(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
21 November 2002 (21.11.2002)

PCT

(10) International Publication Number
WO 02/092000 A2

(51) International Patent Classification[7]: A61K

(21) International Application Number: PCT/US02/14877

(22) International Filing Date: 13 May 2002 (13.05.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/290,071	11 May 2001 (11.05.2001)	US
60/291,311	17 May 2001 (17.05.2001)	US
60/353,058	1 February 2002 (01.02.2002)	US
60/361,293	4 March 2002 (04.03.2002)	US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

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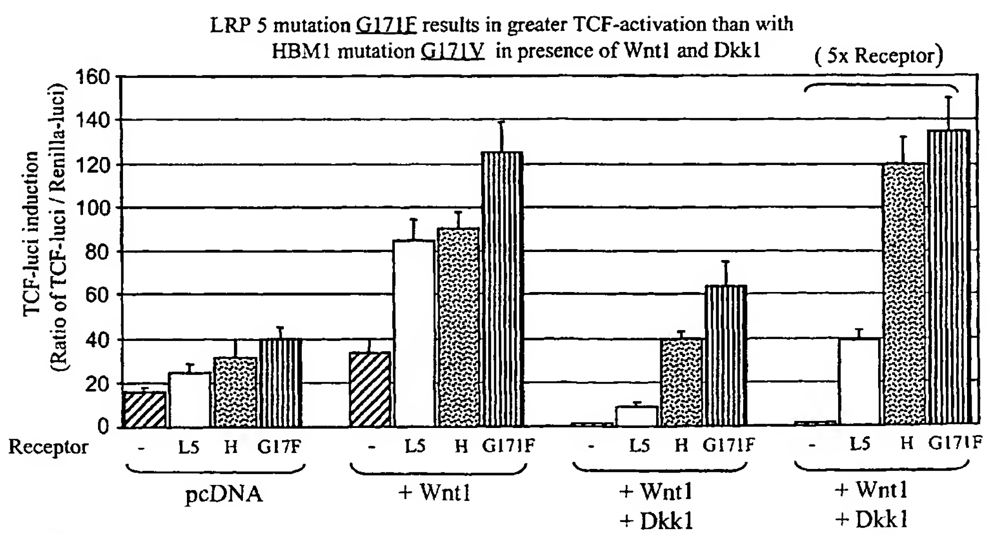
(54) Title: HBM VARIANTS THAT MODULATE BONE MASS AND LIPID LEVELS



• G171F mutation involves the ringed R group (F) alteration and leads to marginally greater TCF-luci activation than that with HBM1 mutation G171V.

(57) Abstract: ABSTRACT The present invention relates to methods and materials used to express an HBM-like polypeptide derived from HBM, LRP5 or LRP6 in animal cells and transgenic animals. The present invention also relates to transgenic animals expressing the HBM-like polypeptides. The invention provides nucleic acids, including coding sequences, oligonucleotide primers and probes, proteins, cloning vectors, expression vectors, transformed hosts, methods of developing pharmaceutical compositions, methods of identifying molecules involved in bone development, and methods of diagnosing and treating diseases involved in bone development and lipid modulation. In preferred embodiments, the present invention is directed to methods for treating, diagnosing and preventing osteoporosis.

WO 02/092000 A2

(84) **Designated States** *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*
— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

HBM VARIANTS THAT MODULATE BONE MASS AND LIPID LEVELS

FIELD OF THE INVENTION

The present invention relates generally to the field of genetics, genomics and molecular biology. The invention relates to methods and materials used to isolate, detect and sequence a high bone mass gene and corresponding wild-type gene, and mutants thereof. The present invention also relates to the high bone mass (HBM) gene, the corresponding wild-type gene, and mutants thereof. The genes identified in the present invention are implicated in the ontology and physiology of bone development. The invention also provides nucleic acids, proteins, cloning vectors, expression vectors, transformed hosts, methods of developing pharmaceutical compositions, methods of identifying molecules involved in bone development, and methods of diagnosing and treating diseases involved in bone development and lipid levels. The invention further relates to transgenic animals for studying the HBM phenotype and related variant phenotypes, the mechanism of action of the *HBM* gene and its variants, and factors and treatments affecting normal and abnormal bone conditions. In preferred embodiments, the present invention is directed to methods for treating, diagnosing, preventing and screening for normal and abnormal conditions of bone, including metabolic bone diseases such as osteoporosis.

BACKGROUND OF THE INVENTION

Two of the most common types of osteoporosis are postmenopausal and senile osteoporosis. Osteoporosis affects men as well as women, and, taken with other abnormalities of bone, presents an ever-increasing health risk for an aging population. The most common type of osteoporosis is that associated with menopause. Most women lose between 20-60% of the bone mass in the trabecular compartment of the bone within 3-6 years after the cessation of menses. This rapid loss is generally associated with an increase of bone resorption and formation. However, the resorptive cycle is more dominant and the result is a net loss of bone mass. Osteoporosis is a common and serious disease among postmenopausal women. There are an estimated 25 million women in the United States alone who are afflicted with this disease. The results of osteoporosis are both personally harmful, and also

account for a large economic loss due to its chronicity and the need for extensive and long-term support (hospitalization and nursing home care) from the disease sequelae. This is especially true in more elderly patients. Additionally, while osteoporosis is generally not thought of as a life-threatening condition, a 20-30% mortality rate is related to hip fractures in elderly women. A large percentage of this mortality rate can be directly associated with postmenopausal osteoporosis. The costs alone associated with the treatment of osteoporotic fractures in the United States is $10 to $15 billion annually. Worldwide incidence of osteoporotic hip fractures is estimated to exceed 1.7 million cases.

The most vulnerable tissue in the bone to the effects of postmenopausal osteoporosis is the trabecular bone. This tissue is often referred to as spongy bone and is particularly concentrated near the ends of the bone near the joints and in the vertebrae of the spine. The trabecular tissue is characterized by small structures which inter-connect with each other as well as the more solid and dense cortical tissue which makes up the outer surface and central shaft of the bone. This crisscross network of trabeculae gives lateral support to the outer cortical structure and is critical to the biomechanical strength of the overall structure. In postmenopausal osteoporosis, it is primarily the net resorption and loss of the trabeculae which lead to the failure and fracture of the bone. In light of the loss of the trabeculae in postmenopausal women, it is not surprising that the most common fractures are those associated with bones which are highly dependent on trabecular support, e.g., the vertebrae, the neck of the femur, and the forearm. Indeed, hip fracture, Colle's fractures, and vertebral crush fractures are indicative of postmenopausal osteoporosis.

One of the earliest generally accepted methods for treatment of postmenopausal osteoporosis was estrogen replacement therapy. Although this therapy frequently is successful, patient compliance is low, primarily due to the undesirable side-effects of chronic estrogen treatment. Frequently cited side-effects of estrogen replacement therapy include reinitiation of menses, bloating, depression, and fear of breast or uterine cancer. In order to limit the known threat of uterine cancer in those women who have not undergone a hysterectomy, a protocol of estrogen and progestin cyclic therapy is often employed. This protocol is similar to that which is used in birth control regimens, and often is not tolerated by women because of the side-effects characteristic of progestin. More recently, certain

antiestrogens, originally developed for the treatment of breast cancer, have been shown in experimental models of postmenopausal osteoporosis to be efficacious. Among these agents is raloxifene (See, U.S. Patent No. 5,393,763, and Black et al, *J. Clin. Invest.,* 93:63-69 (1994)). In addition, tamoxifene, a widely used clinical agent for the treatment of breast cancer, has been shown to increase bone mineral density in post menopausal women suffering from breast cancer (Love et al, *N. Engl. J. Med.*, 326:852-856 (1992)).

Another therapy for the treatment of postmenopausal osteoporosis is the use of calcitonin. Calcitonin is a naturally occurring peptide which inhibits bone resorption and has been approved for this use in many countries (Overgaard et al, *Br. Med. J.*, 305:556-561 (1992)). The use of calcitonin has been somewhat limited, however. Its effects are very modest in increasing bone mineral density and the treatment is very expensive. Another therapy for the treatment of postmenopausal osteoporosis is the use of bis-phosphonates. These compounds were originally developed for use in Paget's disease and malignant hypercalcemia. They have been shown to inhibit bone resorption. Alendronate, one compound of this class, has been approved for the treatment of postmenopausal osteoporosis. These agents may be helpful in the treatment of osteoporosis, but these agents also have potential liabilities which include osteomalacia, extremely long half-life in bone (greater than 2 years), and possible "frozen bone syndrome," e.g., the cessation of normal bone remodeling.

Senile osteoporosis is similar to postmenopausal osteoporosis in that it is marked by the loss of bone mineral density and resulting increase in fracture rate, morbidity, and associated mortality. Generally, it occurs in later life, i.e., after 70 years of age. Historically, senile osteoporosis has been more common in females, but with the advent of a more elderly male population, this disease is becoming a major factor in the health of both sexes. It is not clear what, if any, role hormones such as testosterone or estrogen have in this disease, and its etiology remains obscure. Treatment of this disease has not been very satisfactory. Hormone therapy, estrogen in women and testosterone in men, has shown equivocal results; calcitonin and bis-phosphonates may be of some utility.

The peak mass of the skeleton at maturity is largely under genetic control. Twin studies have shown that the variance in bone mass between adult monozygotic twins is

smaller than between dizygotic twins (Slemenda et al, *J. Bone Miner. Res.*, 6:561-567 (1991); Young et al, *J. Bone Miner. Res.*, 6:561-567 (1995); Pocock et al, *J. Clin. Invest.*, 80:706-710 (1987); Kelly et al, *J. Bone Miner. Res.*, 8:11-17 (1993)), and it has been estimated that up to 60% or more of the variance in skeletal mass is inherited (Krall et al, *J. Bone Miner. Res.*, 10:S367 (1993)). Peak skeletal mass is the most powerful determinant of bone mass in elderly years (Hui et al, *Ann. Int. Med.*, 111:355-361 (1989)), even though the rate of age-related bone loss in adult and later life is also a strong determinant (Hui et al, *Osteoporosis Int.*, 1:30-34 (1995)). Since bone mass is the principal measurable determinant of fracture risk, the inherited peak skeletal mass achieved at maturity is an important determinant of an individual's risk of fracture later in life. Thus, study of the genetic basis of bone mass is of considerable interest in the etiology of fractures due to osteoporosis.

Recently, a strong interest in the genetic control of peak bone mass has developed in the field of osteoporosis. The interest has focused mainly on candidate genes with suitable polymorphisms to test for association with variation in bone mass within the normal range, or has focused on examination of genes and gene loci associated with low bone mass in the range found in patients with osteoporosis. The vitamin D receptor locus (VDR) (Morrison et al, *Nature*, 367:284-287 (1994)), PTH gene (Howard et al, *J. Clin. Endocrinol. Metab.*, 80:2800-2805 (1995); Johnson et al, *J. Bone Miner. Res.*, 8:11-17 (1995); Gong et al, *J. Bone Miner. Res.*, 10:S462 (1995)) and the estrogen receptor gene (Hosoi et al, *J. Bone Miner. Res.*, 10:S170 (1995); Morrison et al, *Nature*, 367:284-287 (1994)) have figured most prominently in this work. These studies are difficult because bone mass (the phenotype) is a continuous, quantitative, polygenic trait, and is confounded by environmental factors such as nutrition, co-morbid disease, age, physical activity, and other factors. Also, this type of study design requires large numbers of subjects. In particular, the results of VDR studies to date have been confusing and contradictory (Garnero et al, *J. Bone Miner. Res.*, 10:1283-1288 (1995); Eisman et al, *J. Bone. Miner. Res.*, 10:1289-1293 (1995); Peacock, *J. Bone Miner. Res.*, 10:1294-1297 (1995)). Furthermore, the work thus far has not shed much light on the mechanism(s) whereby the genetic influences might exert their effect on bone mass.

While it is well known that peak bone mass is largely determined by genetic rather than environmental factors, studies to determine the gene loci (and ultimately the genes)

linked to variation in bone mass are difficult and expensive. Study designs which utilize the power of linkage analysis, e.g., sib-pair or extended family, are generally more informative than simple association studies, although the latter do have value. However, genetic linkage studies involving bone mass are hampered by two major problems. The first problem is the phenotype, as discussed briefly above. Bone mass is a continuous, quantitative trait, and establishing a discrete phenotype is difficult. Each anatomical site for measurement may be influenced by several genes, many of which may be different from site to site. The second problem is the age component of the phenotype. By the time an individual can be identified as having low bone mass, there is a high probability that their parents or other members of prior generations will be deceased and therefore unavailable for study, and younger generations may not have even reached peak bone mass, making their phenotyping uncertain for genetic analysis.

Regardless, linkage analysis can be used to find the location of a gene causing a hereditary "disorder" and does not require any knowledge of the biochemical nature of the disorder, i.e., a mutated protein that is believed to cause the disorder does not need to be known. Traditional approaches depend on assumptions concerning the disease process that might implicate a known protein as a candidate to be evaluated. The genetic localization approach using linkage analysis can be used to first find the general chromosomal region in which the defective gene is located and then to gradually reduce the size of the region in order to determine the location of the specific mutated gene as precisely as possible. After the gene itself is discovered within the candidate region, the messenger RNA and the protein are identified and, along with the DNA, are checked for mutations.

The genetic localization approach has practical implications since the location of the disease can be used for prenatal diagnosis even before the altered gene that causes the disease is found. Linkage analysis can enable families, even many of those that do not have a sick child, to know whether they are carriers of a disease gene and to evaluate the condition of an unborn child through molecular diagnosis. The transmission of a disease within families, then, can be used to find the defective gene. As used herein, reference to "high bone mass" (HBM) is analogous to reference to a disease state, although from a practical standpoint high bone mass can actually help a subject avoid the disease known as osteoporosis.

Linkage analysis is possible because of the nature of inheritance of chromosomes from parents to offspring. During meiosis, the two parental homologues pair to guide their proper separation to daughter cells. While they are lined up and paired, the two homologues exchange pieces of the chromosomes, in an event called "crossing over" or "recombination." The resulting chromosomes are chimeric, that is, they contain parts that originate from both parental homologues. The closer together two sequences are on the chromosome, the less likely that a recombination event will occur between them, and the more closely linked they are. In a linkage analysis experiment, two positions on the chromosomes are followed from one generation to the next to determine the frequency of recombination between them. In a study of an inherited disease, one of the chromosomal positions is marked by the disease gene or its normal counterpart, i.e., the inheritance of the chromosomal region can be determined by examining whether the individual displays symptoms of the disorder or not. The other position is marked by a DNA sequence that shows natural variation in the population such that the two homologues can be distinguished based on the copy of the "marker" sequence that they possess. In every family, the inheritance of the genetic marker sequence is compared to the inheritance of the disease state. If, within a family carrying an autosomal dominant disorder such as high bone mass, every affected individual carries the same form of the marker and all the unaffected individuals carry at least one different form of the marker, there is a great probability that the disease gene and the marker are located close to each other. In this way, chromosomes may be systematically checked with known markers and compared to the disease state. The data obtained from the different families is combined, and analyzed together by a computer using statistical methods. The result is information indicating the probability of linkage between the genetic marker and the disease allowing different distances between them. A positive result can mean that the disease is very close to the marker, while a negative result indicates that it is far away on that chromosome, or on an entirely different chromosome.

Linkage analysis is performed by typing all members of the affected family at a given marker locus and evaluating the co-inheritance of a particular disease state with the marker probe, thereby determining how often the two of them are co-inherited. The recombination frequency can be used as a measure of the genetic distance between two gene loci. A

recombination frequency of 1% is equivalent to 1 map unit, or 1 centiMorgan (cM), which is roughly equivalent to 1,000 kb of DNA. This relationship holds up to frequencies of about 20% or 20 cM.

The entire human genome is 3,300 cM long. In order to find an unknown disease gene within 5-10 cM of a marker locus, the whole human genome can be searched with roughly 330 informative marker loci spaced at approximately 10 cM intervals (Botstein *et al.*, *Am. J. Hum. Genet.*, 32:314-331 (1980)). The reliability of linkage results is established by using a number of statistical methods. The method most commonly used for the analysis of linkage in humans is the LOD score method (Morton, *Prog. Clin. Biol. Res.*, 147:245-265 (1984), Morton *et al.*, *Am. J. Hum. Genet.*, 38:868-883 (1986)) which was incorporated into the computer program, LIPED, by Ott, *Am. J. Hum. Genet.*, 28:528-529 (1976). LOD scores are the logarithm of the ratio of the likelihood that two loci are linked at a given distance to that they are not linked (>50 cM apart). The advantage of using logarithmic values is that they can be summed among families with the same disease. This becomes necessary given the relatively small size of human families.

By convention, a total LOD score greater than + 3.0 (that is, odds of linkage at the specified recombination frequency being 1000 times greater than odds of no linkage) is considered to be significant evidence for linkage at that particular recombination frequency. A total LOD score of less than - 2.0 (that is, odds of no linkage being 100 times greater than odds of linkage at the specified frequency) is considered to be strong evidence that the two loci under consideration are not linked at that particular recombination frequency. Until recently, most linkage analyses have been performed on the basis of two-point data, which is the relationship between the disorder under consideration and a particular genetic marker. However, as a result of the rapid advances in mapping the human genome over the last few years, and concomitant improvements in computer methodology, it has become feasible to carry out linkage analyses using multi-point data. Multi-point analysis provide a simultaneous analysis of linkage between the disease and several linked genetic markers, when the recombination distance among the markers is known.

Multi-point analysis is advantageous for two reasons. First, the informativeness of the pedigree is usually increased. Each pedigree has a certain amount of potential information,

dependent on the number of parents heterozygous for the marker loci and the number of affected individuals in the family. However, few markers are sufficiently polymorphic as to be informative in all those individuals. If multiple markers are considered simultaneously, then the probability of an individual being heterozygous for at least one of the markers is greatly increased. Second, an indication of the position of the disease gene among the markers may be determined. This allows identification of flanking markers, and thus eventually allows isolation of a small region in which the disease gene resides. Lathrop *et al., Proc. Natl. Acad. Sci. USA*, 81:3443-3446 (1984) have written the most widely used computer package, LINKAGE, for multi-point analysis.

There is a need in the art for identifying the gene associated with a high bone mass phenotype. There is also a need for tools for the study of the high bone mass gene and phenotype. More generally there is need for the development of diagnostic tools and treatments. The present invention is directed to these, as well as other, important ends.

SUMMARY OF THE INVENTION

It is an object of the invention to provide a nucleic acid comprising a mutation in LRP5 or LRP6 which results in a HBM phenotype when expressed in a cell, wherein said HBM phenotype results in bone mass modulation and/or lipid level modulation. Another embodiment contemplates that the mutation is located in propeller 1. In another embodiment, the nculeic acid encodes a mutation comprising at least one mutation of Tables 2 or 3 or which results in a mutation of one of the following G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V when expressed in a cell, and wherein expression of the nucleic acid in a subject results in bone mass modulation and/or lipid level modulation. In the instance of LRP6, the mutation is located in a position equivalent to LRP5 such that expression of the nucleic acid in a subject results in bone mass modulation and/or lipid level modulation. In another embodiment, the preferred mutation of LRP5 is G171V, A214V, A65V, M282V, G171K, G171F, G171I or G171Q or in an equivalent location if dealing with LRP6.

Another embodiment contemplated herein is a polypeptide encoded by any of the above nucleic acids, wherein said polypeptide when expressed in a cell modulates Wnt

signaling, LRP5 activity and/or LRP6 activity. The polypeptide can additionally or alternatively modulate bone mass and/or lipid levels when expressed in a subject. These polypeptides or biologically active fragments thereof may preferably contain any of the following mutations of Table 2, G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V in LRP5 or in a equivalent location in LRP6. The most preferred mutations are G171V, A214V, A65V, M282V, G171K, G171F, G171I or G171Q in LRP5 or an equivalent location in LRP6.

Yet another embodiment contemplates antibodies an immunogenic fragments thereof which bind to these proteins. The contemplated antibodies include a monoclonal antibody, a chimeric antibody, a bispecific antibody, a humanized antibody, a primatized® antibody, a human antibody, or a labeled antibody. Preferably, some of the antibodies can discriminate between the wild type and variant forms of LRP5 and LRP6.

Another embodiment contemplates antibodies which bind to polypeptides comprising: ^{208}KLYWADAKLSFIHRAN^{223}, ^{277}ALYSPMDIQVLSQER^{291}, ^{61}GLEDAAAVDFQFSKGA^{73}, ^{234}EGSLTHPFALTLSG^{247}, ^{249}TLYWTDWQTRSIHACN^{264}, ^{144}VLFWQDLDQPRAI^{156}, ^{194}IYWPNGLTIDLEEQKLY^{210}, ^{34}LLLFANRRDVRLVD^{47}, ^{75}GAVYWTDVSEEAIKQ^{89}, ^{121}KLYWTDSETNRIEVA^{135} of LRP5 or an equivalent domain on LRP6 or variants thereof.

The above antibodies can also be used in a composition for modulating bone mass and/or lipid levels in a subject comprising a therapeutically effective amount of the antibody or immunogenic fragment and a pharmaceutically acceptable carrier.

The invention further contemplates a method of diagnosing a HBM like phenotype in a subject comprising: (A) obtaining a biological sample from said subject; (B) exposing the sample to one of the described antibodies or immunogenic fragments; and (C) detecting whether the antibody bound a protein from the biological sample from said subject to determine whether the subject has a HBM-like phenotype.

Another embodiment contemplates a transgenic animal having somatic and/or germ cells comprising a nucleic acid which comprises a promoter region that directs protein expression in animal and/or human cells operably linked to any of the herein described nucleic acids, and wherein said transgenic animal has at least three bone parameters

modulated by the expression of said nucleic acid. The promoter region can be selected from the group consisting of CMV, RSV, SV40, and EF-1a, CMVβbActin, histone, type I collagen, TGFβ1, SX2, cfos/cjun, Cbfa1, Fra/Jun, Dlx5, osteocalcin, osteopontin, bone sialoprotein, and collagenase promoter regions.

A further embodiment of the invention contemplates an animal model for the study of bone density modulation and/or lipid level modulation comprising a first group of animals composed of any of the described transgenic animals and a second group of control animals.

Another embodiment provides for a method of identifying agents which modulate the activity of an HBM-like nucleic acid comprising: (A) transfecting a cell with a vector of claim 11; (B) exposing the transfected cell of step (A) to a compound; and (C) determining whether the compound modulates the activity of the HBM-like nucleic acid. Such agents can include a hormone, a growth factor, a peptide, RNA, siRNA, DNA, a mineral, a vitamin, a natural product, or a synthetic organic compound.

Another aspect of the invention provides for a method for identifying compounds which modulate the interaction of Dkk with the Wnt signaling pathway comprising: (A) transfecting cells with constructs containing any of the described nucleic acids; (B) assessing changes in expression of a reporter element linked to a Wnt-responsive promoter; and (C) identifying as a Dkk/Wnt interaction modulating compound any compound which alters reporter gene expression compared with cells transfected with a Dkk construct alone. The cells are preferably cancer cells, liver cells or bone cells. The reporter element used is TCF-luciferase, tk-Renilla, or a combination thereof.

Yet another embodiment includes a method of diagnosing a subject as expressing a nucleic acid comprising a nucleotide change of Tables 2 or 3 or any other mutations, the method comprising the steps of: (A) obtaining a biological sample from the subject; and (B) assaying for the presence of the nucleotide change which results in HBM phenotype.

The invention also provides agents identified by the above methods which regulate Wnt activity, Dkk activity, bone mass and/or lipid levels.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 shows the pedigree of the individuals used in the genetic linkage studies.

Under each individual is an ID number, the z-score for spinal BMD, and the allele calls for the critical markers on chromosome 11. Solid symbols represent "affected" individuals. Symbols containing "N" are "unaffected" individuals. DNA from 37 individuals was genotyped. Question marks denote unknown genotypes or individuals who were not genotyped.

Fig. 2 depicts the BAC/STS content physical map of the HBM region in 11q13.3. STS markers derived from genes, ESTs, microsatellites, random sequences, and BAC end sequences are denoted above the long horizontal line. For markers that are present in GDB the same nomenclature has been used. Locus names (D11S####) are listed in parentheses after the primary name if available. STSs derived from BAC end sequences are listed with the BAC name first followed by L or R for the left and right end of the clone, respectively. The two large arrows indicate the genetic markers that define the HBM critical region. The horizontal lines below the STSs indicate BAC clones identified by PCR-based screening of a nine-fold coverage BAC library. Open circles indicate that the marker did not amplify the corresponding BAC library address during library screening. Clone names use the following convention: B for BAC, the plate, row and column address, followed by -H indicating the HBM project (i.e., B36F16-H).

Figs. 3A-3F show the genomic structure of Zmax1 (LRP5) with flanking intron sequences. Translation is initiated by the underlined "ATG" in exon 1. The site of the polymorphism in the *HBM* gene is in exon 3 and is represented by the underlined "G," whereby this nucleotide is a "T" in the *HBM* gene. The 3' untranslated region of the mRNA is underlined within exon 23 (exon 1, SEQ ID NO:40; exon 2, SEQ ID NO:41; exon 3, SEQ ID NO:42; exon 4, SEQ ID NO:43; exon 5, SEQ ID NO:44; exon 6, SEQ ID NO:45; exon 7, SEQ ID NO:46; exon 8, SEQ ID NO:47; exon 9, SEQ ID NO:48; exon 10, SEQ ID NO:49; exon 11, SEQ ID NO:50; exon 12, SEQ ID NO:51; exon 13, SEQ ID NO:52; exon 14, SEQ ID NO:53; exon 15, SEQ ID NO:54; exon 16, SEQ ID NO:55; exon 17, SEQ ID NO:56; exon 18, SEQ ID NO:57; exon 19, SEQ ID NO:58; exon 20, SEQ ID NO:59; exon 21, SEQ ID NO:60; exon 22, SEQ ID NO:61; and exon 23; SEQ ID NO:62).

Fig. 4 shows the domain organization of Zmax1 (LRP5), including the YWTD spacers, the extracellular attachment site, the binding site for LDL and calcium, the cysteine-

rich growth factor repeats, the transmembrane region, the ideal PEST region with the CK-II phosphorylation site and the internalization domain. Fig. 4 also shows the site of the glycine to valine change that occurs in the HBM protein. The signal peptide is located at amino acids 1-31, the extracellular domain is located at amino acids 32-1385, the transmembrane segment is located at amino acids 1386-1413, and the cytoplasmic domain is located at amino acids 1414-1615.

Fig. 5 is a schematic illustration of the BAC contigs B527D12 and B200E21 in relation to the *HBM* gene.

Figs. 6A-6J are the nucleotide (SEQ ID NO:1) and amino acid (SEQ ID NO:3) sequences of the wild-type gene, *Zmax1* (*LRP5*). The location for the base pair substitution at nucleotide 582, a guanine to thymine, (SEQ ID NO: 2 and 4) is underlined. This allelic variant is the *HBM* gene. The *HBM* gene encodes for a protein with an amino acid substitution of glycine to valine at position 171. The 5' untranslated region (UTR) boundaries bases 1 to 70, and the 3' UTR boundaries bases 4916-5120.

Figs. 7A and **7B** are northern blot analyses showing the expression of Zmax1 (LRP5) in various tissues.

Fig. 8 is a PCR product analysis.

Fig. 9 is allele specific oligonucleotide detection of the Zmax1 (LRP5) exon 3 mutation.

Fig. 10 is the cellular localization of mouse Zmax1 (LRP5) by *in situ* hybridization at 100X magnification using sense and antisense probes.

Fig. 11 is the cellular localization of mouse Zmax1 (LRP5) by *in situ* hybridization at 400X magnification using sense and antisense probes.

Fig. 12 is the cellular localization of mouse Zmax1 (LRP5) by *in situ* hybridization of osteoblasts in the endosteum at 400X magnification using sense and antisense probes.

Fig. 13 shows antisense inhibition of Zmax1 (LRP5) expression in MC-3T3 cells.

Fig. 14 shows a Zmax1 (LRP5) exon 3 allele specific oligonucleotide (ASO) assay which illustrates the rarity of the HBM allele (right panels; T-specific oligo; 58°C Wash) as compared to the wild-type Zmax1 (LRP5) allele (left panels, G-specific oligo; 55°C Wash). The positive spots appearing in the right panels were positive controls.

Fig. 15 depicts a model representing the potential role of Zmax1 (LRP5) in focal adhesion signaling.

Fig. 16 depicts a schematic of two *Zmax1* (LRP5) gene targeting vectors for the knock-out of endogenous mouse Zmax or conditional knock-in of the HBM polymorphism. B, X, and R indicate *BamHI*, *XbaI*, and *EcoRI* sites in DNA BAC 4735P5 respectively. Exons 3, 4, and 5 are indicated by black rectangles. A G -> T base change is engineered at base 24 of exon 3 to produce the HBM polymorphism. The location of a LoxP flanked cassette containing a neomycin resistance gene and a synthetic pause sequence and probes used for screening and characterizing of ES cell clones are also indicated.

Fig. 17 confirms expression by the transgenic (*i.e.*, HBMMCBA and HBMMTIC) and wild-type (*i.e.*, ZmaxWTCBA and ZmaxWTTIC) plasmid constructs. These constructs were transiently transfected into HOB-02-02 cells and the mRNA levels determined using TaqMan® quantitative PCR. HBMMCBA and ZmaxWTCBA are shown in the left column (*i.e.* CMVβActin) and HBMMTIC and ZmaxWTTIC are shown in the right column (*i.e.* Type I collagen) of the Table.

Fig. 18 depicts a comparison between the human and mouse TaqMan® Primer/Probe sets. HOB (HOB-03-C5) and mouse (MC-3T3-E1) osteoblastic cell mRNA was analyzed using the probes and primers.

Fig. 19 depicts the quantification of human Zmax1 (LRP5) mRNA expressed in a mixed human and mouse RNA background using the TaqMan® Primer/Probe sets. Results are presented in Human Zmax1 (LRP5) mRNA added (ng) versus Human Zmax1 (LRP5) mRNA measured (ng).

Fig. 20 depicts expression of HBM in transgenic mice based on mRNA expression analyzed by TaqMan®.

Fig. 21A-F Panels A-C depict the analysis of various transgenic mouse lines which express the HBMMCBA construct in spine (Fig. 21A), femur (Fig. 21B) and total body (Fig. 21C). Panels D-F depict the analysis of various transgenic mouse lines which express the HBMMTIC construct in spine (Fig. 21D), femur (Fig. 21E) and total body (Fig. 21F).

Fig. 22 depicts changes in BMD in HBM transgenic mice (*i.e.*, HBMMCBA and HBMMTIC constructs) at 5 weeks using *in vivo* pDXA* analysis. The BMD changes are

presented as compared to wild-type animals which were also only 5 weeks old.

Fig. 23 depicts changes in BMD in HBM transgenic mice (*i.e.*, HBMMCBA and HBMMTIC constructs) at 9 weeks using *in vivo* pDXA* analysis. The BMD changes are presented as compared to wild-type animals which were also only 9 weeks old.

Fig. 24 (A-D) presents the sequence of the insert of the gene, HBMGI_2AS, subcloned into the vector (SEQ ID NO:759).

Fig. 25 (A-D) presents the sequence of the insert of the gene, ZMAXGI_3AS, subcloned into the vector (SEQ ID NO:760).

Fig. 26 (A-C) presents an alignment of human (SEQ ID NO:761) and mouse (SEQ ID NO:762) Zmax1 (LRP5) amino acid sequences.

Fig. 27 (A-C) presents an alignment of human LRP5 (Zmax1) (SEQ ID NO:763) and LRP6 (SEQ ID NO:764) amino acid sequences.

Fig. 28 shows a schematic of the components of the Wnt signal transduction pathway. Schematic obtained from: http://www.stanford.edu/~rnusse/pathways/cell2.html.

Fig. 29 shows that the mutation G171F in LRP5 produces a greater activation of the Wnt pathway than LRP5 which is consistent with HBM activity.

Fig. 30 shows that the mutation M282V in LRP5 produces an activation of the Wnt pathway which is consistent with HBM activity in U2OS cells.

Fig. 31 shows a table of proteins identified in a Y2H screen using a Dkk-1 bait sequence. These proteins are identified by both their nucleic acid and amino acid accession numbers.

Fig. 32 shows the differential binding of an antibody generated to a sequence (a.a. 165-177) containing the HBM mutation in LRP5 in LRP5 and HBM virus-infected cells.

Fig. 33 shows a diagram of the *Xenopus* Embryo Assay for Wnt activity.

Fig. 34 shows the effects of Zmax/LRP5 and HBM on Wnt signaling in the *Xenopus* embryo assay.

Fig. 35 shows the effects of Zmax/LRP5 and HBM on induction of secondary axis formation in the *Xenopus* embryo assay.

Fig. 36 shows the effects of human Dkk-1 on the repression of the canonical Wnt pathway.

Fig. 37 shows the effects of human Dkk-1 on Zmax/LRP5 and HBM-mediated Wnt signaling.

Fig. 38 shows a table of peptide aptamer insert sequences identified in a Y2H screen using a LRP5 ligand binding domain bait sequence.

Fig. 39 shows pcDNA3.1 construct names with nucleotide sequences for LRP5-binding peptide aptamers, Dkk-1 peptides and control constructs.

Fig. 40 shows the results of a minimum interaction domain mapping screen of Dkk-1 with LRP5. At the top, a map of Dkk-1 showing the location of the signal sequence, and cysteine rich domains 1 and 2. Below, the extent of domains examined using LRP5 LBD baits, LBD1 and LBD4. To the right, scoring of the binding results observed in the experiment.

Fig. 41 shows the effects of Dkk-1 and Dkk-2 on Wnt1 signaling with coreceptors LRP5, HBM, and LRP6 in HOB03CE6 cells.

Fig. 42 shows the effects of Dkk-1 and Dkk-2 on Wnt3a signaling with coreceptors LRP5, HBM, and LRP6 in HOB03CE6 cells.

Fig. 43 demonstrates that the LRP5-LBD peptide aptamer 262 activates Wnt signaling in the presence of Wnt3a in U2OS cells.

Fig. 44 shows the amino acid sequences for the corresponding LRP5-binding peptides, Dkk-1 peptide aptamers and control constructs in Figure 39.

Fig. 45 shows that Dkk-1 represses Wnt3a-mediated Wnt signaling in U2OS bone cells using the cell-based reporter gene assay for high throughput screening.

Fig. 46 demonstrates that Wnt1-HBM generated signaling is not efficiently inhibited by Dkk-1 in U2OS bone cells while LRP5 and LRP6-mediated signaling are using the cell-based reporter gene assay for high throughput screening.

Fig. 47 shows that the TCF signal in the cell-based reporter gene assay for high throughput screening can be modulated by Dkk-1 and Dkk-1-AP without Wnt DNA transfection.

Fig. 48 shows the morphological results in the Xenopus assay using aptamers 261 and 262 from the LRP5-LBD to activate Wnt signaling.

Fig. 49 demonstrates that LRP5-LBD aptamers 261 and 262 induce Wnt signaling

over other LRP5 aptamers.

Fig. 50 depicts the LRP5 domain structure. The symbols are defined at the upper right. The structural domains are numbered successively from top to bottom corresponding to the N-terminal to C-terminal ends of the protein as Propeller 1, EGF-like Domain 1, Propeller 2, EGF-like Domain 2, and so forth. The structure was determined using the motifs and nomenclature described in Springer *et al.*, 1998 *J. Mol. Biol.* 283: 837-62.

Fig. 51 CLUSTALW (1.8) multiple sequence alignment of the β-propeller segments of LRP5 from human (af077820h) and mouse (af064984m and af077847m), LRP6 from human (af074264h) and mouse (af074265m), and the sequences from proteins with modeled 6-bladed β-propellers: chicken LRP1(**1lpx**) and human nidogen (**1ndx**). For the LPRs, the final suffix letter designates which of the four propeller domains the sequence comes from (a => prop. #1, b => prop. #2, etc.). The final four lines give the secondary structure assignments predicted by DSC for all sequences given in this alignment (H = helix, E = strand and C = coil) and the weights assigned to each structural type at each position on a scale of 0 (least probable) to 9 (most probable). Sequences corresponding to Springer's models' strand positions are underlined and color-coded according to which of the six blades they belong to. In the propeller geometry, alternate loops fall on opposite faces of the disc-shaped domain. The loops on the "top" face (*i.e.*, opposite the points of entry and exit of the chain from the structure) are colored red. The position of the G171V mutation is marked with "*".

Fig. 52 displays the functional effect of mutations on side chain interactions in HBM protein as compared the wild-type Zmax1 (LRP5) protein. It also shows the side chain interactions of G171F, an HBM like variant.

Fig. 53 displays the structural change due to the OPPG mutation versus the wild-type, Zmax1 (LRP5). Panel A depicts the homology model of LRP5's second propeller domain; Panel B depicts the third propeller domain and Panel C depicts the second propeller domain with two mutations.

DETAILED DESCRIPTION OF THE INVENTION

1. **Definitions**

To aid in the understanding of the specification and claims, the following definitions are provided.

"Gene" refers to a DNA sequence that encodes through its template or messenger RNA a sequence of amino acids characteristic of a specific peptide. The term "gene" includes intervening, non-coding regions, as well as regulatory regions, and can include 5' and 3' ends.

By "nucleic acid" is meant to include single stranded and double stranded nucleic acids including, but not limited to DNAs, RNAs (e.g., mRNA, tRNAs, siRNAs), cDNAs, recombinant DNA (rDNA), rRNAs, antisense nucleic acids, oligonucleotides, and oligomers, and polynucleotides. The term may also include hybrids such as triple stranded regions of RNA and/or DNA or double stranded RNA:DNA hybrids. The term also is contemplated to include modified nucleic acids such as, but not limited to biotinylated nucleic acids, tritylated nucleic acids, fluorophor labeled nucleic acids, inosine, and the like.

"Gene sequence" refers to a nucleic acid molecule, including DNA which contains a non-transcribed or non-translated sequence, which comprises a gene. The term is also intended to include any combination of gene(s), gene fragment(s), non-transcribed sequence(s) or non-translated sequence(s) which are present on the same DNA molecule.

The nucleic acid sequences of the present invention may be derived from a variety of sources including DNA, cDNA, synthetic DNA, synthetic RNA or combinations thereof. Such sequences may comprise genomic DNA which may or may not include naturally occurring introns. Moreover, such genomic DNA may be obtained in association with promoter regions and/or poly (A) sequences. The sequences, genomic DNA or cDNA may be obtained in any of several ways. Genomic DNA can be extracted and purified from suitable cells by means well known in the art. Alternatively, mRNA can be isolated from a cell and used to produce cDNA by reverse transcription or other means.

"cDNA" refers to complementary or copy DNA produced from an RNA template by the action of RNA-dependent DNA polymerase (reverse transcriptase). Thus, a "cDNA clone" means a duplex DNA sequence for which one strand is complementary to an RNA

molecule of interest, carried in a cloning vector or PCR amplified. cDNA can also be single stranded after first strand synthesis by reverse transcriptase. In this form, it is a useful PCR template and does not need to be carried in a cloning vector. This term includes genes from which the intervening sequences have been removed. Thus, the term "gene", as sometimes used generically, can also include nucleic acid molecules comprising cDNA and cDNA clones.

"Recombinant DNA" means a molecule that has been engineered by splicing *in vitro* a cDNA or genomic DNA sequence or altering a sequence by methods such as PCR mutagenesis.

"Cloning" refers to the use of *in vitro* recombination techniques to insert a particular gene or other DNA sequence into a vector molecule. In order to successfully clone a desired gene, it is necessary to use methods for generating DNA fragments, for joining the fragments to vector molecules, for introducing the composite DNA molecule into a host cell in which it can replicate, and for selecting the clone having the target gene from amongst the recipient host cells.

"cDNA library" refers to a collection of recombinant DNA molecules containing cDNA inserts which together comprise the entire or a partial repertoire of genes expressed in a particular tissue or cell source. Such a cDNA library can be prepared by methods known to one skilled in the art and described by, for example, Cowell and Austin, "cDNA Library Protocols," *Methods in Molecular Biology* (1997).

"Cloning vehicle" refers to a plasmid or phage DNA or other DNA sequence which is able to replicate in a host cell. This term can also include artificial chromosomes such as BACs and YACs. The cloning vehicle is characterized by one or more endonuclease recognition sites at which such DNA sequences may be cut in a determinable fashion without loss of an essential biological function of the DNA, which may contain a marker suitable for use in the identification of transformed cells.

"Expression" refers to the process comprising transcription of a gene sequence and subsequent processing steps, such as translation of a resultant mRNA to produce the final end product of a gene. The end product may be a protein (such as an enzyme or receptor) or a nucleic acid (such as a tRNA, antisense RNA, or other regulatory factor). The term

"expression control sequence" refers to a sequence of nucleotides that control or regulate expression of structural genes when operably linked to those genes. These include, for example, the lac systems, the trp system, major operator and promoter regions of the phage lambda, the control region of fd coat protein and other sequences known to control the expression of genes in prokaryotic or eukaryotic cells. Expression control sequences will vary depending on whether the vector is designed to express the operably linked gene in a prokaryotic or eukaryotic host, and may contain transcriptional elements such as enhancer elements, termination sequences, tissue-specificity elements and/or translational initiation and termination sites.

"Expression vehicle" refers to a vehicle or vector similar to a cloning vehicle but which is capable of expressing a gene which has been cloned into it, after transformation into a host. The cloned gene is usually placed under the control of (i.e., operably linked to) an expression control sequence.

"Operator" refers to a DNA sequence capable of interacting with the specific repressor, thereby controlling the transcription of adjacent gene(s).

"Promoter" refers to a DNA sequence that can be recognized by an RNA polymerase. The presence of such a sequence permits the RNA polymerase to bind and initiate transcription of operably linked gene sequences.

"Promoter region" is intended to include the promoter as well as other gene sequences which may be necessary for the initiation of transcription. The presence of a promoter region is sufficient to cause the expression of an operably linked gene sequence. The term "promoter" is sometimes used in the art to generically indicate a promoter region. Many different promoters are known in the art which direct expression of a gene in a certain cell types. Tissue-specific promoters can comprise nucleic acid sequences which cause a greater (or decreased) level of expression in cells of a certain tissue type.

"Operably linked" means that the promoter controls the initiation of expression of the gene. A promoter is operably linked to a sequence of proximal DNA if upon introduction into a host cell the promoter determines the transcription of the proximal DNA sequence(s) into one or more species of RNA. A promoter is operably linked to a DNA sequence if the promoter is capable of initiating transcription of that DNA sequence.

"Prokaryote" refers to all organisms without a true nucleus, including bacteria.

"Eukaryote" refers to organisms and cells that have a true nucleus, including mammalian cells.

"Host" includes prokaryotes and eukaryotes, such as yeast and filamentous fungi, as well as plant and animal cells. The term includes an organism or cell that is the recipient of a replicable expression vehicle.

The term "animal" is used herein to include all vertebrate animals, except humans. It also includes an individual animal in all stages of development, including embryonic and fetal stages. Preferred animals include higher eukaryotes such as avians, rodents (e.g., mice, rabbits, rats, chinchillas, guinea pigs, hamsters and the like), and mammals. Preferred mammals include bovine, equine, feline, canine, ovine, caprine, porcine, buffalo, humans, and primates.

A "transgenic animal" is an animal containing one or more cells bearing genetic information received, directly or indirectly, by deliberate genetic manipulation or by inheritance from a manipulated progenitor at a subcellular level, such as by microinjection or infection with a recombinant viral vector (e.g., adenovirus, retrovirus, herpes virus, adeno-associated virus, lentivirus). This introduced DNA molecule may be integrated within a chromosome, or it may be extra-chromosomally replicating DNA.

"Embryonic stem cells" or "ES cells" as used herein are cells or cell lines usually derived from embryos which are pluripotent meaning that they are un-differentiated cells. These cells are also capable of incorporating exogenous DNA by homologous recombination and subsequently developing into any tissue in the body when incorporated into a host embryo. It is possible to isolate pluripotent cells from sources other than embryonic tissue by methods which are well understood in the art.

Embryonic stem cells in mice have enabled researchers to select for transgenic cells and perform gene targeting. This allows more genetic engineering than is possible with other transgenic techniques. For example, mouse ES cells are relatively easy to grow as colonies *in vitro*. The cells can be transfected by standard procedures and transgenic cells clonally selected by antibiotic resistance. See, for example, Doetschman *et al.*., 1994, *Gene transfer in embryonic stem cells*. In Pinkert (Ed.) Transgenic Animal Technology: A Laboratory

Handbook. Academic Press Inc., New York, pp.115-146. Furthermore, the efficiency of this process is such that sufficient transgenic colonies (hundreds to thousands) can be produced to allow a second selection for homologous recombinants. Mouse ES cells can then be combined with a normal host embryo and, because they retain their potency, can develop into all the tissues in the resulting chimeric animal, including the germ cells. The transgenic modification can then be transmitted to subsequent generations.

Methods for deriving embryonic stem (ES) cell lines *in vitro* from early preimplantation mouse embryos are well known. See for example, Evans *et al.*, 1981 *Nature* 29: 154-6 and Martin, 1981, *Proc. Nat. Acad. Sci. USA*, 78: 7634-8. ES cells can be passaged in an undifferentiated state, provided that a feeder layer of fibroblast cells or a differentiation inhibiting source is present.

The term "somatic cell" indicates any animal or human cell which is not a sperm or egg cell or is capable of becoming a sperm or egg cell. The term "germ cell" or "germ-line cell" refers to any cell which is either a sperm or egg cell or is capable of developing into a sperm or egg cell and can therefore pass its genetic information to offspring. The term "germ cell-line transgenic animal" refers to a transgenic animal in which the genetic information was incorporated in a germ line cell, thereby conferring the ability to transfer the information to offspring. If such offspring in fact possess some or all of that information, then they, too, are transgenic animals.

The genetic alteration of genetic information may be foreign to the species of animal to which the recipient belongs, or foreign only to the particular individual recipient. In the last case, the altered or introduced gene may be expressed differently than the native gene.

"Fragment" of a gene refers to any portion of a gene sequence. A "biologically active fragment" refers to any portion of the gene that retains at least one biological activity of that gene. For example, the fragment can perhaps hybridize to its cognate sequence or is capable of being translated into a polypeptide fragment encoded by the gene from which it is derived.

"Variant" refers to a gene that is substantially similar in structure and biological activity or immunological characteristics to either the entire gene or to a fragment of the gene. Provided that the two genes possess a similar activity, they are considered variant as that term is used herein even if the sequence of encoded amino acid residues is not identical.

Preferentially, as used herein (unless otherwise defined) the variant is one of LRP5, HBM or LRP6. The variant preferably is one that yields an HBM-like phenotype (i.e., enhances bones mass and/or modulates lipid levels). These variants include missense mutations, single nucleotide polymorphisms (SNPs), mutations which result in changes in the amino acid sequence of the protein encoded by the gene or nucleic acid, and combinations thereof, as well as com in the exon domains of the *HBM* gene and mutations in LRP5 or LRP6 which result in an HBM like phenotype.

"Amplification of nucleic acids" refers to methods such as polymerase chain reaction (PCR), ligation amplification (or ligase chain reaction, LCR) and amplification methods based on the use of Q-beta replicase. These methods are well known in the art and described, for example, in U.S. Patent Nos. 4,683,195 and 4,683,202. Reagents and hardware for conducting PCR are commercially available. Primers useful for amplifying sequences from the HBM region are preferably complementary to, and hybridize specifically to sequences in the HBM region or in regions that flank a target region therein. HBM sequences generated by amplification may be sequenced directly. Alternatively, the amplified sequence(s) may be cloned prior to sequence analysis.

"Antibodies" may refer to polyclonal and/or monoclonal antibodies and fragments thereof, and immunologic binding equivalents thereof, that can bind to the HBM proteins and fragments thereof or to nucleic acid sequences from the HBM region, particularly from the HBM locus or a portion thereof. Preferred antibodies also include those capable of binding to LRP5, LRP6 and HBM variants. The term antibody is used both to refer to a homogeneous molecular entity, or a mixture such as a serum product made up of a plurality of different molecular entities. Proteins may be prepared synthetically in a protein synthesizer and coupled to a carrier molecule and injected over several months into rabbits. Rabbit sera is tested for immunoreactivity to the HBM protein or fragment. Monoclonal antibodies may be made by injecting mice with the proteins, or fragments thereof. Monoclonal antibodies will be screened by ELISA and tested for specific immunoreactivity with HBM protein or fragments thereof. Harlow *et al.*, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1988) and *Using Antibodies: A Laboratory Manual*, Harlow, Ed and Lane, David (Cold Spring Harbor Press, 1999). These antibodies will be

useful in assays as well as pharmaceuticals. By "antibody" is meant to include but not limited to polyclonal, monoclonal, chimeric, human, humanized, bispecific, multispecific, primatized™ antibodies.

"HBM protein" refers to a protein that is identical to a Zmax1 (LRP5) protein except that it contains an alteration of glycine 171 to a valine. An HBM protein is defined for any organism that encodes a Zmax1 (LRP5) true homolog. For example, a mouse HBM protein refers to the mouse Zmax1 (LRP5) protein having the glycine 170 to valine substitution.

By "HBM-like" is meant a variant of LRP5, LRP6 or HBM which when expressed in a cell is capable of modulating bone mass, lipid levels, Dkk activity, and/or Wnt activity.

In one embodiment of the present invention, "*HBM* gene" refers to the genomic DNA sequence found in individuals showing the HBM characteristic or phenotype, where the sequence encodes the protein indicated by SEQ ID NO: 4. The *HBM* gene and the *Zmax1* (*LRP5*) gene are allelic. The protein encoded by the *HBM* gene has the property of causing elevated bone mass, while the protein encoded by the *Zmax1* (*LRP5*) gene does not. The *HBM* gene and the *Zmax1* (*LRP5*) gene differ in that the *HBM* gene has a thymine at position 582, while the *Zmax1* gene has a guanine at position 582. The *HBM* gene comprises the nucleic acid sequence shown as SEQ ID NO: 2. The *HBM* gene may also be referred to as an "HBM polymorphism." Other *HBM* genes may further have silent mutations, such as those discussed in Section 3 below.

In alternative embodiments of the present invention, "HBM gene" may also refer to any allelic variant of Zmax1 (LRP5) or LRP6 which results in the HBM phenotype. Such variants may include alteration from the wild-type protein coding sequence as described herein and/or alteration in expression control sequences of Zmax1 (LRP5) or contains an amino acid mutation in LRP5 or LRP6, such that the resulting protein produces a phenotype which enhances bone mass and/or modulates lipid levels. A preferred example of such a variant is an alteration of the endogenous Zmax1 (LRP5) promoter region resulting in increased expression of the Zmax1 (LRP5) protein.

"Normal," "wild-type," "unaffected", "Zmax1", "Zmax", "LR3" and "LRP5" all refer to the genomic DNA sequence that encodes the protein indicated by SEQ ID NO: 3. LRP5 has also been referred to LRP7 in mouse. Zmax1, LRP5 and Zmax may be used

interchangeably throughout the specification and are meant to be the same gene, perhaps only relating to the gene in a different organism. The *Zmax1* gene has a guanine at position 582 in the human sequence. The *Zmax1* gene of human comprises the nucleic acid sequence shown as SEQ ID NO: 1. "Normal," "wild-type," "unaffected", "Zmax1" and "LRP5" also refer to allelic variants of the genomic sequence that encodes proteins that do not contribute to elevated bone mass. The *Zmax1* (*LRP5*) gene is common in the human population, while the *HBM* gene is rare.

"5YWTD+EGF" refers to a repeat unit found in the Zmax1 (LRP5) protein, consisting of five YWTD repeats followed by an EGF repeat.

"Bone development" generally refers to any process involved in the change of bone over time, including, for example, normal development, changes that occur during disease states, and changes that occur during aging. This may refer to structural changes in and dynamic rate changes such as growth rates, resorption rates, bone repair rates, and etc. "Bone development disorder" particularly refers to any disorders in bone development including, for example, changes that occur during disease states and changes that occur during aging. Bone development may be progressive or cyclical in nature. Aspects of bone that may change during development include, for example, mineralization, formation of specific anatomical features, and relative or absolute numbers of various cell types.

"Bone modulation" or "modulation of bone formation" refers to the ability to affect any of the physiological processes involved in bone remodeling, as will be appreciated by one skilled in the art, including, for example, bone resorption and appositional bone growth, by, *inter alia*, osteoclastic and osteoblastic activity, and may comprise some or all of bone formation and development as used herein.

Bone is a dynamic tissue that is continually adapting and renewing itself through the removal of old or unnecessary bone by osteoclasts and the rebuilding of new bone by osteoblasts. The nature of the coupling between these processes is responsible both for the modeling of bone during growth as well as the maintenance of adult skeletal integrity through remodeling and repair to meet the everyday needs of mechanical usage. There are a number of diseases of bone that result from an uncoupling of the balance between bone resorption and formation. With aging there is a gradual “physiologic” imbalance in bone turnover, which is

particularly exacerbated in women due to menopausal loss of estrogen support, that leads to a progressive loss of bone. The reduction in bone mass and deterioration in bone architecture results in an increase in bone fragility and susceptibility to spontaneous fractures. For every 10 percent of bone that is lost the risk of fracture doubles. Individuals with bone mineral density (BMD) in the spine or proximal femur 2.5 or more standard deviations below normal peak bone mass are classified as osteoporotic. However, osteopenic individuals with BMD between 1 and 2.5 standard deviations below the norm are clearly at risk of suffering bone loss related disorders.

Bone modulation may be assessed by measuring parameters such as bone mineral density (BMD) and bone mineral content (BMC) by pDXA X-ray methods, bone size, thickness or volume as measured by X-ray, bone formation rates as measured for example by calcien labeling, total, trabecular, and mid-shaft density as measured by pQCT and/or mCT methods, connectivity and other histological parameters as measured by mCT methods, mechanical bending and compressive strengths as preferably measured in femur and vertebrae respectively. Due to the nature of these measurements, each may be more or less appropriate for a given situation as the skilled practitioner will appreciate. Furthermore, parameters and methodologies such as a clinical history of freedom from fracture, bone shape, bone morphology, connectivity, normal histology, fracture repair rates, and other bone quality parameters are known and used in the art. Most preferably, bone quality may be assessed by the compressive strength of vertebra when such a measurement is appropriate. Bone modulation may also be assessed by rates of change in the various parameters. Most preferably, bone modulation is assessed at more than one age.

"Normal bone density" refers to a bone density within two standard deviations of a Z score of 0 in the context of the HBM linkage study. In a general context, the range of normal bone density parameters is determined by routine statistical methods. A normal parameter is within about 1 or 2 standard deviations of the age and sex normalized parameter, preferably about 2 standard deviations. A statistical measure of meaningfulness is the P value which can represent the likelihood that the associated measurement is significantly different from the mean. Significant P values are $P < 0.05$, 0.01, 0.005, and 0.001, preferably at least $P < 0.01$.

"HBM" refers to "high bone mass" although this term may also be expressed in terms

of bone density, mineral content, and size.

The "HBM phenotype" and "HBM-like phenotype" may be characterized by an increase of about 2 or more standard deviations, preferably 2, 2.5, 3, or more standard deviations in 1, 2, 3, 4, 5, or more quantitative parameters of bone modulation, preferably bone density and mineral content and bone strength parameters, above the age and sex norm for that parameter. The HBM phenotype and HBM-like phenotype are characterized by statistically significant increases in at least one parameter, preferably at least 2 parameters, and more preferably at least 3 or more parameters. The HBM phenotype and the HBM-like phenotype may also be characterized by an increase in one or more bone quality parameters and most preferably increasing parameters are not accompanied by a decrease in any bone quality parameters. Most preferably, an increase in bone modulation parameters and/or bone quality measurements is observed at more than one age. The HBM phenotype and HBM-like phenotype also includes changes of lipid levels, Wnt activity and/or Dkk activity.

A "Zmax1 system" or "LRP5 system" refers to a purified protein, cell extract, cell, animal, human or any other composition of matter in which Zmax1 (LRP5) is present in a normal or mutant form.

The terms "isolated" and "purified" refer to a substance altered by hand of man from the natural environment. An isolated peptide may be for example in a substantially pure form or otherwise displaced from its native environment such as by expression in an isolated cell line or transgenic animal. An isolated sequence may for example be a molecule in substantially pure form or displaced from its native environment such that at least one end of said isolated sequence is not contiguous with the sequence it would be contiguous with in nature.

A "surrogate marker" refers to a diagnostic indication, symptom, sign or other feature that can be observed in a cell, tissue, human or animal that is correlated with the *HBM* gene or elevated bone mass or both, but that is easier to measure than bone density. The general concept of a surrogate marker is well accepted in diagnostic medicine.

The present invention encompasses the *Zmax1* (*LRP5*) gene and Zmax1 (LRP5) protein in the forms indicated by SEQ ID NOS: 1 and 3, respectively, and other closely related variants, as well as the adjacent chromosomal regions of Zmax1 (LRP5) necessary for

its accurate expression. In a preferred embodiment, the present invention is directed to at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO: 1.

The present invention further encompasses variants of the *LRP6* gene and its corresponding protein which result in an enhanced bone mass and/or modulate lipids and/or modulate the Wnt signaling pathway.

"Biologically active" refers to those forms of proteins and polypeptides, including conservatively substituted variants, alleles of genes encoding a protein or polypeptide fragments of proteins which retain a biological and/or immunological activity of the wild-type protein or polypeptide. Preferably the activity is one which induces a change in LRP5, LRP6, or Dkk activity, such as inhibiting the interaction of LRP5 or LRP6 or variants thereof with Dkk, or Dkk with another ligand binding partner (*e.g.,* Dkk-1 with a Dkk-1 interacting protein such as those shown in Fig. 31). By biologically active is also meant to include any form which modulates Wnt signaling.

By "modulate"and "regulate" is meant methods, conditions, or agents which increase or decrease the wild-type activity of an enzyme, inhibitor, signal transducer, receptor, transcription activator, co-factor, and the like. This change in activity can be an increase or decrease of mRNA translation, mRNA or DNA transcription, and/or mRNA or protein degradation, which may in turn correspond to an increase or decrease in biological activity.

By " modulated activity" and "regulated activity" is meant any activity, condition, disease or phenotype which is modulated by a biologically active form of a protein. Modulation may be effected by affecting the concentration or subcellular localization of biologically active protein, *i.e.*, by regulating expression or degradation, or by direct agonistic or antagonistic effect as, for example, through inhibition, activation, binding, or release of substrate, modification either chemically or structurally, or by direct or indirect interaction which may involve additional factors.

By "effective amount" or "dose effective amount" or "therapeutically effective amount" is meant an amount of an agent which modulates a biological activity of the polypeptide of the invention.

By "immunologically active" is meant any immunoglobulin protein or fragment thereof which recognizes and binds to an antigen.

By "Dkk" is meant to refer to the nucleic acids and proteins of members of the Dkk (Dickkopf) family. This includes, but is not limited to, Dkk-1, Dkk-2, Dkk-3, Dkk-4, Soggy, and related Dkk proteins. Dkk-1 is a preferred embodiment of the present invention. However, the Dkk proteins have substantial homology and one skilled in the art will appreciate that all of the embodiments of the present invention utilizing Dkk-1 may also be utilized with the other Dkk proteins.

By "Dkk-1" is meant to refer to the Dkk-1 protein and nucleic acids which encode the Dkk-1 protein. Dkk-1 refers to Dickkopf-1, and in *Xenopus* it is related to at least Dkk-2, Dkk-3, and Dkk-4 (*see* Krupnik *et al.*, 1999 *Gene* 238: 301-313). Dkk-1 was first identified in *Xenopus* (Glinka *et al.*, 1998 *Nature* 391: 357-62). It was recognized as a factor capable of inducing ectopic head formation in the presence of inhibition of the BMP pathway. It was then also found to inhibit the axis-inducing activity of several *Xenopus* Wnt molecules by acting as an extracellular antagonist of Wnt signaling. Mammalian homologs have been found including Dkk-1, Dkk-2, Dkk-3, Dkk-4 and soggy (Fedi *et al.*, 1999 *J. Biol. Chem.* 274: 19465-72; and Krupnick *et al.* 1999). Human Dkk-1 was also referred to as sk (Fedi *et al.* 1999). As used herein, Dkk-1 is meant to include proteins from any species having a Wnt pathway in which Dkk-1 interacts. Particularly preferred are mammalian species (*e.g.*, murine, caprine, canine, bovine, feline, equine, primate, ovine, porcine and the like), with particularly preferred mammals being humans. Nucleic acid sequences encoding Dkk-1 include, but are not limited to human Dkk-1 (GenBank Accession Nos. AH009834, XM_005730, AF261158, AF261157, AF177394, AF127563 and NM_012242), *Mus musculus* dickkopf homolog 1 (GenBank Accession No. NM_010051), and *Danio rerio* dickkopf-1 (GenBank Accession Nos. AF116852 and AB023488). The genomic sequences with exon annotation are GenBank Accession Nos. AF261157 and AF261158. Also contemplated are homologs of these sequences which have Dkk-1 activity in the Wnt pathway. Dkk-1 amino acid sequences include, but are not limited to human dickkopf homolog 1 (GenBank Accession Nos. AAG15544, BAA34651, NP_036374, AAF02674, AAD21087, and XP_005730), *Danio rerio* (zebrafish) dickkopf1 (GenBank Accession Nos. BAA82135 and AAD22461) and murine dickkopf-1 (GenBank Accession Nos. O54908 and NP_034181). Variants and homologs of these sequences which possess Dkk-1 activity are

also included when referring to Dkk-1.

By "LRP5 mediated", "LRP6 mediated", and "Dkk mediated" disorder, condition or disease is any abnormal state that involves LRP5, LRP6 and/or Dkk activity. The abnormal state can be induced by environmental exposure or drug administration. Alternatively, the disease or disorder can be due to a genetic defect. Dkk mediated diseases, disorders and conditions include but are not limited to bone mass disorders or conditions and lipid disorders and conditions. For example, bone mass disorders/conditions/diseases, which may be mediated by Dkk, LRP5 and/or LRP6 include but are not limited to age related loss of bone, bone fractures (*e.g.*, hip fracture, Colle's fracture, vertebral crush fractures), chondrodystrophies, drug-induced disorders (e.g., osteoporosis due to administration of glucocorticoids or heparin and osteomalacia due to administration of aluminum hydroxide, anticonvulsants, or glutethimide), high bone turnover, hypercalcemia, hyperostosis, osteoarthritis, osteogenesis imperfecta, osteomalacia, osteomyelitis, osteoporosis, Paget's disease, and rickets.

Lipid disorders/diseases/conditions, which may be mediated by Dkk, LRP5, and/or LRP6 include but are not limited to familial lipoprotein lipase deficiency, familial apoprotein CII deficiency, familial type 3 hyperlipoproteinemia, familial hypercholesterolemia, familial hypertriglyceridemia, multiple lipoprotein-type hyperlipidemia, elevated lipid levels due to dialysis and/or diabetes, and elevated lipid levels of unknown etiologies

The term "recognizes and binds," when used to define interactions of antisense nucleotides or siRNA's (small inhibitory RNA) with a target sequence, means that a particular antisense or small inhibitory RNA (siRNA) sequence is substantially complementary to the target sequence, and thus will specifically bind to a portion of an mRNA encoding polypeptide. As such, typically the sequences will be highly complementary to the mRNA target sequence, and will have no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 base mismatches throughout the sequence. In many instances, it may be desirable for the sequences to be exact matches, i.e. be completely complementary to the sequence to which the oligonucleotide specifically binds, and therefore have zero mismatches along the complementary stretch. As such, highly complementary sequences will typically bind quite specifically to the target sequence region of the mRNA and will therefore be highly efficient in reducing, and/or even

inhibiting the translation of the target mRNA sequence into polypeptide product.

Substantially complementary oligonucleotide sequences will be greater than about 80 percent complementary (or '% exact-match') to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and will, more preferably be greater than about 85 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds. In certain aspects, as described above, it will be desirable to have even more substantially complementary oligonucleotide sequences for use in the practice of the invention, and in such instances, the oligonucleotide sequences will be greater than about 90 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and may in certain embodiments be greater than about 95 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and even up to and including 96%, 97%, 98%, 99%, and even 100% exact match complementary to the target mRNA to which the designed oligonucleotide specifically binds.

Percent similarity or percent complementary of any of the disclosed sequences may be determined, for example, by comparing sequence information using the GAP computer program, version 6.0, available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch (1970). Briefly, the GAP program defines similarity as the number of aligned symbols (i.e., nucleotides or amino acids) which are similar, divided by the total number of symbols in the shorter of the two sequences. The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess (1986), (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

By "mimetic" is meant a compound or molecule that performs the same function or behaves similarly to the compound mimicked.

By "reporter element" is meant a polynucleotide that encodes a polypeptide capable of being detected in a screening assays. Examples of polypeptides encoded by reporter elements include, but are not limited to, lacZ, GFP, luciferase, and chloramphenicol acetyltransferase.

2. Introduction

The present invention also encompasses the HBM gene and HBM protein in the forms indicated by SEQ ID NO: 2 and 4, respectively, and other closely related variants, as well as the adjacent chromosomal regions of the HBM gene necessary for its accurate expression. In a preferred embodiment, the present invention is directed to at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO: 2. More preferably, the present invention is directed to at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO: 2, wherein one of the 15 contiguous nucleotides is the thymine at nucleotide 582.

The invention also relates to the nucleotide sequence of the *Zmax1* (*LRP5*) gene region, as well as the nucleotide sequence of the HBM region. More particularly, a preferred embodiment are the BAC clones containing segments of the *Zmax1* (*LRP5*) gene region B200E21-H and B527D12-H. A preferred embodiment is the nucleotide sequence of the BAC clones consisting of SEQ ID NOS: 5-12.

The invention also concerns the use of the nucleotide sequence to identify DNA probes for the *Zmax1* (*LRP5*) gene and the *HBM* gene, PCR primers to amplify the *Zmax1* (*LRP5*) gene and the *HBM* gene, nucleotide polymorphisms in the *Zmax1* (*LRP5*) gene and the *HBM* gene, and regulatory elements of the *Zmax1* (*LRP5*) gene and the *HBM* gene.

This invention describes the further localization of the chromosomal location of the *Zmax1* (*LRP5*) gene and *HBM* gene on chromosome 11q13.3, between genetic markers D11S987 and SNP_CONTIG033-6, as well as the DNA sequences of the *Zmax1* (*LRP5*) gene and the *HBM* gene. The chromosomal location was refined by the addition of more genetic markers to the mapping panel used to map the gene, and by the extension of the pedigree to include more individuals. The pedigree extension was critical because the new individuals that have been genotyped harbor critical recombination events that narrow the region. To identify genes in the region on 11q13.3, a set of BAC clones containing this chromosomal region was identified. The BAC clones served as a template for genomic DNA sequencing, and also as a reagent for identifying coding sequences by direct cDNA selection. Genomic sequencing and direct cDNA selection were used to characterize more than 1.5 million base pairs of DNA from 11q13.3. The *Zmax1* (*LRP5*) gene was identified within this region and

the *HBM* gene was then discovered after mutational analysis of affected and unaffected individuals.

When a gene has been genetically localized to a specific chromosomal region, the genes in this region can be characterized at the molecular level by a series of steps that include: cloning of the entire region of DNA in a set of overlapping clones (physical mapping), characterization of genes encoded by these clones by a combination of direct cDNA selection, exon trapping and DNA sequencing (gene identification), and identification of mutations in these genes by comparative DNA sequencing of affected and unaffected members of the HBM kindred (mutation analysis).

Physical mapping is accomplished by screening libraries of human DNA cloned in vectors that are propagated in *E. coli* or *S. cereviseae* using PCR assays designed to amplify unique molecular landmarks in the chromosomal region of interest. To generate a physical map of the HBM candidate region, a library of human DNA cloned in Bacterial Artificial Chromosomes (BACs) was screened with a set of Sequence Tagged Site (STS) markers that had been previously mapped to chromosome 11q12-q13 by the efforts of the Human Genome Project.

STSs are unique molecular landmarks in the human genome that can be assayed by PCR. Through the combined efforts of the Human Genome Project, the location of thousands of STSs on the twenty-two autosomes and two sex chromosomes has been determined. For a positional cloning effort, the physical map is tied to the genetic map because the markers used for genetic mapping can also be used as STSs for physical mapping. By screening a BAC library with a combination of STSs derived from genetic markers, genes, and random DNA fragments, a physical map comprised of overlapping clones representing all of the DNA in a chromosomal region of interest can be assembled.

BACs are cloning vectors for large (80 kilobase to 200 kilobase) segments of human or other DNA that are propagated in *E. coli*. To construct a physical map using BACs, a library of BAC clones is screened so that individual clones harboring the DNA sequence corresponding to a given STS or set of STSs are identified. Throughout most of the human genome, the STS markers are spaced approximately 20 to 50 kilobases apart, so that an individual BAC clone typically contains at least two STS markers. In addition, the BAC

libraries that were screened contain enough cloned DNA to cover the human genome six times over. Therefore, an individual STS typically identifies more than one BAC clone. By screening a six-fold coverage BAC library with a series of STS markers spaced approximately 50 kilobases apart, a physical map consisting of a series of overlapping BAC clones, i.e. BAC contigs, can be assembled for any region of the human genome. This map is closely tied to the genetic map because many of the STS markers used to prepare the physical map are also genetic markers.

When constructing a physical map, it often happens that there are gaps in the STS map of the genome that result in the inability to identify BAC clones that are overlapping in a given location. Typically, the physical map is first constructed from a set of STSs that have been identified through the publicly available literature and World Wide Web resources. The initial map consists of several separate BAC contigs that are separated by gaps of unknown molecular distance. To identify BAC clones that fill these gaps, it is necessary to develop new STS markers from the ends of the clones on either side of the gap. This is done by sequencing the terminal 200 to 300 base pairs of the BACs flanking the gap, and developing a PCR assay to amplify a sequence of 100 or more base pairs. If the terminal sequences are demonstrated to be unique within the human genome, then the new STS can be used to screen the BAC library to identify additional BACs that contain the DNA from the gap in the physical map. To assemble a BAC contig that covers a region the size of the HBM candidate region (2,000,000 or more base pairs), it is often necessary to develop new STS markers from the ends of several clones.

After building a BAC contig, this set of overlapping clones serves as a template for identifying the genes encoded in the chromosomal region. Gene identification can be accomplished by many methods. Three methods are commonly used: (1) a set of BACs selected from the BAC contig to represent the entire chromosomal region can be sequenced, and computational methods can be used to identify all of the genes, (2) the BACs from the BAC contig can be used as a reagent to clone cDNAs corresponding to the genes encoded in the region by a method termed direct cDNA selection, or (3) the BACs from the BAC contig can be used to identify coding sequences by selecting for specific DNA sequence motifs in a procedure called exon trapping. The present invention includes genes identified by the first

two methods.

To sequence the entire BAC contig representing the HBM candidate region, a set of BACs was chosen for subcloning into plasmid vectors and subsequent DNA sequencing of these subclones. Since the DNA cloned in the BACs represents genomic DNA, this sequencing is referred to as genomic sequencing to distinguish it from cDNA sequencing. To initiate the genomic sequencing for a chromosomal region of interest, several non-overlapping BAC clones are chosen. DNA for each BAC clone is prepared, and the clones are sheared into random small fragments which are subsequently cloned into standard plasmid vectors such as pUC18. The plasmid clones are then grown to propagate the smaller fragments, and these are the templates for sequencing. To ensure adequate coverage and sequence quality for the BAC DNA sequence, sufficient plasmid clones are sequenced to yield six-fold coverage of the BAC clone. For example, if the BAC is 100 kilobases long, then phagemids are sequenced to yield 600 kilobases of sequence. Since the BAC DNA was randomly sheared prior to cloning in the phagemid vector, the 600 kilobases of raw DNA sequence can be assembled by computational methods into overlapping DNA sequences termed sequence contigs. For the purposes of initial gene identification by computational methods, six-fold coverage of each BAC is sufficient to yield ten to twenty sequence contigs of 1000 base pairs to 20,000 base pairs.

The sequencing strategy employed in this invention was to initially sequence "seed" BACs from the BAC contig in the HBM candidate region. The sequence of the "seed" BACs was then used to identify minimally overlapping BACs from the contig, and these were subsequently sequenced. In this manner, the entire candidate region was sequenced, with several small sequence gaps left in each BAC. This sequence served as the template for computational gene identification. One method for computational gene identification is to compare the sequence of BAC contig to publicly available databases of cDNA and genomic sequences, *e.g.*, unigene, dbEST, GenBank. These comparisons are typically done using the BLAST family of computer algorithms and programs (Altschul *et al.*, *J. Mol. Biol.*, 215:403-410 (1990)). The BAC sequence can also be translated into protein sequence, and the protein sequence can be used to search publicly available protein databases, using a version of BLAST designed to analyze protein sequences (Altschul *et al.*, 1997 *Nucl. Acids Res.* 25:

3389-3402). Another method is to use computer algorithms such as MZEF (Zhang, 1997 *Proc. Natl. Acad. Sci. USA*, 94: 565-568) and GRAIL (Uberbacher *et al.*, 1996 *Methods Enzymol.* 266: 259-281), which predict the location of exons in the sequence based on the presence of specific DNA sequence motifs that are common to all exons, as well as the presence of codon usage typical of human protein encoding sequences.

In addition to identifying genes by computational methods, genes were also identified by direct cDNA selection (Del Mastro *et al.*, 1995 *Genome Res.* 5(2): 185-194). In direct cDNA selection, cDNA pools from tissues of interest are prepared, and the BACs from the candidate region are used in a liquid hybridization assay to capture cDNA which base-pairs to coding regions in the BAC. In the methods described herein, the cDNA pools were created from several different tissues by random priming the first strand cDNA from poly-A RNA, synthesizing the second strand cDNA by standard methods, and adding linkers to the ends of the cDNA fragments. The linkers are used to amplify the cDNA pools. The BAC clones are used as a template for *in vitro* DNA synthesis to create a biotin labeled copy of the BAC DNA. The biotin labeled copy of the BAC DNA is then denatured and incubated with an excess of the PCR amplified, linkered cDNA pools which have also been denatured. The BAC DNA and cDNA are allowed to anneal in solution, and heteroduplexes between the BAC and the cDNA are isolated using streptavidin coated magnetic beads. The cDNA which is captured by the BAC is then amplified using primers complimentary to the linker sequences, and the hybridization/selection process is repeated for a second round. After two rounds of direct cDNA selection, the cDNA fragments are cloned, and a library of these direct selected fragments is created.

The cDNA clones isolated by direct selection are analyzed by two methods. Since a pool of BACs from the HBM candidate region is used to provide the genomic DNA sequence, the cDNAs must be mapped to individual BACs. This is accomplished by arraying the BACs in microtiter dishes, and replicating their DNA in high density grids. Individual cDNA clones are then hybridized to the grid to confirm that they have sequence identity to an individual BAC from the set used for direct selection, and to determine the specific identity of that BAC. cDNA clones that are confirmed to correspond to individual BACs are sequenced. To determine whether the cDNA clones isolated by direct selection share

sequence identity or similarity to previously identified genes, the DNA and protein coding sequences are compared to publicly available databases using the BLAST family of programs.

The combination of genomic DNA sequence and cDNA sequence provided by BAC sequencing and by direct cDNA selection yields an initial list of putative genes in the region. The genes in the region were all candidates for the HBM locus. To further characterize each gene, Northern blots were performed to determine the size of the transcript corresponding to each gene, and to determine which putative exons were transcribed together to make an individual gene. For Northern blot analysis of each gene, probes were prepared from direct selected cDNA clones or by PCR amplifying specific fragments from genomic DNA or from the BAC encoding the putative gene of interest. The Northern blots gave information on the size of the transcript and the tissues in which it was expressed. For transcripts which were not highly expressed, it was sometimes necessary to perform a reverse transcription PCR assay using RNA from the tissues of interest as a template for the reaction.

Gene identification by computational methods and by direct cDNA selection provides unique information about the genes in a region of a chromosome. When genes are identified, then it is possible to examine different individuals for mutations in each gene.

The present invention also encompasses the *HBM* gene and HBM protein in the forms indicated by SEQ ID NO: 2 and 4, respectively, and other closely related variants, as well as the adjacent chromosomal regions of the *HBM* gene necessary for its accurate expression. In a preferred embodiment, the present invention is directed to an isolated nucleic acid sequence of SEQ ID NO: 2, as well as variants thereof. Variants include changes in SEQ ID NO:1 which result in a HBM like phenotype. Examples of such variants are discussed further in Section 3 below and in the examples. These variants preferably have at least about 90%, preferably at least about 95%, or more preferably at least about 98% or more similarity or identity to the nucleic acid sequence of SEQ ID NOS: 1 or 2 or biologically active fragments thereof. Therefore, sequences which are 96%, 97%, and 99% or more similar to SEQ ID NOS: 1 or 2 or biologically active fragments thereof are also contemplated herein.

Determination of the degree of variation between a high bone mass (HBM) variant can be performed using BLAST or FASTA or other suitable algorithm using standard default

parameters. Preferably, identity will be determined for coding regions of SEQ ID NOS: 1-2, but can also include non-coding domains. Additionally, alignment programs can be used to identify conserved sequences or potential motifs across different animal species. Alignment programs can also be used to align the nucleic acid and/or protein sequences of related genes and the proteins that they encode. Preferred alignment programs include CLUSTALW, PILEUP and GAP, and would preferably be used with default parameters. For example, such programs can be used to align the sequences of Zmax1 (LRP5), HBM, and LDL receptor-related protein 6 (LRP6) and sequences related thereto.

By a polynucleotide having a nucleotide sequence at least, for example, 90% "similar" to a reference nucleotide sequence encoding a polypeptide, is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to ten point mutations per each 100 nucleotides of the reference nucleotide sequence. These mutations of the reference sequence may occur at any location in SEQ ID NO: 1 or 2 or in the *LRP6* gene. The mutations may be silent.

Another embodiment contemplates that such polynucleotide variants of SEQ ID NO: 1 or 2 comprise nucleic acid sequences which are at least 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400, or 500 contiguous nucleotides of SEQ ID NO: 1 or 2. More preferably, such polynucleotide variants have a contiguous nucleic acid sequence corresponding with the polymorphism at nucleotide 582 (G→T substitution) of SEQ ID NO: 2 or other variants of SEQ ID NO: 1 or 2, which comprise a mutation which modulates bone mass and/or lipid levels when the polypeptide encoded thereby is administered to a subject. All variants of SEQ ID NO: 1 or 2 contemplated possess the characteristic of encoding a protein or polypeptide which when administered to a subject induces bone modulation. Additional variants which may be responsible for modulating bone mass when administered to a subject may lie within the domain known to contain the HBM polymorphism and which encodes the beta propeller domain (YWTD motifs). Alternatively, other variants of Zmax1 (LRP5) which modulate high bone mass in a subject may be due to mutations in the nucleic acid sequences encoding any of the other conserved domains of Zmax1 (LRP5), such as those set forth in Figure 4 (e.g., the RGD extracellular attachment site, the binding site for LDL and calcium, the cysteine rich growth factor repeats, the ideal PEST region, and the

internalization domain). See Section 3 and the Examples below for additional mutations which may confer enhance bone mass and/or lipid modulation.

HBM polynucleotides and HBM like variants contemplated include those which hybridize under stringent conditions to SEQ ID NO: 2. Hybridization methods are known in the art and include, but are not limited to: (a) washing with 0.1X SSPE (0.62 M NaCl, 0.06 M $NaH_2PO_4 \cdot H_2O$, 0.075 M EDTA, pH 7.4) and 0.1% sodium dodecyl sulfate (SDS) at 50°C; (b) washing with 50% formamide, 5X SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6-8), 0.1% sodium pyrophosphate, 5X Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS and 10% dextran sulfate at 42°C, followed by washing at 42°C in 0.2X SSC and 0.1% SDS; and (c) washing with of 0.5 M $NaPO_4$, 7% SDS at 65°C followed by washing at 60°C in 0.5X SSC and 0.1% SDS. Additional conditions under which HBM variants can be isolated by hybridization to SEQ ID NO: 2 or nucleic acid fragments thereof can be performed by varying the hybridization temperature. High stringency hybridization conditions are those performed at about 20°C below the melting temperature (T_m) of SEQ ID NO: 2 or fragments thereof. Preferred stringency is performed at about 5-10°C below the T_m of SEQ ID NO: 2 or fragments thereof. Additional hybridization conditions can be prepared as described in Chapter 11 of Sambrook *et al.*., Molecular Cloning: A Laboratory Manual (1989), or as would be known to the artisan of ordinary skill.

Alternatively, mammalian libraries (e.g., equine, primate, caprine, bovine, ovine, feline, porcine, and canine) can be probed using degenerate primers and polymerase chain reaction (PCR) techniques to identify variants of SEQ ID NO: 2 or fragments thereof. Preferably primers are utilized which hybridize under stringent conditions to the open reading frame of SEQ ID NO: 2, or to non-coding portions of the sequence. More preferably, such primers hybridize to conserved domains within SEQ ID NO: 2. For example, conserved domains include those coding for the YWTD beta-propeller domains or other domains, such as those listed in Figure 4. Preferred primers are typically 15 nucleotides in length, but can vary to be at least, about 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40 or 50 (and any range in between) nucleotides in length. Heterologous hybridization is to amplify the target gene or nucleic acid sequence using degenerate PCR primers. Probes for variants of SEQ ID NO: 2

and the polypeptide encoded thereby can be obtained by preparing mixed oligonucleotides of greater than 10, preferably of 15 or more, nucleotides in length representing all possible nucleotide sequences which could encode the corresponding amino acid sequences (e.g., SEQ ID NO: 4 fragments thereof). This method is clearly documented by Gould *et al.*, 1989 *Proc. Natl. Acad. Sci. USA* 86(6): 1934-8.

Another embodiment includes nucleic acids which encode an HBM polypeptide or HBM like variant which is at least about 90% similar to SEQ ID NO: 4 and fragments thereof, and which when administered to a subject modulate bone mass in that subject. HBM variants may have a valine corresponding to position 171 of SEQ ID NO: 4 (Gly to Val substitution) or 170 of the mouse homolog, or an amino acid change elsewhere in propeller 1 or in the protein which results in enhanced bone mass and/or lipid modulation. Other preferred embodiments include high bone mass polypeptides which have at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 500 or more contiguous amino acids of SEQ ID NO: 3 or 4, with a mutation in the sequence resulting in enhanced bone mass and/or modulated lipid levels. Such contemplated contiguous sequences preferably overlap with a polymorphism corresponding to high bone mass, such as valine-171 of SEQ ID NO: 4, other mutations in propeller 1 or is predicted from the model provided in the Examples. Also contemplated are the polynucleotides encoding polypeptides which are at least about 95%, 96%, 97%, 98% and 99% or more similar to SEQ ID NO: 3 or 4 and fragments thereof, wherein these polypeptide contain at least one mutation (e.g., valine-171 or like mutation).

In another embodiment, a synthetic nucleic acid encoding SEQ ID NO: 4 is contemplated wherein the nucleic acid sequence has been conservatively substituted based on the degeneracy of the code such that no amino acids are altered in SEQ ID NO: 4, but perhaps wherein the resulting synthetic polynucleotide encoding said SEQ ID NO: 4 is one that is at least, about 50% similar to SEQ ID NO: 2. Alternatively, SEQ ID NO: 4 may contain any of the silent mutations identified in Section 3 below .

By a polypeptide having an amino acid sequence of at least, for example, 95% "identity" to a reference amino acid sequence of SEQ ID NO: 3 or 4 or fragment thereof is intended that the amino acid sequence of the polypeptide is identical to the reference

sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid sequence of SEQ ID NO: 3 or 4 and has an HBM like phenotype. In other words, to obtain a polypeptide having an amino acid sequence 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

Additional HBM polypeptides and nucleic acids which encode said HBM polypeptides are contemplated wherein amino acid residues are conservatively substituted. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247: 1306-10 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. These studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. Numerous phenotypic substitutions are described in Bowie *et al.*, *supra*, and the references cited therein, which are herein incorporated by reference in their entirety. Preferred substitutions would be in domains which are less conserved across species, and which do not correspond to a structurally or functionally important domain (e.g., a binding site, catalytic site, or beta propeller or other domain described in Figure 4).

Recent studies have indicated that LRP5 participates in the Wnt signal transduction pathway. The Wnt pathway is critical in limb early embryological development. A recently published sketch of the components of Wnt signaling is shown in Fig. 28 (Nusse, 2001

http://www.stanford.edu/~rnusse/pathways/cell2. html) (*see also*, Nusse, 2001 *Nature* 411: 255-6; and Mao *et al.*, 2001 *Nature* 411: 321-5).

Briefly summarized, Wnt proteins are secreted proteins which interact with the transmembrane protein Frizzled (Fz). LRP proteins, such as LRP5 and LRP6, are believed to modulate the Wnt signal in a complex with Fz (Tamai *et al.*, 2000 *Nature* 407: 530-5). The Wnt pathway acts intracellularly through the Disheveled protein (Dsh) which in turn inhibits glycogen synthetase kinase-3 (GSK3) from phosphorylating β-catenin. Phosphorylated β-catenin is rapidly degraded following ubiquitination. However, the stabilized β-catenin accumulates and translocates to the nucleus where it acts as a cofactor of the T-cell factor (TCF) transcription activator complex.

The protein dickkopf-1 (Dkk-1) is reported to be an antagonist of Wnt pathway. Dkk-1 is required for head formation in early development (Glinka *et al.*, 1998 *Nature* 391: 357-62). Dkk-1 and its function in the Wnt pathway are described in *e.g.*, Krupnik, *et al.*, 1999 *Gene* 238: 301-13; Fedi *et al.*, 1999 *J. Biol. Chem.* 274: 19465-72; *see also* for Dkk-1 and the Wnt pathway, Wu *et al.*, 2000 *Curr. Biol.* 10: 1611-4; Shinya *et al.*, 2000 *Mech. Dev.* 98: 3-17; Mukhopadhyay *et al.*, 2001 *Dev. Cell.* 1: 423-434; and in PCT Patent Application No. WO 00/52047, and in references cited in each. It has been known that Dkk-1 acts upstream of Dsh, however the nature of the mechanism of inhibition by Dkk-1 is just beginning to be elucidated. Dkk-1 is expressed in the mouse embryonic limb bud and its disruption results in abnormal limb morphogensis, among other developmental defects (Gotewold *et al.*, 1999 *Mech. Dev.* 89:151-3; and Mukhopadhyay *et al.*, 2001 *Dev. Cell.* 1: 423-34).

Related U.S. Serial No. 60/291,311 (herein incorporated by reference in its entirety) disclosed a novel interaction between Dkk-1 (GenBank Accession No. XM 005730) and LRP5. The interaction between Dkk-1 and LRP5 was discovered by a yeast two hybrid (Y2H) screen for proteins which interact with the ligand binding domain of LRP5. The two-hybrid screen is a common procedure in the art, which is described, for example, by Gietz *et al.*, 1997 *Mol. Cell. Biochem.* 172: 67-79; Young, 1998 *Biol. Reprod.* 58: 302-11; Brent *et al.*, 1997 *Ann. Rev. Genet.* 31: 663-704; and Lu *et al.*, eds., Yeast Hybrid Technologies, Eaton Publishing, Natick MA, (2000). More recently, other studies confirm that Dkk-1 is a binding partner for LRP and modulates the Wnt pathway via direct binding with LRP (R.

Nusse, 2001 *Nature* 411: 255-6; Bafico *et al.*, 2001 *Nat. Cell Biol.* 3: 683-6; Semënov, 2001 *Curr. Biol.* 11: 951-61; Mao, 2001 *Nature* 411: 321-5 (2001); Zorn, 2001 *Curr. Biol.* 11: R592-5); and Li *et al.*, 2002 *J. Biol Chem.* 277: 5977-81).

Mao and colleagues (2001) identified Dkk-1 as a ligand for LRP6. Mao *et al.* suggest that Dkk-1 and LRP6 interact antagonistically where Dkk proteins inhibit the Wnt coreceptor functions of LRP6. Using co-immunoprecipitation, the group verified that the Dkk-1/LRP6 interaction was direct. Dkk-2 was also found to directly bind LRP6. Contrary to data contained in provisional application 60/291,311, Mao *et al.* report that no interaction was detected between any Dkk protein and LRP5, as well as no interaction with LDLR, VLDLR, ApoER, or LRP). Additionally, Mao *et al.* demonstrated that LRP6 can titrate Dkk-1's effects of inhibiting Wnt signaling using the commercial TCF-luciferase reporter gene assay (TOPFLASH). A similar conclusion was drawn from analogous studies in *Xenopus* embryos. Deletion analyses of LRP6 functional domains revealed that EGF repeats (beta-propellers) 3 and 4 were necessary for Dkk-1 binding and that the ligand binding domains of LRP6 had no effect on Dkk-1 binding. The findings of Mao *et al.* contrast with data obtained by the present inventors indication that the ligand binding domains of LRP5 were necessary and sufficient for Dkk-1 binding in yeast. Using classical biochemical ligand-receptor studies, Mao *et al.* determined a Kd=0.34 nM for Dkk-1/LRP6 and a Kd=0.73 nM for Dkk-2/LRP6.

Semenov *et al.* (2001) verified the Mao group's results and confirmed by coimmunoprecipitation that Dkk-1 does not directly bind to Wnt or Frizzled but rather interacts with LRP6. Their Scatchard analyses found a Kd=0.5 nM for Dkk-1/LRP6. Semenov *et al.* also demonstrated that Dkk-1 could abolish an LRP5/Frizzled8 complex implying that Dkk-1 can also repress Wnt signaling via interactions with LRP5. A Dkk-1 mutant where cysteine 220 was changed to alanine abolished LRP6 binding and was unable to repress Wnt signaling. Studies in *Xenopus* embryos confirmed the results and revealed a functional consequence of Dkk-1/LRP6: repression of Wnt signaling. Their *Xenopus* work also suggested that LRP6/Dkk-1 may be specific for the canonical, β-catenin-mediated, Wnt pathways as opposed to the Wnt Planar Cell Polarity pathway.

Bafico *et al.* (2001) employed a ^{125}I-labeled Dkk-1 molecule to identify LRP6 as its sole membrane receptor with a Kd=0.39 nM. Again, the functional consequences of the Dkk-

1/LRP6 interaction was a repression of the canonical Wnt signaling even when Dkk-1 was added at extremely low concentrations (30 pM).

Not wishing to be bound by theory, it is believed that the present invention provides an explanation for the mechanism of Dkk-1 inhibition of the Wnt pathway and provides a mechanism whereby the Wnt pathway may be modulated. The present application and related U.S. Serial No. 60/291,311 (which is herein incorporated by reference in its entirety) describe Dkk-1/LRP5 interactions and demonstrate that the interaction between LRP5/LRP6/HBM, and Dkk can be used in a method as an intervention point in the Wnt pathway for an anabolic bone therapeutic or a modulator of lipid metabolism.

As detailed in the Examples, Dkk-1 is able to repress LRP5-mediated Wnt signaling but not HBM-mediated Wnt signaling. This observation is of particular interest because the HBM mutation in LRP5 is a gain of function or activation mutation. That is, Wnt signaling, via the canonical pathway, is enhanced with HBM versus LRP5. Thus, other HBM-like mutations would also function similarly. The present data suggest the mechanism of this functional activation: the inability of Dkk-1 to repress HBM-mediated Wnt signaling. Further investigations of other Wnt or Dkk family members show differential activities in the canonical Wnt pathway that demonstrate the complexity and variability in Wnt signaling that can be achieved depending on the LRP/Dkk/Wnt/Frizzled repertoire that is expressed in a particular cell or tissue. This may attest to the apparent bone specificity of the HBM or HBM like phenotypes in humans and in the HBM transgenic animals.

Furthermore, the present data reveal the importance and functional consequence for the potential structural perturbation of the first beta-propeller domain of LRP5. Our data identified the ligand binding domain of LRP5 as the interacting region with Dkk-1 while the Mao *et al.* publication demonstrated the functional role of propellers 3 and 4 in their LRP6/Dkk-1 studies. In the present invention, we implicate the first beta propeller domain, via the HBM mutation at residue 171, as having a functional consequence in the Dkk-1-mediated Wnt pathway. The involvement of position 171 of propeller 1 may be direct or indirect with Dkk-1. Direct involvement could arise from perturbations of the 3-dimensional structure of the HBM extracellular domain that render Dkk-1 unable to bind. Alternatively, residue 171 of propeller 1 may directly interact with Dkk-1; however, by itself, it is

insufficient to bind and requires other LRP5 domains. Potential indirect candidate molecules may be among the proteins identified the Dkk-1 yeast-two-hybrid experiments.

It may be that the disruption of Dkk activity is not necessarily mediated by enhancing or preventing the binding of Dkk to LRP5/LRP6/HBM. More than one mechanism may be involved. Indeed, the inventors have observed that Dkk-1 binds LRP5, LRP6, and HBM. It is able to effectively inhibit LRP6, and to a slightly lesser extent, LRP5 activity. Further, has been observed that different members of the Dkk family differentially affect LRP5/LRP6/HBM activity. For example, Dkk-1 inhibits LRP5/LRP6/HBM activity while another Dkk may enhance LRP5/LRP6/HBM activity. An endpoint to consider is the modulation of the LRP5/LRP6/HBM activity, not simply binding.

The present disclosure shows that targeting the modulation of the Dkk-1/LRP5 interaction is a therapeutic intervention point for an HBM or HBM-like mimetic agent. A therapeutic agent of the invention may be a small molecule, peptide or nucleic acid aptamer, antibody, or other peptide/protein, etc. Methods of reducing Dkk-1 expression may also be therapeutic using methodologies such as: RNA interference (i.e., siRNAs), small hairpin RNAs (shRNAs), antisense oligonucleotides, morpholino oligonucleotides, PNAs, antibodies to Dkk-1 or Dkk-1 interacting proteins, decoy or scavenger LRP5 or LRP6 receptors, and knockdown of Dkk-1 or Dkk-1 interactor transcription. For discussion of small hairpin RNAs, see Yu *et al.*, 2002 *Proc. Natl. Acad. Sci. USA* 99: 6047-52; Tuschl, 2002 *Nature Biotech.* 20: 446-8; Lee *et al.*, 2002 *Nature Biotech.* 19: 500-5; Paddison *et al.*, 2002 *Genes & Devel.* 16: 948-58; and Brummelkamp *et al.*, 2002 *Science* 296: 550-3.

In an embodiment of the present invention, the activity of Dkk-1 or the activity of a Dkk-1 interacting protein may be modulated for example by binding with a peptide aptamer of the present invention. In another embodiment, LRP5 activity may be modulated by a reagent provided by the present invention (*e.g.*, a peptide aptamer). In another embodiment, the Dkk-1/LRP5 interaction may be modulated by a reagent of the present invention (*e.g.*, a Dkk-1 interacting protein such as those identified in Fig. 31). In another embodiment, the Wnt signal transduction pathway may be modulated by use of one or more of the above methods. In a preferred embodiment of the present invention, the Dkk-1 mediated activity of the Wnt pathway may be specifically modulated by one or more of the above methods. In

another preferred embodiment of the present invention, the Wnt signal transduction pathway may be stimulated by down-regulating Dkk-1 interacting protein activity; such down-regulation could, for example, yield greater LRP5 activity. In a more preferred embodiment, by stimulating LRP5 activity, bone mass regulation may be stimulated to restore or maintain a more optimal level. In another preferred embodiment, by stimulating LRP5 activity, lipid metabolism may be stimulated to restore or maintain a more optimal level. Alternative embodiments provide methods for screening candidate drugs and therapies directed to correction of bone mass disorders or lipid metabolism disorders. And, preferred embodiments of the present invention provide drugs and therapies developed by the use of the reagents and/or methods of the present invention. One skilled in the art will understand that the present invention provides important research tools to develop an effective model of osteoporosis, to increase understanding of bone mass and lipid modulation, and to modulate bone mass and lipid metabolism. For a more detailed description of Dkk-1 and Dkk-1 interacting protein modulation, please refer to U.S. Serial No. 60/361,293, which is herein incorporated by reference in its entirety.

3. Alternative Variants of LRP5/LRP6 Having HBM Activity

A structural model of the LRP5/Zmax1 first beta-propeller module was generated based on a model prediction in Springer *et al.*, 1998 *J. Mol. Biol.* 283: 837-862. Based on the model, certain amino acid residues were identified as important variants of LRP5/HBM/Zmax1. The model and modifications thereof are discussed in more detail in the Examples. The following three categories provide examples of such variants:

The shape of the beta-propeller resembles a disk with inward-sloping sides and a hole down the middle. Residue 171 is in a loop on the outer or top surface of the domain in blade 4 of propeller module 1. Thus, variants comprising changed residues in structurally equivalent positions in other blades; as well as residues that are slightly more interior to the binding pocket, but still accessible to the surface, are important embodiments of the present invention for the study of bone mass modulation by LRP5/HBM, for the development of pharmaceuticals and treatments of bone mass disorders, and for other objectives of the present invention. The following Table contains examples of such variants:

TABLE 1

Variant	Effect of Mutation
A214V	a position equivalent to 171 in blade 5 of propeller 1; alanine is not conserved in other propellers
E128V	a position equivalent to 171 in blade 3 of propeller 1; glutamate is not conserved in other propellers
A65V	a position equivalent to 171 in blade 2 of propeller 1; alanine is conserved in propellers 1-3 but not 4
G199V	an accessible interior position in blade 5 of propeller 1; glycine is conserved in propellers 1-3 but not 4
M282V	accessible interior position in blade 1 of propeller 1; methionine is conserved in propellers 1-3 but not 4

These mutations were further analyzed based on a more sophisticated model, as discussed and described in Example 11 below.

LRP5/Zmax1 has four beta-propeller structures; the first three beta-propeller modules conserve a glycine in the position corresponding to residue 171 in human LRP5/Zmax1. Therefore, variants bearing a valine in the equivalent positions in the other propellers are important embodiments of the present invention. The following variants are useful for the study of bone mass modulation by LRP5/HBM, for the development of pharmaceuticals and treatments of bone mass disorders, and for other objectives of the present invention: G479V, G781V, and Q1087V of SEQ ID NO: 3, which demonstrate that propeller 1 is an important determinant of an HBM or HBM-like effect.

The G171V HBM polymorphism (SEQ ID NO: 4) results in "occupied space" of the beta-propeller 1, with the side-chain from the valine residue sticking out into an open binding pocket and potentially altering a ligand/protein interaction. The glycine residue is conserved in LRP5/Zmax1 propellers 1, 2 and 3 but is a glutamine in propeller 4. Therefore, the following variants of LRP5/HBM are important embodiments of the present invention for the study of bone mass modulation by LRP5/HBM, for the development of pharmaceuticals and treatments of bone mass disorders, and for other objectives of the present invention:

G171K: introduces a charged side-chain

G171F: introduces a ringed side-chain

G171I: introduces a branched side-chain

G171Q: introduces the propeller 4 residue

These substitutions along with substitutions in other regions of propeller 1 of SEQ ID NO: 3 (i.e., A214V and M282V) have been shown to produce an HBM-like effect by TCF assay (Figs. 29 and 30). Thus these substitutions in other propeller 1 domains would similarly have an expectation of producing an HBM-like phenotype readily assayable by TCF assay.

Furthermore, LRP6 is the closest homolog of LRP5/Zmax1. LRP6 has a beta-propeller structure predicted to be similar, if not identical to Zmax1. The position corresponding to glycine 171 of human LRP5/Zmax1 is glycine 158 of human LRP6. Thus, corresponding variants of LRP6 are an important embodiment of the present invention for the study of the specificity of LRP5/Zmax1 versus its related family member, for the development of pharmaceuticals and treatments of bone mass disorders, and for other objectives of the present invention. Specifically, for example, a glycine to valine substitution at the structurally equivalent position, residue 158, of human LRP6 and similar variants of other species' LRP6 homologs represent important research tools.

Site-directed mutants of LRP5 were generated in the full-length human LRP5 cDNA using the QuikChange XL-Site-Directed Mutagenesis Kit (catalog #200516, Stratagene, La Jolla, CA) following the manufacturer's protocol. The mutant sequences were introduced using complementary synthetic oligonucleotides:

Mutation	Complementary oligos
A65V:	5'-TGGTCAGCGGCCTGGAGGATGTGGCCGCAGTGGACTTCC-3' 5'-GGAAGTCCACTGCGGCCACATCCTCCAGGCCGCTGACCA-3'
E128V	5'-AAGCTGTACTGGACGGACTCAGTGACCAACCGCATCGAGG-3' 5'-CCTCGATGCGGTTGGTCACTGAGTCCGTCCAGTACAGCTT-3'
G171K	5'-ATGTACTGGACAGACTGGAAGGAGACGCCCCGGATTGAGCG-3' 5'-CGCTCAATCCGGGGCGTCTCCTTCCAGTCTGTCCAGTACAT-3'
G171F	5'-ATGTACTGGACAGACTGGTTTGAGACGCCCCGGATTGAGCG-3' 5'-CGCTCAATCCGGGGCGTCTCAAACCAGTCTGTCCAGTACAT-3'
G171I	5'-ATGTACTGGACAGACTGGATTGAGACGCCCCGGATTGAGCG-3' 5'-CGCTCAATCCGGGGCGTCTCAATCCAGTCTGTCCAGTACAT-3'

Mutation	Complementary oligos
G171Q	5'-ATGTACTGGACAGACTGGCAGGAGACGCCCCGGATTGAGCG-3' 5'-CGCTCAATCCGGGGCGTCTCCTGCCAGTCTGTCCAGTACAT-3'
G199V	5'-CGGACATTTACTGGCCCAATGTACTGACCATCGACCTGGAGG-3' 5'-CCTCCAGGTCGATGGTCAGTACATTGGGCCAGTAAATGTCCG-3'
A214V	5'-AGCTCTACTGGGCTGACGTCAAGCTCAGCTTCATCCACCG-3' 5'-CGGTGGATGAAGCTGAGCTTGACGTCAGCCCAGTAGAGCT-3'
M282V	5'-GAGTGCCCTCTACTCACCCGTGGACATCCAGGTGCTGAGCC-3' 5'-GGCTCAGCACCTGGATGTCCACGGGTGAGTAGAGGGCACTC-3'
G479V	5'-CATGTACTGGACAGACTGGGTAGAGAACCCTAAAATCGAGTGTGC-3' 5'-GCACACTCGATTTTAGGGTTCTCTACCCAGTCTGTCCAGTACATG-3'
G781V	5'-CATCTACTGGACCGAGTGGGTCGGCAAGCCGAGGATCGTGCG-3' 5'-CGCACGATCCTCGGCTTGCCGACCCACTCGGTCCAGTAGATG-3'
Q1087V	5'-GTACTTCACCAACATGGTGGACCGGGCAGCCAAGATCGAACG-3' 5'-CGTTCGATCTTGGCTGCCCGGTCCACCATGTTGGTGAAGTAC-3'
G158V of LRP6	5'-GTACTGGACAGACTGGGTAGAAGTGCCAAAGATAGAACGTGC-3' 5'-GCACGTTCTATCTTTGGCACTTCTACCCAGTCTGTCCAGTAC-3'

All constructs were sequence verified to ensure that only the engineered modification was present in the gene. Once verified, each variant was functionally evaluated in the TCF-luciferase assay in U2OS cells (essentially as described in Example 6. Other functional evaluations could also be performed, such as the *Xenopus* embryo assay (essentially as described in Example 5), or other assays to evaluate Wnt signaling, Dkk modulation, or anabolic bone effect. Binding of these mutants to Dkk, LRP-interacting proteins, Dkk-interacting proteins, or peptide aptamers to any of the preceding could also be investigated in a variety of ways such as in a two-hybrid system (such as in yeast as described in this application), or other methods.

Figure 29 shows the effects of the G171F mutation in propeller 1 of LRP5. This mutation is at the same position as HBM's G171V substitution. Expression of G171F results in an HBM effect. That is, in the presence of Wnt, G171F is able to activate the TCF-luciferase reporter construct. In fact, it may activate the reporter to a greater extent than either LRP5 or HBM. Furthermore, in the presence of Dkk1 and Wnt1, G171F is less susceptible than LRP5 to modulation by Dkk. These data exemplify that the G171F variant

modulates Wnt signaling in a manner similar to HBM. In addition, this data confirms that HBM's valine residue at 171 is not the only modification at 171 that can result in an HBM effect. Together these data support an important role for LRP5 propeller 1 in modulating Wnt pathway activity; in responding to Dkk modulation; and, in the ability to generate an HBM effect.

Figure 30 shows the effects of the M282V mutation in propeller 1 of LRP5. M282 expression results in an HBM-effect. That is, in the presence of Wnt, M282 is able to activate the TCF-luciferase reporter construct. Furthermore, in the presence of Dkk1 and Wnt1, M282V is less susceptible than LRP5 to modulation by Dkk. These data show that the M282V variant modulates Wnt signaling in a manner similar to HBM. In addition, this data confirms that modifications of other residues in propeller 1 of LRP5 can result in an HBM effect.

These data support an "occupied space" model of the HBM mutation in propeller 1 and show that multiple mutations of propeller 1 are capable of generating an HBM effect; the original G171V HBM mutation is not unique in this ability. Moreover, various perturbations in propeller 1 can modulate Dkk activity.

These data illustrate the molecular mechanism of Dkk modulation of LRP signaling. Using the methods disclosed herein and in U.S. Application 60/290,071, generation of a comprehensive mutant panel will reveal residues in LRP that function in Dkk modulation of Wnt signaling. Such variants of LRP5 and LRP6 that modulate Dkk activity and the residues which distinguish them from LRP5 and LRP6 are points for therapeutic intervention by small molecule compound, antibody, peptide aptamer, or other agents. Furthermore, models of each HBM-effect mutation/polymorphism may be used in rational drug design of an HBM mimetic agent.

These and the examples provided *infra* are only a few illustrative examples presented to better describe the present invention. Variants of LRP5 which have demonstrated HBM activity in assays include A65V, G171I, G171V (HBM), G171F, M282V, G171K, G171Q and A214V. Clearly, other variants may be contemplated within the scope of the present invention. Furthermore, wherever HBM is recited in the methods of the invention, it should be understood that any such alternative variant of LRP5 or LRP6 which demonstrates HBM

like biological activity is also encompassed by those claims.

Additional mutations may also result in conformational changes such as those described above and in the Examples below. These mutations may also result in a HBM-like phenotype when expressed. The following mutations have been identified in Table 2 based on familial genetics in the exons of Zmax1 (LRP5).

TABLE 2: Mutations in the Exons of LRP5

Exon	Location (ATG as nt 1)	Reference	Change	Met as AA1	AA Change
2	249	CGAGGAGGCCATC	C/T	S83	None
2	266	AGACCTACCT	A/G	Q89	G→R
3	512	GTGAGACGCC	G/T	G171	G→V
6	1199	CGTACCTGGACGGG	C/T	A400	A→V
8	1647	CGGGTTCACGCTGC	C/T	F549	None
9	1932	GGCCTTCTTGGTCT	G/A	E644	None
9	1999	GTGGCCATCCCGCT	G/A	V667	V→M
10	2220	CAGAATCGAAGTG	C/T	N740	None
14	3107	GGACACTGTT	G/A	R1036	R→Q
15	3297	CGGCACCGAGCG	C/T	D1099	None
15	3357	AGACAACACACTG	A/G	V1119	None
16	3564	GACTCGCATC	G/A	R1188	None
18	3989	CGGACTGTGA	C/T	A1330	A→V
20	4137	CAGCCCGGCCCAC	C/T	D1379	None
20	4248	GGGGGCCAACGG	G/A	A1416	None
20	4565	CGGCCACTGC	C/T	P1522	P→L
23	4635	CGACGTGTGTGACA	C/T	T1545	None

By, for example "C/T" is meant there is a C to T mutation.

Additional mutations have also been identified in the introns, which may result in splice variants are provided in Table 3 below.

TABLE 3: Mutations in the Introns of LRP5

Exon	Nucleotide Position with respect to Exon	Sequence with SNP Location Underlined	Nucleotide
2	+53	CTCTCTCTCGAATT	C/T
5	-4	TCAGTCCACACTCG	T/C
5	+8	GGGCGGGGGCTGGG	G/A
7	-50	GCAGAGACCAGAC	G/A
8	-118	TGCTCTTGGGCATT	T/G
9	-131	TGGGGGTGAGTCCT	T/C
10	+6	TGTTTGCCTGTCCC	T/C
11	-173	ATGTGTGTGGCAG	A/G
11	-152	GGTCTCGCCCTTC	G/A
11	-49	CGGTGAGAGCAGAC	C/T
11	+37	CGGGGCAGCCGGG	C/T
11	+78	GTACCCTGTGGCCT	G/A
12	+80	CTCATCTGGGGTTC	C/G
12	+141	ATGATGCTACCTGG	A/G
15	-166	CGGGAATTTGGAGA	C/T
15	-149	TTGTTCAACTAGTA	T/C
15	-52	TCCGAGGAGACGC	T/G
17	-213	TTGTTTCCGGCATC	T/C
17	-82	CATTTGGCCCCTA	C/T
18	-72	GCCCAGTCAC	G/A
18	-63	CGCCATTGCC	C/T
18	-30	GTGTGATGTT	G/A
18	+23	TGATCTGGAGGAGG	T/C
18	+47	GTCTGGGCAGCTTT	G/C
18	+54	CACCGTCAGTGCT	C/A

Exon	Nucleotide Position with respect to Exon	Sequence with SNP Location Underlined	Nucleotide
22	-118	GGCACCTGCC	G/A

These splice variants may also produce an altered phenotype capable of conferring a HBM-like effect.

These mutations were identified using 80 ng of genomic DNA, which was PCR amplified with the primers indicated in Table 4 below with M13F (TGTAAAACGACGGCCAGT) attached to the 5' end of the Forward primer or M13R (AGGAAACAGCTATGACCAT) attached to the 5' end of the Reverse primer. 4 μl of the PCR reaction was diluted to a final volume of 100 μl with water. Sequencing was performed using ET and M13F and M13R primers or by the ABI-PRISM® Big-Dye™ method of Applied Biosystems using the indicated nested sequencing primers. The sequences are assembled on consed with the appropriate reference sequence.

The PCR mixes used are as follows

Promega:	50 mM KCl, 10 mM Tris-HCl, pH 9.0, 0.1% Triton X-100, 1.5 mM $MgCl_2$
Invitrogen D:	60 mM Tris-HCl, pH 8.5, 15 mM $(NH_4)_2SO_4$, 3.5 mM $MgCl_2$
Invitrogen J:	60 mM Tris-HCL, pH 9.5, 15 mM $(NH_4)_2SO_4$, 2.0 mM $MgCl_2$
InvitrogenM:	60 mM Tris-HCl, pH 10.0, 15 mM $(NH_4)_2SO_4$, 1.5 mM $MgCl_2$

To all the PCT mixes, 120 μM of all 4 dNTPs was added, 0.4 μM of the forward and reverse primers, 80 ng genomic DNA, 1 U of AmpliTaq® DNA polymerase, and 1.1 U of TaqStart antibody (Clontech). The PCR reaction is than run as follows: 94°C, 2 min; (94°C, 30 sec; X-anneal-temp, 30 sec; 72°C, 2 min) for 35 cycles and 72°C for 3 min.

TABLE 4: Forward and Reverse Primers

Exon	F-primer(PCR)	R-primer(PCR)	anneal temp	Prod. Size	PCR buffer	F-primer(seq)	R-primer(seq)
1	GAGACGCGGCGCGGCTTC	CGCCCCAACTCGCTCCCAAC	2-cycle-68	429	dmso	TCCCGCGCGCCCAGCTC	TCGCCAAGTCGCTTCCG
2	AAGGAACTGGAGGTCTTG	CAGAGTCACACCCTTTTTC	62	670	promega	GGCATGGGCAGGGCAGT	TGAAAAACAACTTGGGCTC
3	CCAAGTTCTGAGAAGTCC	AATACCTGAAACCATACCTG	58	523	promega	TGCATTCCTCAGGGCCC	TTGGTTATTTCCGATGGG
4	GGCGTAGTGGTGGGCATCAG	CCCAGCCAGCCACACACCTC	62	680	dmso	ACTGTCGGGGGACCCTC	ATTGCAGCAGGTACCCC
5	GGGAAATTGCAGGCCGTCTG	CTGAGGACCAAGGCGGAGAG	58	633	promega	AGGCTGAGGGCCCCATG	CAGGATTGACCTCCTGG
6	CACCTAACATCACCAGCC	GATGCAAGACAGTGTCCC	62	672	promega	CCTGGCTGAGTATTTCC	TCAATCTCCCTCTCGCC
7	ACACCGACATTTACGAGCAC	AAATAGCAGAGCACAGGCAC	58	484	promega+10% dmso	CGACATTTACTGACACCA	CCATCGGTGCCTCGCCA
8	TCTCAAACAAACAAACAAACAAAAA	TCCTTGGCCAGATACTGTCAC	60	638	promega	ACAAACAAACAAAGCGTCA	CTTTCCTGTCCTGCCCT
9	TGTGTGGCGGGAATAAAG	TTGAGGCAGGAACAGAGG	60	648	promega	CTGTGCACATTGGAGCT	CAAGGTTTTCCCATAAAGG
10	ATGTCTACAAAACACGCTG	CTAATCACTGAGGGCCAC	60	744	promega	GTTCTGGCCTGGCGTGG	ACGGACAGCCTGCCACC
11	TCACCTTACGAGTGAGCC	AGCCTCTCCCGACATAAC	60	677	promega	ACTGTGGGAATTCAGGG	TGCAGCAAAGGCACCCA
12-1	GAAAACCAGCAAAAGCCC	TGTCCATCACGAAGTCCAG	60	677	promega	ATGAGGGCGGCCATGTG	GCGGTTCCGGCCGCTAG
12-2	ACAGCGATTATATCTACTGGAC	ATGGAAAGCACTCAGCAC	60	622	promega	AGACTGGAATCTGCACAG	TGTGCTGGCAGTATGAG
13	AGAATGAAATTCCCCATAGCG	AGACAAAAGTCCTGTGGGGTC	52	676	Invitrogen D	TCCCGTGGACCTCCAGC	ACAACGGGGAAACCCAG
14	GAGAGACCCCCACACCAATAC	CAGGTGGAAAGTCTCCCCAG	63	571	promega	TGGGATTTGACTTTCAGG	CCTGTGAGAGGCTGGCA
15	CAGTTGGATTTAGGGCCTACC	CAGCTGTCAGTGTGAGGACAA	60	656	promega	CTCACCCATTGTGGTCG	AACACGCTACACACAAAG
16	AACTGATGGCCTTCATCCC	TCTTAAAACGCTGTTCGTGGT	60	699	promega	GAGCCCAGCCCAGGTGG	GATTTGTTCTGCGGCAAAAG
17	AGACTGATGGTATGGGCACAG	ATTTGTGAGATGCAGGAAACG	60	662	promega	TAGAGACTGGTGCAGAC	CAGTACTTAGAGGAAAATTC
18	ATTCTCCCAGCCTCTCTTCTG	GCAGGAAGGTGAGATAGACCC	58	722	promega	GGTTGGGGCTGGAGGTG	TCACAGTCTGCCTTCAAG
19	GGGGTCTGTTACTCCTTGCAT	CAGCTCACAGTCTGTCCTCCT	60	645	promega	GGCGTAGACCTCCCCAC	CCGCTGCCCTGGGAAAG
20	ACGTTACCCTGAGGTTGGC	AGGCCTCTGTGTTGAAGGATT	60	640	promega	AGGCTCCCCAGGCCTAG	CTGATGCCAAGCACAGG
21	TTGGAGGAGGTACCATGTGTC	GGTGGATTTGGGTGAGATTTT	55	643	Invitrogen J	TCCCGTTTCACAGATGAG	CAGATTATCCACAATCAAC
22	TTCTGCTGATTTCTGAACCC	TTGCCTTTCACTGAGATGAC	58	558	promega+10%dmso	AACATGCAGTGCCCGCT	CTTCGGGGCAGGTGGCT
23	GGCCTGCATCTTCTGGAGC	CATTCCCTCCACGGGGAC	62	683	promega	TGGCCAGTGGACAGGCC	ACACAACTCAAATGCACAC

4. Genotyping of Microsatellite Markers

To narrow the genetic interval to a region smaller than that originally reported by Johnson *et al.*, 1997 *Am. J. Hum. Genet.*, 60:1326-1332, additional microsatellite markers on chromosome 11q12-13 were typed. The new markers included: D11S4191, D11S1883, D11S1785, D11S4113, D11S4136, D11S4139, (Dib *et al.*, 1996 *Nature*, 380:152-154), FGF3 (Polymeropolous *et al.*, 1990 *Nucl. Acid Res.*, 18: 7468), as well as GTC_HBM_Marker_1, GTC_HBM_Marker_2, GTC_HBM_Marker_3, GTC_HBM_Marker_4, GTC_HBM_Marker_5, GTC_HBM_Marker_6, and GTC_HBM_Marker_7 (*See* Fig. 2).

Blood (20 ml) was drawn into lavender cap (EDTA containing) tubes by a certified phlebotomist. The blood was stored refrigerated until DNA extraction. DNA has been extracted from blood stored for up to 7 days in the refrigerator without reduction in the quality or quantity of yield. For those subjects that have blood drawn at distant sites, a shipping protocol was successfully used on more than a dozen occasions. Blood samples were shipped by overnight express in a styrofoam container with freezer packs to provide cooling. Lavender cap tubes were placed on individual plastic shipping tubes and then into "zip-lock" biohazard bags. When the samples arrived the next day, they were immediately processed to extract DNA.

The DNA extraction procedure used a kit purchased from Gentra Systems, Inc. (Minneapolis, Minnesota). Briefly, the procedure involved adding 3 volumes of a red blood cell lysis buffer to the whole blood. After incubations for 10 minutes at room temperature, the solution was centrifuged in a Beckman tabletop centrifuge at 2,000 X g for 10 minutes. The white blood cell pellet was resuspended in Cell Lysis Buffer. Once the pellet was completely resuspended and free of cell clumps, the solution was digested with RNase A for 15 minutes at 37°C. Proteins were precipitated by addition of the provided Protein Precipitation Solution and removed by centrifugation. The DNA was precipitated out of the supernatant by addition of isopropanol. This method was simple and fast, requiring only 1-2 hours, and allowed for the processing of dozens of samples simultaneously. The yield of DNA was routinely >8 mg for a 20 ml sample of whole blood and had a MW of >50 kb. DNA was archived by storing coded 50 µg aliquots at -80°C as an ethanol precipitate.

DNA was genotyped using one fluorescently labeled oligonucleotide primer and one

unlabeled oligonucleotide primer. Labeled and unlabeled oligonucleotides were obtained from Integrated DNA Technologies, Inc. (Coralville, Iowa). All other reagents for microsatellite genotyping were purchased from Perkin Elmer-Applied Biosystems, Inc. ("PE-ABI") (Norwalk, Connecticut). Individual PCR reactions were performed for each marker, as described by PE-ABI using AmpliTaq™ DNA Polymerase. The reactions were added to 3.5 µl of loading buffer containing deionized formamide, blue dextran and TAMRA 350 size standards (PE-ABI). After heating at 95°C for 5 minutes to denature the DNA, the samples were loaded and electrophoresed as described in the operator's manual for the Model 377 DNA Sequencer (PE-ABI, Foster City, California). After gel electrophoresis, the data was analyzed using PE-ABI GENESCAN™ and GENOTYPER™ software. First, within the GENESCAN™ software, the lane tracking was manually optimized prior to the first step of analysis. After the gel lane data was extracted, the standard curve profiles of each lane were examined and verified for linearity and size calling. Lanes, which had problems with either of these parameters, were re-tracked and verified. Once all lanes were tracked and the size standards were correctly identified, the data were imported into GENOTYPER™ for allele identification To expedite allele calling (binning), the program Linkage Designer from the Internet web-site of Dr. Guy Van Camp (http://alt.www.uia.ac.be/u/dnalab/ld.html) was used. This program greatly facilitates the importing of data generated by GENOTYPER™ into the pedigree drawing program Cyrillic (Version 2.0, Cherwell Scientific Publishing Limited, Oxford, Great Britain) and subsequent linkage analysis using the program LINKAGE (Lathrop *et al.*, 1985 *Am. J. Hum. Genet.* 37: 482-98).

5. **Linkage Analysis**

Fig. 1 demonstrates the pedigree of the individuals used in the genetic linkage studies for this invention. Specifically, two-point linkage analysis was performed using the MLINK and LINKMAP components of the program LINKAGE (Lathrop *et al.*, 1985 *Am. J. Hum. Genet.*, 37: 482-98). Pedigree/marker data was exported from Cyrillic as a pre-file into the Makeped program and converted into a suitable ped-file for linkage analysis.

The original linkage analysis was performed using three models: (i) an autosomal dominant, fully penetrant model, (ii) an autosomal dominant model with reduced penetrance,

and (iii) a quantitative trait model. The HBM locus was mapped to chromosome 11q12-13 by analyzing DNA for linked markers from 22 members of a large, extended kindred. A highly automated technology was used with a panel of 345 fluorescent markers which spanned the 22 autosomes at a spacing interval ranging from 6-22 cM. Only markers from this region of chromosome 11 showed evidence of linkage (LOD score ~3.0). The highest LOD score (5.74) obtained by two-point and multipoint analysis was D11S987 (map position 55 in Fig. 2). The 95% confidence interval placed the HBM locus between markers D11S905 and D11S937 (map position 41-71 in Fig. 2). Haplotype analysis also places the *Zmax1* (*LRP5*) gene in this same region. Further descriptions of the markers D11S987, D11S905, and D11S937 can be found in Gyapay *et al.*, 1994 *Nature Genetics*, Vol. 7.

In this invention, the inventors report the narrowing of the HBM interval to the region between markers D11S987 and GTC_HBM_Marker_5. These two markers lie between the delimiting markers from the original analysis (D11S905 and D11S937) and are approximately 3 cM from one another. The narrowing of the interval was accomplished using genotypic data from the markers D11S4191, D11S1883, D11S1785, D11S4113, D11S4136, D11S4139, (Dib *et al.*, 1996 *Nature* 380: 152-4), FGF3 (Polymeropolous *et al.*, 1990 *Nucl. Acid Res.*, 18: 7468) (information about the genetic markers can be found at the Internet site of the Genome Database, http://gdbwww.gdb.org/), as well as the markers GTC_HBM_Marker_1, GTC_HBM_Marker_2, GTC_HBM_Marker_3, GTC_HBM_Marker_4, GTC_HBM_Marker_5, GTC_HBM_Marker_6, and GTC_HBM_Marker_7.

As shown in Fig. 1, haplotype analysis with the above genetic markers identifies recombination events (crossovers) in individuals 9019 and 9020 that significantly refine the interval of chromosome 11 to which the *Zmax1* (*LRP5*) gene is localized. Individual 9019 is an HBM-affected individual that inherits a portion of chromosome 11 from the maternal chromosome with the *HBM* gene, and a portion from the chromosome 11 homologue. The portion inherited from the *HBM* gene-carrying chromosome includes markers D11S935, D11S1313, GTC_HBM_Marker_4, D11S987, D11S1296, GTC_HBM_Marker_6, GTC_HBM_Marker_2, D11S970, GTC_HBM_Marker_3, D11S4113, GTC_HBM_Marker_1, GTC_HBM_Marker_7 and GTC_HBM_Marker_5. The portion

from D11S4136 and continuing in the telomeric direction is derived from the non-HBM chromosome. This data places the *Zmax1* (*LRP5*) gene in a location centromeric to the marker GTC_HBM_Marker_5. Individual 9020 is an unaffected individual who also exhibits a critical recombination event. This individual inherits a recombinant paternal chromosome 11 that includes markers D11S935, D11S1313, GTC_HBM_Marker_4, D11S987, D11S1296 and GTC_HBM_Marker_6 from her father's (individual 0115) chromosome 11 homologue that carries the *HBM* gene, and markers GTC_HBM_Marker_2, D11S970, GTC_HBM_Marker_3, GTC_HBM_Marker_1, GTC_HBM_Marker_7, GTC_HBM_Marker_5, D11S4136, D11S4139, D11S1314, and D11S937 from her father's chromosome 11 that does not carry the *HBM* gene. Marker D11S4113 is uninformative due to its homozygous nature in individual 0115. This recombination event places the centromeric boundary of the HBM region between markers D11S1296 and D11S987.

Two-point linkage analysis was also used to confirm the location of the *Zmax1* (*LRP5*) gene on chromosome 11. The linkage results for two point linkage analysis under a model of full penetrance are presented in Table 5 below. This table lists the genetic markers in the first column and the recombination fractions across the top of the table. Each cell of the column shows the LOD score for an individual marker tested for linkage to the *Zmax1* (*LRP5*) gene at the recombination fraction shown in the first row. For example, the peak LOD score of 7.66 occurs at marker D11S970, which is within the interval defined by haplotype analysis.

TABLE 5

Marker	0.0	0.05	0.1	0.15	0.2	0.25	0.3	0.35	0.4
D11S935	- infinity	0.39	0.49	0.47	0.41	0.33	0.25	0.17	0.10
D11S1313	- infinity	2.64	2.86	2.80	2.59	2.30	1.93	1.49	1.00
D11S987	- infinity	5.49	5.18	4.70	4.13	3.49	2.79	2.03	1.26
D11S4113	4.35	3.99	3.62	3.24	2.83	2.40	1.94	1.46	0.97
D11S1337	2.29	2.06	1.81	1.55	1.27	0.99	0.70	0.42	0.18
D11S970	7.66	6.99	6.29	5.56	4.79	3.99	3.15	2.30	1.44
D11S4136	6.34	5.79	5.22	4.61	3.98	3.30	2.59	1.85	1.11
D11S4139	6.80	6.28	5.73	5.13	4.50	3.84	3.13	2.38	1.59
FGF3	0.59	3.23	3.15	2.91	2.61	2.25	1.84	1.40	0.92
D11S1314	6.96	6.49	5.94	5.34	4.69	4.01	3.27	2.49	1.67
D11S937	-infinity	4.98	4.86	4.52	4.06	3.51	2.88	2.20	1.47

A single nucleotide polymorphism (SNP) further defines the HBM region. This SNP is termed SNP_Contig033-6 and is located 25 kb centromeric to the genetic marker GTC_HBM_Marker_5. This SNP is telomeric to the genetic marker GTC_HBM_Marker_7. SNP_Contig033-6 is present in HBM-affected individual 0113. However, the HBM-affected individual 9019, who is the son of 0113, does not carry this SNP. Therefore, this indicates that the crossover is centromeric to this SNP. The primer sequence for the genetic markers GTC_HBM_Marker_5 and GTC_HBM_Marker_7 is shown in Table 6 below.

TABLE 6

Marker	Primer (Forward)	Primer (Reverse)
GTC_HBM_ Marker_5	TTTTGGGTACACAATTCAGTCG (SEQ ID NO:63)	AAAACTGTGGGTGCTTCTGG (SEQ ID NO:65)
GTC_HBM_ Marker_7	GTGATTGAGCCAATCCTGAGA (SEQ ID NO:64)	TGAGCCAAATAAACCCCTTCT (SEQ ID NO:66)

The kindred described have several features of great interest, notably that their bones, while very dense, have an absolutely normal shape. The outer dimensions of the skeletons of

the HBM-affected individuals are normal, and, while medullary cavities are present, there is no interference with hematopoiesis. The HBM-affected members seem to be resistant to fracture, and there are no neurologic symptoms, and no symptoms of impairment of any organ or system function in the members examined. HBM-affected members of the kindred live to advanced age without undue illness or disability. Furthermore, the HBM phenotype matches no other bone disorders such as osteoporosis, osteoporosis pseudoglioma, Engelmann's disease, Ribbing's disease, hyperphosphatasemia, Van Buchem's disease, melorheostosis, osteopetrosis, pycnodysostosis, sclerostenosis, osteopoikilosis, acromegaly, Paget's disease, fibrous dysplasia, tubular stenosis, osteogenesis imperfecta, hypoparathyroidism, pseudohypoparathyroidism, pseudopseudohypoparathyroidism, primary and secondary hyperparathyroidism and associated syndromes, hypercalciuria, medullary carcinoma of the thyroid gland, osteomalacia and other diseases. Clearly, the HBM locus in this family has a very powerful and substantial role in regulating bone density, and its identification is an important step in understanding the pathway(s) that regulate bone density and the pathogenesis of diseases such as osteoporosis.

In addition, older individuals carrying the *HBM* gene, and therefore expression of the HBM protein, do not show loss of bone mass characteristic of normal individuals. In other words, the *HBM* gene is a suppressor of osteoporosis. In essence, individuals carrying the *HBM* gene are dosed with the HBM protein, and, as a result, do not develop osteoporosis. This *in vivo* observation is strong evidence that treatment of normal individuals with the *HBM* gene or protein, or a fragment thereof, will ameliorate osteoporosis.

6. <u>Physical Mapping</u>

To provide reagents for the cloning and characterization of the HBM locus, the genetic mapping data described above were used to construct a physical map of the region containing Zmax1 (LRP5) on chromosome 11q13.3. The physical map consists of an ordered set of molecular landmarks, and a set of BAC clones that contain the *Zmax1* (*LRP5*) gene region from chromosome 11q13.3.

Various publicly available mapping resources were utilized to identify existing STS markers (Olson *et al.*, 1989 *Science* 245:1434-5) in the HBM region. Resources included the

GDB, the Whitehead Institute Genome Center, dbSTS and dbEST (NCBI), 11db, the University of Texas Southwestern GESTEC, the Stanford Human Genome Center, and several literature references (Courseaux *et al.*, 1997 *Genomics* 40: 13-23; Courseaux *et al.*, 1996 *Genomics* 37: 354-65; Guru *et al.*, 1997 *Genomics* 42: 436-45; Hosoda *et al.*, 1997 *Genes Cells* 2: 345-57; James *et al.*, 1994 *Nat. Genet.* 8: 70-76; Kitamura *et al.*, 1997 *DNA Research*, 4: 281-9; Lemmens *et al.*, 1997 *Genomics* 44: 94-100; and Smith *et al.*, 1997 *Genome Res.* 7: 835-42). Maps were integrated manually to identify markers mapping to the region containing Zmax1 (LRP5).

Primers for existing STSs were obtained from the GDB or literature references are listed in Table 6 below. Thus, Table 7 shows the STS markers used to prepare the physical map of the *Zmax1* (*LRP5*) gene region.

TABLE 7: HBM STS Table

STS Name	Locus Name	Type	GDB Access. #	Size (kb)	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	Gene Name
ACTN3		Gene	GDB:197568	0.164	67: CTGGACTACGTGGCCTTCTC	68: TTCAGAAGCACTTGGCTGG	Actinin, alpha 3 - skeletal muscle
PC-B/PC-Y		Gene	GDB:197884	0.125	69: CTCAGTGCCATGAAGATGGA	70: CAAGATCACTCGATCTCCAGG	Pyruvate Carboxylase
	D11S2161E	Gene		0.322	71: GTTTCAGGAGACTCAGAGTC	72: TTCTGCAGGTTGCTGTTGAG	Adenosine Receptor (A2) Gene
ADRBK1		Gene	GDB:4590179	0.117	73: TTATTGTGATTTCCCGTGGC	74: GCCCTCTGTCCTGACTTCAGG	Beta-adrenergic receptor kinase
PSANK3		GENE		0.259	75: GAGAAAGAAATAAGGGGACC	76: TGCTTTGTAAAGCACTGAGA	sim. to Human endogenous retrovirus mRNA long terminal repeat
PP1(1/2)/PP1(2/2)		Gene	GDB:197566	0.208	77:GAAGTACGGGCAGTTCAGTGGCCT	78: ATACACCAAGGTCCATGTTCCCCGT	Protein phosphatase 1, catalytic subunit, alpha isoform
GSTP1.PCR1		Gene	GDB:270066	0.19	79:AGCCTGGGCCACAGCGTGAGACTACGT	80: TCCCGGAGCTTGCACACCCGCTTCACA	Glutathione S-transferase pi
NDUFV1		Gene		0.521	81:CATGTGCCCACCTCATTCAT	82: CAAGATTCTGTAGCTTCTGG	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD)
PSANK2		GENE		0.157	83: CAGAGAAGTCAAGGGACTTG	84: ATCCTCTCACATCCCACACT	Aldehyde Dehydrogenase 8 (ALDH8)
PSANK1		EST		0.3	85: CAAGGCTAAAAGACGAAAAA	86: TCAGGAGCATTTCATCTTTT	Human ribosomal protein L37 (PSANK1) pseudogene.
UT5620	D11S1917	MSAT	GDB:314521	0.211	87: AAGTCGAGGCTGCAAGGAG	88: GCCCTGTGTTCCTTTCAGTA	
AFM289ya9	D11S1337	MSAT	GDB:199805	0.287	89: AAGGTGTGAGGATCACTGG	90: AGCTCATGGGGGCTATT	
GALN		Gene		0.322	91: GCTTCTCCGAGTGTATCAAC	92: ATGGCAGAGGACTTAGAACA	Preprogalanin (GAL1)
pMS51	D11S97	VNTR	GDB:177850		93: GATCAGCGAACTTCCTCTCGGCTC	94: TCCACATTGAGGACTGTGGGAACG	
BCL1(1)/BCL1(2)		Gene		0.205	95: GCTAATCACAGTCTAACCGA	96: TTGCACTGTCTTGGATGCA	B-cell CLL/lymphoma 1 - Cyclin D1 (PRAD1 gene)
CCND1		Gene	GDB:4590141	0.248	97: GCACAGCTGTAGTGGGGTTCTAGGC	98: CAGGCGCAAAGGACATGCACACGGC	Cyclin D1
FGF4		Gene	GDB:4590113	0.549	99: CACCGATGAGTGCACGTTCAAGGAG	100: CAGACAGAGATGCTCCACGCCATAC	Fibroblast growth factor 4
FGF3.PCR1		Gene	GDB:188627	0.161	101: TTTCTGGGTGTGTCTGAAT	102: ACACAGTTGCTCTAAAGGGT	Fibroblast growth factor 3
AFM164ZF12	D11S913	MSAT	GDB:188151	0.22	103: CATTTGGGAAATCCAGAAGA	104: TAGGTGTCTTATTTTTTGTTGCTTC	
AFMA190YD5		MSAT	GDB:1222329	0.275	105: GACATACCATGAACACTATAAGAGG	106: CAACCCATACCAGGGATAAG	
SHGC-15295	D11S4689	STS	GDB:740600	0.147	107: GAACAAGAGGGGTAAGTTGGC	108: TGAGGACACAGATACTGATGGG	
SHGC-3084	D11S4540	STS	GDB:740102	0.167	109: GAAGTGTTCCCTCTTAAATTCTTTG	110: GAACTATATTGTAGTTAGTGAGGAG	
SHGC-14407	D11S4664	STS	GDB:740516	0.158	111: CCTGTAACCCCCAGTCCC	112: TCTTGCTTCCTAAGTTTCTCGG	
SHGC-10946	D11S4327	Gene	GDB:674522	0.311	113: ACTCCATCCACCTCATCACTG	114: TGCTGTTTGCCTCATCTGAC	Choline Kinase
S515	D11S703	STS	GDB:196290	0.166	115: GTGGACAGGCATAGCTGAGG	116: TGTTCACTCTTCTGCCTGCAG	
AFM147XD10	D11S1889	MSAT	GDB:307895	0.183	117: AGCTGGACTCTCACAGAATG	118: CAAGAGGCTGGTAGAAGGTG	
AFMA131YE5	D11S987	MSAT	GDB:195002	0.082	119: GACTCCAGTCTGGGCAATAAAAGC	120: GGTGGCAGCATGACCTCTAAAG	
AFMb358xa9	D11S4178	MSAT	GDB:611922	0.237	121: CAGGCCCAGTCTCTTG	122: CGTGTCCAGATGAAAGTG	
AFMa272yb5	D11S4113	MSAT	GDB:608115	0.218	123: ACCTCACGGTGTAATCCC	124: CTTGAAGCCCATCTTTGC	
WI-17803		EST	GDB:4581644	0.15	125: TATTTGCAAAGCTTGAGACTTCT	126: AATCACTGTGCTTTGTTGCC	
SGC31923		EST	GDB:4578606	0.126	127: ACTTTATTGTCAGCGTGGGC	128: ACTCCCTCGATGGCTTCC	
WI-7741	D11S4364	GENE	GDB:677652	0.324	129: GAGCAGGGGAGAGAAGGC	130: CCCAACTGGCTTGTTTTATTG	Transformation-sensistive protein IEF SSP 3521
SGC35223		EST	GDB:4582598	0.13	131: AGCCACTTTATTGTTATTTTGATGC	132: AAGAGTGAACAAAAGCAAACATACC	ZNF162 - splicing factor 1
WI-16754		EST	GDB:4578377	0.15	133: GTGGAGTGTGGGATTGGG	134: TACTGTTCTTGATAAGTATGTCGGC	
WI-6315	D11S4418	EST	GDB:678804	0.224	135: ATGCTTTTGCATGATTCTAATTATT	136: TCCCCCAAAAGAATGTAAAGG	
WI-16915		EST	GDB:4584055	0.125	137: CTGGTCTTCCTTGTGTGCTG	138: ATCACCCAGGCCAGGGAT	Mitogen inducible gene (MIG-2)
SGC30608		EST		0.128	139:TCAGAAGCAGAACTGTTTTTAACA	140: CCTGCTTGAAAGTTCTAGAGCC	
WI-17663		EST	GDB:4583346	0.126	141: CAAGCCGGGTTTTATTGAAA	142: GATGCCAGGACCATGGAC	
WI-6383		Gene	GDB:1222237	0.199	143: GCATATAGAAACAATTTATTGCCG	144: CTCTGAAGCAGGGACCAGAG	Human tat interactive protein (TIP60)
SGC31567		Gene	GDB:4578432	0.207	145: CTACCACACCACACCAGGC	146: CAAGCGAAAGCTGCCTTC	Calcium activated neutral protease large subunit, muCANP, calpain
SGC30658		EST	GDB:4584037	0.15	147: GTTGTCTTGACTTCAGGTCTGTC	148: TTTTCCTTCAACAATCACTACTCC	
SGC34590		EST		0.13	149: GCGTGGGGATATAGAGGTCA	150: TACGTGGCCAAGAAGCTAGG	
SGC33927		EST	GDB:4582382	0.15	151: TAATATATCCCCAGTCTAAGGCAT	152: AGCTTGCAGATGGAGCCC	
WI-8671		EST	GDB:1222235	0.124	153: TGGTTTTAAACCTTTAATGAGAAAA	154: TGTTGATCTATACCCTGTTTCCG	
WI-12334		EST	GDB:1222257	0.127	155: AATTATTTAAAAGAGAGGAAAGGCA	156: TGGCTGTGAACTTCCTCTGA	
WI-18402		EST	GDB:4581874	0.113	157: GGTTACAGAAAAACATTTGAGAGAT	158: TGAGCTTTAGTTCCCTTCTCTG	
WI-18671		EST	GDB:4584947	0.131	159: TTGAAAAACCATTTATTTCACCG	160: TCTGCGGCTGTTGGATTT	Hlark
WI-12856		EST	GDB:4576606	0.209	161: TTGAAAAACCATTTATTTCACCG	162: TGTTCTCTTCTCCCAGCAGG	Hlark
SGC33767		EST	GDB:4581106	0.15	163: CTTTATTGAAAACATTGAGTGCA	164: TTGTCAAATTCCCCCCAAAA	
AFM343YB5		MSAT	GDB:1222332	0.181	165: AAACCACGACCNCCAA	166: CCCTGGAAAGGTAAGATGCT	
SGC33744		EST	GDB:4575826	0.15	167: CTTTTGGTAGAGACAAGGTCTCA	168: TATCTGTCTGTAGTGCTTCAAATGT	
SGC32272		EST	GDB:4581592	0.135	169: GACGAAGGTGATTCAGGGC	170: ACTGAAGAACTCTTGTCCT	
SGC34148		EST	GDB:4583084	0.1	171: CAGATAAAAGAGTCACTATGGCTCA	172: CACTTCTCCCACTTTGTCCC	
WI-18546		EST	GDB:4574598	0.133	173: TTATTGATAAGCATTAGTGAACCCC	174: TGGCAAGTTAGGCACAGTCA	Human 1.1 kb mRNA upregulated in retinoic acid treated HL-60 neutrophilic cells
SGC31103		EST	GDB:4567265	0.1	175: CTATGCCCAGAGATGAACAGG	176: TCCACTAAGGGCTATGTCGC	
SGC30028		Gene	GDB:4580505	0.128	177: GCCAGCTTTATTGAGTAAACTTCC	178: CACTGGAGACTACAAGTGGTGG	Human pyruvate carboxylase precursor
WI-2875	D11S4407	STS	GDB:678546	0.125	179: CATCCCAACCATCACTCAGT	180: GGGGACTAGCTTACAGATTTGA	
SGC36985		Gene	GDB:4577182	0.223	181: AGACTACATTTTGGAACCAGTGG	182: TGAAAGGATATTTATAGCCTGGA	LAR-interacting protein 1b
GCT16B07	D11S4270	STS	GDB:626245	0.137	183: GAAGGTTTTGTCCCTCGATC	184: TGAGGGTTGGGAAGATCATA	
WI-6504	D11S3974	EST	GDB:588142	0.174	185: CCTTCATAGCCACACCCG	186: CAGCTAACTGTTGACATGCCA	
SGC31049		EST	GDB:4580093	0.15	187: TCTTTACTGTGCTTACAACTTTCCT	188: CAACAGTGCAGTCGGTATCG	
TIGR-A002J17		EST	GDB:1222193	0.199	189: AGATCAGCAAGCAGATAG	190: CATTCCACATGGATAGAC	NDUFV1
WI-5996	D11S2382	EST	GDB:458683	0.1	191: CATACCTATGAGGTGTGCTACAGG	192: GCATTTTCTCATCATCCTTGC	amplaxin (EMS1)
WI-16987		EST	GDB:4575848	0.15	193: TTACAGCCACCAAGGTTTCC	194: AGGTGTGTGTGCCAGGTTGA	Nuclear mitotic apparatus protein 1, NUMA
SGC31912		EST	GDB:4567868	0.101	195: CACTGTTATCTCATTAACTGTGAGG	196: TTTGATTTTGTGTCTCCCAAA	

TABLE 7: HBM STS Table

STS Name	Locus Name	Type	GDB Access. #	Size (kb)	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	Gene Name
WI-13500		EST	GDB:4577893	0.15	197: CCCCACTCCCACTTTTATTT	198: CCAGTCACCTTTACTAGTCCTTTG	
CHLC.GAAT1B01.P7933	D11S971	MSAT	GDB:684255	0.103	199: AGGACACAGCCTGCATCTAG	200: ACCAGGCATTGCACTAAAAG	
SGC35519		Gene	GDB:4577180	0.134	201: GATGGGTCACACTAACCTGTCA	202: ACATTTATATTTGGACATGCAACC	LAR-interacting protein 1a mRNA
WI-11974		EST	GDB:1222255	0.108	203: AGCATCTTTAATGTGTCAGGCA	204: ATGTGCTGGGCTGGAAAG	Carnitine palmitoyl transferase I
WI-15244		Gene	GDB:4574740	0.108	205: TCACATTCAAAAATCGGCAA	206: CTGCCTGTGTGGTGTCGC	Beta-adrenergic receptor kinase 1, ADRB1
WI-17496		EST	GDB:4583336	0.131	207: TGTTTTATTTCTCAGTACAAAGCCA	208: GACCTCCTGTGACACCACG	
WI-9159	D11S4381	EST	GDB:678144	0.111	209: CCACCAAATTATTTATAGTTCTGCG	210: GTAAGATTCTCCACTGTTGCACC	FGF4
WI-4232		STS	GDB:1222250	0.175	211: CCTATAATGGGCTGGACCAA	212: ACTCCTCATGTGAAGTCACCG	
SHGC-4167		EST	GDB:4566789	0.161	213: CAGTGTGCACGTTTTCATTT	214: CAGCATCTTCAGCACTTACC	Human DNA helicase gen (SMBP2)
WI-14303		EST	GDB:4576938	0.15	215: CTGCATTTATTATGAGAATCAACAG	216: TGCTGCTGGGAGTCAGAGTC	
WI-16597		EST	GDB:4585666	0.13	217: CAGGGCACTGAGATACACTTACC	218: AAGGATCAAGCAGGCATTTG	
RC29S1CATTFOR/RC29S1CATTREV	D11S970	MSAT	GDB:191084	0.15	219: ACACATCTCTTCTGTGCCCC	220: TGAACCCTGGAGGCAGAG	
UT979	D11S1296	MSAT	GDB:198525	0.362	221: CATTCCCCAGTTTGCAGAC	222: GTGCTGGGATTACAGGTGT	
1281/1282	D11S1959E	EST	GDB:335216	0.07	223: GCAGAGAAGTCCTGTTAGCC	224: CCATGCTAGAGAAGCACAAC	
D11S468	D11S468	STS		0.096	225: AGTGTGGGGCAGGACCTCTG	226: CAGACAGATAGCCCTGGGTTC	
D11S668	D11S668	STS	GDB:179349	0.143	227: TCCCTCATCCCCTTGTCTGT	228: AGCCCCCCTGGGGATAATC	
RH18048		Gene	GDB:4572853	0.188	229: GATGCTTACCTACCACGGC	230: AGGATTCCTATCTGGGCTATG	Aldehyde dehydrogenase (ALDH8)
IGHMBP2		Gene	GDB:4590087	0.699	231: TGGCAGACCATGCTCCGCCT	232: GAGAAGGCCGGGAGGCTCTG	Human DNA helicase gen (SMBP2)
NUMA		Gene	GDB:4590244	0.277	233: CTCCATCACAACCAGATTTGAGGCT	234: GGGTGTGAGCTGCTGCTGAAGG	Nuclear mitotic apparatus protein 1, NUMA
KRN1		Gene	GDB:4590232	0.228	235: AGTGGGAAACCTCAGGTAGCTCCCGA	236: CAGTTTGGCTCAGACATATGGGGGCA	High sulphur keratin, KRN
Cda1ff06	D11S2302E	EST	GDB:445887	0.091	237: CATTAAGTAGTGGGGGGACAG	238: CAAAGCGACAGTGAGTTAGGG	
RH10753		Gene	GDB:4563588	0.194	239: GGAGTAGACCATGATTACTG	240: CATGGTCTATTTATTCTCG	protein phosphatase 2A , PP2A
EMS1		Gene	GDB:459016	0.64	241: CGCCCTGGATCCTCACACTACA	242: GGGCATCAGGGGATGGGTAGA	Amplaxin
SHGC-11098	DXS9736	Gene	GDB:737674	0.137	243: GCTCCTATCTGTGTTTTGAATGG	244: CCGTGGCATAAGATAAGTAAACG	Androgen Receptor
INPPL1		Gene	GDB:4590093	0.382	245: CTTGGAGCGCTATGAGGAGGGC	246: ATGGCAACTGACCTTCCGTCCTG	51C protein,inositol polyphosphate phosphatase-like 1
RH18051		EST	GDB:4572859	0.195	247: TTGGAGTCACAGGGGC	248: CAGCACTATCCTTGGGG	NOF1
Cda1cc11	D11S2297E	EST	GDB:445869	0.1	249: AACAAAGCTGCTTAGCACCTG	250: GATGAGGACCAACTGGTGAC	
1249/1250	D11S1957E	EST	GDB:335210	0.247	251: TTTTCCAATAATGTGACTTC	252: CAATCCCAACCGTAACAGGC	
NDUFV1	D11S2245E	EST	GDB:445695		253: CTTGATCTCGCCCAGGAAC	254: GCTCGCTGAAGGATGAAGAC	NDUFV1
AFMb032zg5	D11S4136	MSAT	GDB:609546	0.19	255: GAATCGCTTGAACCCAG	256: CCAGGTGGTCTTAACGG	
AFMa059xg9	D11S4196	MSAT	GDB:614025	0.2	257: GAACGTTNTTCATGTAGGCGT	258: TAATGGTCGCTGTCCC	
Cda17c12	D11S2288E	EST	GDB:445842	0.158	259: AGGGAAAATGGTATGTGGGGAG	260: GCAGTGTGTGAAGGCAGG	
SHGC-1364	D11S951E	EST	GDB:4562765	0.137	261: AGTGGACAAAATGAGGAAAACAGG	262: CCAACACAGTTTGCTCACATGCC	
RH17410		EST	GDB:4571587	0.126	263: TGACATCTTTGCATTATGGC	264: AGTTATCCCACCTGATACCG	
RH17414		EST	GDB:4571595	0.121	265: AGCTCTTGCTTCTCAGTCCA	266: CAAAAGTTGTTTCTGTGTTTGTTC	
RH17770		EST	GDB:4572301	0.267	267:GCCTCTCAAAGTAGTTGGAACC	268: TGTGTATCCATAGTGCAAAACAG	
SEA		EST	GDB:4590169	0.13	269: CTCAAGGCCAGGCATCACT	270: GGACTCTTCCATGCCAGTG	S13 avian erythroblastosis oncogene homolog
RH10689		EST	GDB:4563460	0.107	271: AATGATGATCTCAACTCTG	272: ACTGAAGAACTCTTGTCCT	
TIGR-A006P20		EST	GDB:4587692	0.236	273: GACATCTGTTAGTCTCATAATTC	274: GGTAACAGTGTCTTGCTT	
TIGR-A007D15		Gene	GDB:4588398	0.24	275: CTATGTACAAAACAGGAAGAG	276: ATCCTAGTTTCCTCTCCTT	Menin gene (MEN1)
TIGR-A008B14		EST	GDB:4588882	0.141	277: GTAAATGAGAAACAGACAAATGA	278: CTATTGGATGTGATATGTTATGG	
TIGR-A008K11		EST	GDB:4589094	0.203	279: AAGTAGAAACAAAATGAGGGAC	280: CCTACCCCAAGGTAACAG	
TIGR-A008P15		EST	GDB:4589662	0.182	281: ACTTCCTATAAATGGAGGTGAG	282: GAGGAGCTTCAAGAGGAA	
TIGR-A008T11		EST	GDB:4589278	0.138	283: CATACTCCTAGACTCAAGGAATC	284: GAATGATGTACATGAATTCTTTG	
TIGR-A008U48		EST	GDB:4589364	0.107	285: GTGTTGAGGAGAAAAGCACT	286: CTCCCAGTAGTCACATTCC	
TIGR-A008X45		EST	GDB:4589838	0.242	287: CAAGTTACAAATAACTTAAGCCG	288: CAAGACCCTATCTCTACAAAAAC	
SHGC-11839	D11S4611	Gene	GDB:740339	0.151	289: TTTATTAGAAGTGACTCTTGGCCC	290: GACTACCTGCCCTCAGCTTG	Folate receptor 2 (FBP2)
NIB1242	D11S4929E	EST	GDB:3888276	0.149	291: TTCTCATGTACAAAGCGGTC	292: CCACTGGCTTCTCTCTTTTT	cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A)
SHGC-13599	D22S1553	Gene	GDB:737558	0.147	293: CACCAGAAGGTTGGGGTG	294: ACTATTACGACATGAACGCGG	Macrophage Migration Inhibitory factor
SHGC-11867	D11S4331	Gene	GDB:674684	0.14	295: CTCATGCTGGATGACCCC	296: TTGCCTTTCTTGAAACTTAATTCC	P2U Purinoceptor
SHGC-15349	D12S2124	EST	GDB:740819	0.141	297: TCACAGCCTTCAGTCAGGG	298: ACATGCTGTGGCACCATG	
Bda84a05	D11S2235E	EST	GDB:445662	0.095	299: CCTGAGCTACTGCCACAG	300: CCCTGACTTGGACAGTGTCC	
Bda99d07	D11S2238E	EST	GDB:445674	0.09	301: TCAGAGTCACTCCTGCCC	302: CAAATTCAAGCTCATCCAGACC	
folr1		Gene	GDB:197840	0.3	303: CGGCATTTCATCCAGGAC	304: GGTGTAGGAGGTGCGACAAT	Folate receptor2 (FBP2)
NIB1738	D11S4284	EST	GDB:626260	0.173	305: TTCCATTTATTGAGCACCTG	306: CTTAAGCCACTGTGTTTTGG	
WI-7351	D11S4433	Gene	GDB:679143	0.324	307: CCTCCTACACCTGCAAAAGC	308: TGGAAGAACCCCAGAGGAC	Folate receptor3 (FBP3)
WI-14325		EST	GDB:4578507	0.132	309: AAAGCACAAAAGTAACAGCAACA	310: GTGTGTGGGCCACAATATTG	
WI-15192		EST	GDB:4575806	0.15	311: AGAGCACCTTTCCTCAGCAC	312: AGAATCTCATCACAGGGGCG	
WI-17872		EST	GDB:4577492	0.141	313: AAAAAGGACAGTGTCTAAAATTTGA	314: AATTGTTTTTGTTTGTTTTTTGAGT	
SHGC-30732		EST	GDB:4567830	0.105	315: GATTTAGGGAGTACAAGTGCGG	316: GGGGACAAATTATACTTTATTCAGG	
stSG4288		EST	GDB:4566057	0.123	317: CCATCATCATATTGGTGTGACC	318: TGGCTGCCCAAGAAGAAG	
WI-13814		EST	GDB:4579290	0.15	319: TTAAGATGCCATTAAACTCATGAC	320: CCAAGGAGATGACCAAGTGG	(DRES9
WI-14122		Gene	GDB:4576114	0.126	321: CCATCTCTTTTATCAGGGTTGG	322: CTCTGTGCAAGTAAGCATCTTACA	Human VEGF related factor isoform VRF186 precursor (VRF)
2729/2730	D11S4057	EST	GDB:596509	0.118	323: CGACTGTGTATTTTCCACAG	324: AGAAGCCCATATCAATGCAC	
SHGC-31329		EST	GDB:4567386	0.15	325: AGCTTAAAGTAGGACAACCATGG	326: GGATGCTTCACTCCAGAAAG	

TABLE 7: HBM STS Table

STS Name	Locus Name	Type	GDB Access. #	Size (kb)	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	Gene Name
SGC33858		EST	GDB:4578600	0.127	327: TGTTGTTTATTTCCACCTGCC	328: AGAGTGGCTGCAGGCCAG	
WI-12191		EST	GDB:1222208	0.15	329: TTTTTTTTTTTACACGAATTTGAGG	330: TGAGGAAGTAAAAACAGGTCATC	
WI-13701		EST	GDB:4574892	0.15	331: ATGAAATCTTAAGCAGAATCCCA	332: CACAGAGTCCCAGGGTCTGT	
WI-14069		EST	GDB:4584373	0.15	333: AAAGGCCTTTATTTATCTCTCTCTG	334: GCCTCAGAGCTGGTGGGT	
WI-14272		EST	GDB:4578525	0.125	335: GCTTCTAAGTCTTAGAGTCAGCTGG	336: AGCCCACAGTCAGCCTACC	
WI-17347		EST	GDB:4578523	0.127	337: TTGGTTAAATGATGCCCAGA	338: TGGTCCCACTCACATCCC	
stSG1561		EST	GDB:4564415	0.215	339: ACACAGCATGCAGGGAGAG	340: ATCCCTGGTGCTTAGGTGG	
stSG1938		EST	GDB:4564568	0.137	341: GATGGAAGTAGCTCCTCTCGG	342: GGAAGGCCAGCAAGTACTACC	
stSG2759		EST	GDB:4565137	0.141	343: CCGGTGCTTGGAAAGATG	344: GAAGTGTCTCTGTTGGGGGA	
RH97		EST	GDB:4559690	0.17	345: TTACAGGCATGAGTCACTACGC	346: ACCACTCTCACAGCCCTTACA	
stSG4794		EST	GDB:4573113	0.141	347: CCCTCCCTCCACACACAC	348: GCTCACTGAACTTTCAGGGC	
stSG4957		EST	GDB:4569051	0.171	349: AGATACGGGCAAAACACTGG	350: GTTGAATATAGAGCAGGGCCC	
stSG4974		EST	GDB:4569063	0.166	351: TTCTGAGGTCAGGGCTGTCT	352: AGCTTGGAAAATCTCGTGTCA	
stSG8144		EST	GDB:4573137	0.17	353: ACTCAGTCCCTCCCACCC	354: TCCTCTCACTCCTTCCCAGA	
stSG9275		EST	GDB:4569999	0.19	355: GTGATCACGGCTCAACCTG	356: TGGAGGACTGCTTGAGCC	
SHGC-10667	D11S4583	Gene	GDB:740246	0.277	357: CTGCAGCTGCCTCAGTTTC	358: TCAAAAGTGCTGGTGACAGC	Human protein kinase (MLK-3)
SHGC-11930		Gene	GDB:1231223	0.21	359: ATTTCCAGAGCCAGCTCAAA	360: CTTTAATGTTGTGATGACACAAAGC	FGF3
SHGC-32786		EST	GDB:4567878	0.125	361: GATCATGCACTGTTGACCAC	362: TACATTTGAAACATTTAAAACCTGA	
FKBP2		Gene		0.064	363: AACTGAGCTGTAACCAGACTGGGA	364: TGGAACAGTCTGGTCCTGATGG	FK506-Binding Protein Precursor (FKBP-13)
WI-13116		EST	GDB:4585099	0.202	365: TTATCCCTTTATTGTTTCTCCTTTG	366: TGGTCACCTGTATTTATTGCTAGG	
MDU1		Gene	GDB:4590064	0.859	367: TCTTCAAAGCCTCTGCAGTACC	368: CTCATCTCCAACCTGTCTAACC	4F2 CellL-Surface Antigen Heavy Chain (4F2HC)
S453	D11S579	STS	GDB:196276	0.108	369: GTGGCTGCAGCTAATGTAAGACAC	370: CAGCAGAGACAATGGCGTAAGTCC	
STS1-cSRL-112e11	D11S3866	STS	GDB:547681	0.135	371: CTGATTGAGAACCAGAACAG	372: TAAAGCCCTATAACCTCTCC	
STS1-cSRL-44a3	D11S3830	STS	GTC:547609	0.118	373: TAGTAAGGGACCTTCACCAG	374: AGATGTTTGGTATGACTTGG	
STS1-cSRL-31b12	D11S2439	STS	GDB:459728	0.123	375: GATGATTAAACTCTCCTGGC	376: GAGACAGCTAAGCACTCATG	
cSRL-4f9	D11S1137	STS	GDB:197824	0.196	377: GAGGTGGTGGGCACCTGTA	378: AGAGGGGAGGAACACACCTT	Folate receptor2 (FBP2)
SHGC-10323	D11S4351	Gene	GDB:676135	0.141	379: GACCAGAGTCTGCCCAGAAG	380: TCCCCAGCTCTATCCCAAC	Collagen binding protein 2, colligin-2 gene (CBP2)
WI-9219		Gene	GDB:678179	0.1	381: GGAGGGATGGACAAGTCTGA	382: GTCCAGCTCGCTGACTATCC	Retinal outer segment membrane protein 1, ROM1
GTC_ZNF		Gene		0.172	383: TCAAAACACAGTCATCTCCA	384: GCAAAGGCTTTACCATATTG	ZNF126
AFMa152yh1	D11S4087	MSAT	GDB:603797	0.158	385: GCTCAGCACCCCCATT	386: TCCCTGCTCGGGAAAC	
AFMb331zh5	D11S4162	MSAT	GDB:611241	0.263	387: GTTCTCCAGAGAGACAGCAC	388: GAGAGCAACACTATTGCCC	
AFMb038yb9	D11S4139	MSAT	GDB:609621	0.151	389: TATAGACTTCAGCCCTGCTGC	390: CCTCTGTAGGATGCAGTTGG	
AFM212xe3	D11S1314	MSAT	GDB:199292	0.209	391: TTGCTACGCACTCCTCTACT	392: GTGAAGGCAGGAAATGTGAC	
WI-18813		EST		0.13	393: ATCCTAGACCAGAGGAGCCC	394: CTCCCCCTGGTCCAGTTATT	Serine/threonine kinase
WI-19549		EST		0.252	395: AACTTTCATTTGCCAAGGGA	396: AGCAGATCTGCTCTTGCGAT	
WI-20154		EST		0.25	397: bACAGTTGTCATCGGTAGGCA	398: AAAAGTATGAATGGGATGGAGC	
WI-22393		EST	GDB:4583084	0.142	399: GTGCAGGTGGCGTTTATTTT	400: CCCTATATCTCCGTGTGCTCC	DRES9
WI-7587		EST	GDB:1223732	0.274	401: GCTCTAGTGGGAAACCTCAGG	402: GAATTCCAGGCTCTTGCTTG	Ultra high-sulphur keratin protein (KRN1)
EST455579		EST		0.273	403: GGTTTGGTCTCAAAGGCAAA	404: CCAGTACATGGTGGTCACCA	
WI-21134		EST		0.293	405: GCTGCCTTGGAATTTCTGTT	406: GTGCTGTGGTGGGGAAAG	Fas-associating death domain-containing protein, FADD
WI-21698		EST		0.25	407: ATTCAAGCTCATCCAGACCC	408: GGACTGGCCCTTTGAAACTC	
SHGC-7373	D11S4567	STS	GDB:740192	0.225	409: ATATTGACCGTGCACAAATACG	410: AGACCTGGGAAAAGTGGAGAA	
SHGC-36533		STS		0.125	411: ATTGGCAGTGGAAAATGCTT	412: TTAATCTTTTGTCAACTTCCTGATT	
ARIX		Gene		0.242	413: tctgtcctcctttcaccggaagc	414: ggataaagaaactccgctctgctggtaga	Arix homeodomain protein, neuroendocrine specific, tx factor
CLCI.PCR		Gene	GDB:6262613		415: TCAGGGCCTGTGTTGCCGCACTCTG	416: AGCGATGTAAAGGGTACCAGTGCCGAGG	Chloride channel current inducer, ICLN gene
B188N21-HL		STS			417: AGGCATGCAAGCTTCTTA	418: CCGGGAGGAGACATCTAT	
B234C17-HR		STS			419: TGGTAAGCACAGAAAATGC	420: AATGGATGGGGGATTATT	
B235G10-HR		STS			421: CTGGACGTTATGTCTGCC	422: AGAGGCCCAGTCACAGAT	
B247F23-HR		STS			423: ATCACTCTGAACTGCCACT	424: CCCTTCTGTTTTTCTGTTTT	
B337H24-HL		STS			425: CAAGCTTTGAAGGAAGAG	426: TAGGACGTTAAGTGAGGAC	
B337L5-HL		STS			427: GCTCTGCAGTGGGTAAAA	428: ACTCTCCAAGACTGTGCG	
B382N10-HR		STS			429: CCCTTTCTGAGGCAAGAT	430: GACCACCTGGGAGAGAAC	
B12I1-HR		STS			431: CGCTATGAGTCCCATCTG	432: GATCAGCTGCAATGAAGG	
B180D17-HR		STS			433: TTGAGTACACGGGGTGAC	434: CGCAGGACTGAAAGATGA	
B236E6-HR		STS			435: ACCTGTCTCCTCTCCTGG	436: TGCTTTTCTTCTGTGGGA	
B278E22-HR		STS			437: ATGACCAGCAAGCATTGT	438: GTACTGGGATTACAGGCG	
B312F21-HR		STS			439: GCAGAAGGTCCTTTGGAT	440: TTTGCAGGATTCATGCTT	
B337H24-HR		STS			441: CGACATTCTTTTCTGGAGG	442: ACCTTTGCATGTTGGTTTT	
B358H9-HR		STS			443: GCACTTTTCCTTCCTTCC	444: TGCTTTGCTTTCTTCTGG	
B148N18-HL		STS			445: ACAGCTCCAGAGAGAAGGA	446: GCAGTCACTTGAAACCAGA	
B172N12-HL		STS			447: AGGCATCAAGCTTTCCTT	448: GGTTTAGAGAACCGAGCC	
B172N12-HR		STS			449: GTGGTGCTGCAAGTTACC	450: GGAATCCCTTTCTTTCCA	
B215J11-HR		STS			451: GACCATTTGTTACGCAGC	452: GATGGGTGTGAATGAACAA	
B223E5-HR		STS			453: CTCAAGCTTCTGTTCATGC	454: GCTGTGAGTGTCTTGGCT	
B312B3-HR		STS			455: TACAGAAAACCGCAGCTC	456: GCCACCAAAGGAAAGATT	

TABLE 7: HBM STS Table

STS Name	Locus Name	Type	GDB Access. #	Size (kb)	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	Gene Name
B328G19-HL		STS			457: AAAAGGAGGGAATCATGG	458: TCACTTAGCAGGAGGCAG	
B328G19-HR		STS			459: CTGAGCATCCGATGAGAC	460: GTGCAAAATGAGCAGCTT	
B329I10-HL		STS			461: TCTAACCCCTTACTGGGC	462: TCCTCAAACTGGGAATGA	
B329I10-HR		STS			463: TTTACACAGGACCAGGGA	464: ATCTCCCCCACTCAGAAG	
B368G19-HL		STS			465: GTCCACGGGCTTTATTCT	466: TGAGCATAAATTTCATTAGCTG	
B368G19-HR		STS			467: GGAAGAGCAAAATAAATCCA	468: GGTGCACAGAATTGTTCAT	
B36F16-HL		STS			469: AGCACGCTTATTTCATGG	470: GTAACACCAGCAGGGACA	
B250K11-HR		STS			471: TCCTGCTGCATTATGGAT	472: GGGGGTGAGAAGTAGGAA	
B338D17-HR		STS			473: ATGGGGATTAAATACGGG	474: AGCTAGCATTGGGCTCTT	
B268I23-HL		STS			475: CTGAGGAGAAGAGGCTGG	476: CGCCTTACAAGGCAAGTA	
B268I23-HR		STS			477: AGGATGCTTGCTAGGGTT	478: CACAAGTGTCTGGAAGGC	
B371E15-HR		STS			479: GGTCTCAGGAGCCCTTTA	480: ACATGCCACTCTTCTCACTAA	
B312F21-HL		STS			481: ACTTAACCAAGGATGGGG	482: CAACCCACGAGCATAAGA	
B338D17-HL		STS			483: TAGGCTCTGCACTCTTGG	484: ACCCACGGAGTCTCTCTC	
B369H19-HL		STS			485: TAAAGGCGGTGAAGTGAG	486: CTACCGCTCTCCTAGGCT	
B369H19-HR		STS			487: TGGGGCCAGATAATTCTT	488: CTGGTGTTTGGTGGTGTT	
B444M11-HR		STS			489: AAGGAAGAGGTCACCAGG	490: CACAAATTCCATTTCCCA	
B269L23-HL		STS			491: TCAATAGGTGATCCAACATTT	492: AAAGTCCCACAAAGGGTC	
B250K11-HL		STS			493: GGGTAGGGGGATCTTTTT	494: TGTGGAACATTCATTGGC	
B269L23-HR		STS			495: GTCCTGGGAAAGATGGAA	496: TCAAAGCGTCTCCCATAA	
B364H4-HL		STS			497: TCTTTCGCTGTACTTGGC	498: TGGGAGGTCAGAGTGATG	
B364H4-HR		STS			499: GGACAGTGTATGTGTTGGG	500: AGGCAGCTGTTTTTGTGA	
B473O3-HR		STS			501: CTTCTTGAGTCCCGTGTG	502: CAACCGAGAATCCTCTAGC	
B180D17-HL		STS			503: GCTGGGAGAGAATCACAA	504: GCTTTGCAGAAGAGACCA	
B200E21-HL		STS			505: ACGCTGTCAGGTCACACT	506: GGAGGATGCTCAGGTGAT	
B200E21-HR		STS			507: TAGGGGGATCTTTTTCCA	508: GAGCAATTTGAAAAGCCA	
B14L15-HR		STS			509: ATGGTCCAGCTCCTCTGT	510: ATAGAGCACCCCATCTCC	
B442P6-HR		STS			511: AACATTGCTGTTAGCCCA	512: GCAATCGAAACAGCATTC	
B188N21-HR		STS			513: ATGAGTTGGCAGCTGAAG	514: AATGAAGGTCTTGCCTCC	
GTC-ARRB1		Gene		0.067	515: GAGGAGAAGATCCACAAGCG	516: TCTCTGGGGCATACTGAACC	Beta-arrestin-1
B508A5-HL		STS			517: CTGAGCTTTTGGCACTGT	518: CTGCTAGGTGACAGCAGG	
B36F16-HR		STS			519: TGTATGAGTCTGGAGGGTGT	520: ACACCTGGCTGAGGAAAT	
B117N18-HL		STS			521: GCAGGGGACGTGATAATA	522: TTTTGCTTCCTACCATGC	
B14L15-HL		STS			523: AAAATTGTGAGCACCTCC	524: TTTATATTTAAAGTGGCTTTGTT	
B21K22-HL		STS			525: GTGCAAAGCCCACAGTAT	526: AGGAAAATGCAAGAGCAG	
B21K22-HR		STS			527: CCACTGAATTGCATACTTTG	528: TCTGGGTCCAGTCTGCTA	
B223E5-HL		STS			529: AGATTTTGGGGAGTCAGG	530: GCGCTCAAGCAATTCTC	
B278E22-HL		STS			531: CAAGCCCCAAAGTAGTCA	532: GAATCATCCAATCCACGA	
B444M11-HL		STS			533: AGCCTCCAGGTGACTACC	534: GAAGGACATGGTCAGCAG	
B543O19-HR		STS			535: ATGCTTTCAGCATTTTCG	536: TGATCCGTGGTAGGGTTA	
B117N18-HR		STS			537: GTCGGATTGGTTTCACAA	538: TTTTATGGGAATTTCAGCC	
B543O19-HL		STS			539: TTTGGAAAAGAACAGAAATGT	540: GGCTAGTCTTTCCTGAACC	
B442P6-HL		STS			541: CCTTAATGCCCCTGATTC	542: GCGTTTACAAGCTGAGGA	
B367H4-HR		STS			543: TCAAGCTTGCTTTCTCAA	544: GTAGCCCAGCAAGTGTCT	
B250E21-HR		STS			545: CCTGGCTGGAGATAGGAT	546: CTTCCCCTCTGCCTATGT	
B250E21-HL		STS			547: GGCACGTACTTCCTACCA	548: GGTGCTTCTTACAGGCAA	
B248C16-HR		STS			549: ACCCAGGCTGGTGTGT	550: ACTGAGTTAATTATCACTCCCCT	
B248C16-HL		STS			551: GATGCATTTTGCTTCACC	552: TCTGCTTTTAGAGCTGTTAGC	
B160D8-HR		STS			553: TCAAGCTTCAAAGAGCAGA	554: GGAGTACATCCCAGGACC	
B539L7-HR		STS			555: TGGTGCTTTTAAATCCAGA	556: CTCCCTTACTTACTTGCATTG	
B473O3-HL		STS			557: TCTTCTCCCAGGGAATCT	558: TTTATGTCCCCTGAGCAC	
AFMa190xd9	D11S4095	STS	GDB:606064	0.193	559: TCCCTGGCTATCTTGAATC	560: CTTGACTGGGTCCACG	
ARRB1(2)		STS			561: CGAGACGCCAGTAGATACCA	562: CATCCTCCATGCCTTTCAGT	
ARRB1(1)		STS			563: AGTTCCAGAGAACGAGACGC	564: CTTGTCATCCTCCATGCCTT	
P102F3S		STS	GDB:6054145		565: GAGCGTGAGAGGTTGAGGAG	566: AAACAAACTCCAGACGCACC	
N172A		STS	GDB:6054146	0.208	567: CTGAACCACTACCTGTATGACCTG	568: CTAACTACTTACTCCTACAGGGCCC	
N60A		STS	GDB:6054147	0.23	569: GAAGCATTTCAATACTTTAACTG	570: CCACTCCAGTGCACCCAATC	
cCI11-44A		STS	GDB:6054148	0.239	571: CTTCTCCTGGCCACTCTGAC	572: GGTTTACCTTTGAATCCCAGC	
CN1677-2A		STS	GDB:6054149	0.271	573: TGAGGATGAATGAGCACATAGG	574: TTTGTGGTCCATTGAGTAGGC	
cCI11-524B		STS	GDB:6054150	0.221	575: AGGGGAAGGAATGTGCTTGG	576: TTCGGCTGAGCGGGCAGTGT	
P117F3T		STS	GDB:6054151	0.168	577: ATTGAAGGTCCTCCAAAAGAATGCTGCAGC	578: AGAACGTCAACATATCTTTTTGGGGGACAC	
ARRB1(3)		Gene			579: TTGTATTTGAGGACTTTGCTCG	580: CGGTACCATCCTCCTCTTCC	
B215J11-HL		STS		0.122	581: TTTTTGCCTCATCTATGCCC	582: GGGTGACAGAGCAAGACTCC	
B317G1-HR		STS			583: TTGCTCAAGTTCTCCTGG	584: ACCTTGTTTTGAGGGGAG	
B317G1-HL		STS			585: CTTGGCTATTTGGACAGC	586: GGGCATTTACTCACTTGC	

TABLE 7: HBM STS Table

STS Name	Locus Name	Type	GDB Access. #	Size (kb)	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	Gene Name
B292J18-HR		STS			587: CTTGTGTCAGTTGTCAGGG	588: TGGAATTGTTGTGTCTTGG	
B10A18-HL		STS			589: CCAGTTCCACTGGATGTT	590: ATGGGCTGTGTTTCTCAA	
B10A18-HR		STS			591: CTGCCTATCCCTGGACTT	592: AGTTTGTCCCTAGTGCCC	
B527D12-HL		STS			593: CAACACGTCTGACATCCAT	594: GGATAGTGCACACCCA	
B372J11-HR		STS			595: TGGGTGGTACTATTGTTCCCAT	596: AGTTCCAGCCCCCTTACCAG	
B372J11-HL		STS			597: GGCCACTATCATCCCTGTGT	598: TTTCACATGGGAAGAACACG	
B37E17-HR(GS)		STS			599: ACAGTGACACTAGGGACGGG	600: TGCCAGGATGGAGATAACAA	
B37E17-HL(GS)		STS			601: CCTGTGGCACACATATCACC	602: ACAACCAAGAATGGAGCCAC	
B34F22-HR(GS)		STS			603: TGCTGTGTAACAAGTCCCCA	604: TGAACGGAGGACCTACCAAG	
B34F22-HL(GS)		STS			605: GCAGGGTCCGACTCACTAAG	606: GCTGTGAGTTCCCTTTACGC	
B648P22-HR1		STS			607: ACAGTGGGGACAAAGACAGG	608: TACAGGGCACCTCCCAGTAG	
B82A4-HR2		STS			609: TCTTCTGTTAAGGTTTCCCCC	610: TGTCTCAAACCTCCCTCTGC	
B648P22-HL		STS			611: AACATATTTCCTCCCCAGCC	612: CAGTCCCAGCCAATGAGAAC	
B82L11-HL (GS)		STS			613: CTCCTCTGCATGGGAGAATC	614: AGACCTGGGACCAGTCTGTG	
B86J13-HL (GS)		STS			615: GGGAGACGACGTCACAAGAT	616: TGATGTTGGGAAGATGGTGA	
144A24-HL		STS			617: CAGGCATCTTCTATGTGCCA	618: GGGAGGCACAAGTTCTTTCA	
B82L11-HR (GS)		STS			619: ACTTCGTGGCACTGAGTGTG	620: CCTTTCTTACGGATGAGGCA	
B86J13-HR (GS)		STS			621: GGCTGCTGAGCTCTTCTGAT	622: TGGGTCTCTCTGCCTGACTT	
B82L11-HL2(GS)		STS			623: TCACCTACTTCCAGCTTCCG	624: AGACCTGGGACCAGTCTGTG	
B82L11-HL3(GS)		STS			625: CTCCTCTGCATGGGAGAATC	626: AATTCAGGAGACCTGGGACC	

Novel STSs were developed either from publicly available genomic sequence or from sequence-derived BAC insert ends. Primers were chosen using a script which automatically performs vector and repetitive sequence masking using Cross_match (P. Green, Univ. of Washington) and subsequent primer picking using Primer3 (Rozen, Skaletsky (1996, 1997). Primer3 is available at: www.genome.wi.mit.edu/genome_software/other/primer3 .html.

Polymerase chain reaction (PCR) conditions for each primer pair were initially optimized with respect to $MgCl_2$ concentration. The standard buffer was 10 mM Tris-HCl (pH 8.3), 50 mM KCl, $MgCl_2$, 0.2 mM each dNTP, 0.2 µM each primer, 2.7 ng/µl human DNA, 0.25 units of AmpliTaq (Perkin Elmer) and $MgCl_2$ concentrations of 1.0 mM, 1.5 mM, 2.0 mM or 2.4 mM. Cycling conditions included an initial denaturation at 94°C for 2 minutes followed by 40 cycles at 94°C for 15 seconds, 55°C for 25 seconds, and 72°C for 25 seconds followed by a final extension at 72°C for 3 minutes. Depending on the results from the initial round of optimization the conditions were further optimized if necessary. Variables included increasing the annealing temperature to 58°C or 60°C, increasing the cycle number to 42 and the annealing and extension times to 30 seconds, and using AmpliTaq™ Gold (Perkin Elmer).

BAC clones (Kim *et al.*, 1996 *Genomics* 32: 213-8; and Shizuya *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89: 8794-7) containing STS markers of interest were obtained by PCR-based screening of DNA pools from a total human BAC library purchased from Research Genetics. DNA pools derived from library plates 1-596 were used corresponding to nine genomic equivalents of human DNA. The initial screening process involved PCR reactions of individual markers against superpools, i.e., a mixture of DNA derived from all BAC clones from eight 384-well library plates. For each positive superpool, plate (8), row (16) and column (24), pools were screened to identify a unique library address. PCR products were electrophoresed in 2% agarose gels (Sigma) containing 0.5 µg/ml ethidium bromide in 1X TBE at 150 volts for 45 min. The electrophoresis units used were the Model A3-1 systems from Owl Scientific Products. Typically, gels contained 10 tiers of lanes with 50 wells/tier. Molecular weight markers (100 bp ladder, Life Technologies, Bethesda, MD) were loaded at both ends of the gel. Images of the gels were captured with a Kodak DC40 CCD camera and processed with Kodak 1D software. The gel data were exported as tab delimited text files;

names of the files included information about the library screened, the gel image files and the marker screened. These data were automatically imported using a customized Perl script into Filemaker™ PRO (Claris Corp.) databases for data storage and analysis. In cases where incomplete or ambiguous clone address information was obtained, additional experiments were performed to recover a unique, complete library address.

Recovery of clonal BAC cultures from the library involved streaking out a sample from the library well onto LB agar (Maniatis *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1982)) containing 12.5 μg/ml chloramphenicol (Sigma). Two individual colonies and a portion of the initial streak quadrant were tested with appropriate STS markers by colony PCR for verification. Positive clones were stored in LB broth containing 12.5 μg/ml chloramphenicol and 15% glycerol at -70°C.

Several different types of DNA preparation methods were used for isolation of BAC DNA. The manual alkaline lysis miniprep protocol listed below (Maniatis *et al.*, 1982) was successfully used for most applications, i.e., restriction mapping, CHEF gel analysis, FISH mapping, but was not successfully reproducible by endsequencing. The Autogen and Qiagen protocols were used specifically for BAC DNA preparation for endsequencing purposes.

Bacteria were grown in 15 ml Terrific Broth containing 12.5 μg/ml chloramphenicol in a 50 ml conical tube at 37°C for 20 hrs with shaking at 300 rpm. The cultures were centrifuged in a Sorvall RT 6000 D at 3000 rpm (~1800xg) at 4°C for 15 min. The supernatant was then aspirated as completely as possible. In some cases, cell pellets were frozen at -20°C at this step for up to 2 weeks. The pellet was then vortexed to homogenize the cells and minimize clumping. 250 μl of P1 solution (50 mM glucose, 15 mM Tris-HCl, pH 8, 10 mM EDTA, and 100 μg/ml RNase A) was added and the mixture pipetted up and down to mix. The mixture was then transferred to a 2 ml Eppendorf tube. 350 μl of P2 solution (0.2 N NaOH, 1% SDS) was then added, the mixture mixed gently and incubated for 5 min at room temperature. 350 μl of P3 solution (3 M KOAc, pH 5.5) was added and the mixture mixed gently until a white precipitate formed. The solution was incubated on ice for 5 min and then centrifuged at 4°C in a microfuge for 10 min. The supernatant was transferred carefully (avoiding the white precipitate) to a fresh 2 ml Eppendorf tube, and 0.9

ml of isopropanol was added, the solution mixed and left on ice for 5 min. The samples were centrifuged for 10 min, and the supernatant removed carefully. Pellets were washed in 70% ethanol and air dried for 5 min. Pellets were resuspended in 200 µl of TE8 (10 mM Tris-HCl, pH 8.0, 1.0 mM EDTA), and RNase A (Boehringer Mannheim) added to 100 µg/ml. Samples were incubated at 37°C for 30 min, then precipitated by addition of $C_2H_3O_2Na{\cdot}3H_2O$ to 0.5 M and 2 volumes of ethanol. Samples were centrifuged for 10 min, and the pellets washed with 70% ethanol followed by air drying and dissolving in 50 μl TE8. Typical yields for this DNA prep were 3-5 μg/15 ml bacterial culture. Ten to 15 µl were used for *Hind*III restriction analysis; 5 µl was used for *Not*I digestion and clone insert sizing by CHEF gel electrophoresis.

BACs were inoculated into 15 ml of 2X LB Broth containing 12.5 µg/ml chloramphenicol in a 50 ml conical tube. Four tubes were inoculated for each clone. Cultures were grown overnight (~16 hr) at 37°C with vigorous shaking (>300 rpm). Standard conditions for BAC DNA isolation were followed as recommended by the Autogen 740 manufacturer. 3 ml samples of culture were placed into Autogen tubes for a total of 60 ml or 20 tubes per clone. Samples were dissolved finally in 100 µl TE8 with 15 seconds of shaking as part of the Autogen protocol. After the Autogen protocol was finished DNA solutions were transferred from each individual tube and pooled into a 2 ml Eppendorf tube. Tubes with large amounts of debris (carry over from the pelleting debris step) were avoided. The tubes were then rinsed with 0.5 ml of TE8 successively and this solution added to the pooled material. DNA solutions were stored at 4°C; clumping tended to occur upon freezing at -20°C. This DNA was either used directly for restriction mapping, CHEF gel analysis or FISH mapping or was further purified as described below for use in endsequencing reactions.

The volume of DNA solutions was adjusted to 2 ml with TE8, samples were then mixed gently and heated at 65°C for 10 min. The DNA solutions were then centrifuged at 4°C for 5 min and the supernatants transferred to a 15 ml conical tube. The NaCl concentration was then adjusted to 0.75 M (~0.3 ml of 5 M NaCl to the 2 ml sample). The total volume was then adjusted to 6 ml with Qiagen column equilibration buffer (Buffer QBT). The supernatant containing the DNA was then applied to the column and allowed to enter by gravity flow. Columns were washed twice with 10 ml of Qiagen Buffer QC. Bound

DNA was then eluted with four separate 1 ml aliquots of Buffer QF kept at 65°C. DNA was precipitated with 0.7 volumes of isopropanol (~2.8 ml). Each sample was then transferred to 4 individual 2.2 ml Eppendorf tubes and incubated at room temperature for 2 hr or overnight. Samples were centrifuged in a microfuge for 10 min. at 4°C. The supernatant was removed carefully and 1 ml of 70% ethanol was added. Samples were centrifuged again and because the DNA pellets were often loose at this stage, the supernatant removed carefully. Samples were centrifuged again to concentrate remaining liquid which was removed with a micropipet tip. DNA pellets were then dried in a desiccator for 10 min. 20 µl of sterile distilled and deionized H_2O was added to each tube which was then placed at 4°C overnight. The four 20 µl samples for each clone were pooled and the tubes rinsed with another 20 µl of sterile distilled and deionized H_2O for a final volume of 100 µl. Samples were then heated at 65°C for 5 min. and then mixed gently. Typical yields were 2-5 µg/60 ml culture as assessed by *Not*I digestion and comparison with uncut lambda DNA.

3 ml of LB Broth containing 12.5 µg/ml of chloramphenicol was dispensed into autoclaved Autogen tubes. A single tube was used for each clone. For inoculation, glycerol stocks were removed from -70°C storage and placed on dry ice. A small portion of the glycerol stock was removed from the original tube with a sterile toothpick and transferred into the Autogen tube; the toothpick was left in the Autogen tube for at least two minutes before discarding. After inoculation the tubes were covered with tape making sure the seal was tight. When all samples were inoculated, the tube units were transferred into an Autogen rack holder and placed into a rotary shaker at 37°C for 16-17 hours at 250 rpm. Following growth, standard conditions for BAC DNA preparation, as defined by the manufacturer, were used to program the Autogen. Samples were not dissolved in TE8 as part of the program and DNA pellets were left dry. When the program was complete, the tubes were removed from the output tray and 30 µl of sterile distilled and deionized H_2O was added directly to the bottom of the tube. The tubes were then gently shaken for 2-5 seconds and then covered with parafilm and incubated at room temperature for 1-3 hours. DNA samples were then transferred to an Eppendorf tube and used either directly for sequencing or stored at 4°C for later use.

7. **BAC Clone Characterization for Physical Mapping**

DNA samples prepared either by manual alkaline lysis or the Autogen protocol were digested with *Hind*III for analysis of restriction fragment sizes. This data were used to compare the extent of overlap among clones. Typically 1-2 μg were used for each reaction. Reaction mixtures included: 1X Buffer 2 (New England Biolabs), 0.1 mg/ml bovine serum albumin (New England Biolabs), 50 μg/ml RNase A (Boehringer Mannheim), and 20 units of *Hind*III (New England Biolabs) in a final volume of 25 μl. Digestions were incubated at 37°C for 4-6 hours. BAC DNA was also digested with NotI for estimation of insert size by CHEF gel analysis (see below). Reaction conditions were identical to those for *Hind*III except that 20 units of *Not*I were used. Six μl of 6X Ficoll loading buffer containing bromphenol blue and xylene cyanol was added prior to electrophoresis.

*Hind*III digests were analyzed on 0.6% agarose (Seakem, FMC Bioproducts) in 1X TBE containing 0.5 μg/ml ethidium bromide. Gels (20 cm X 25 cm) were electrophoresed in a Model A4 electrophoresis unit (Owl Scientific) at 50 volts for 20-24 hrs. Molecular weight size markers included undigested lambda DNA, *Hind*III digested lambda DNA, and *Hae*III digested _X174 DNA. Molecular weight markers were heated at 65°C for 2 min prior to loading the gel. Images were captured with a Kodak DC40 CCD camera and analyzed with Kodak 1D software.

*Not*I digests were analyzed on a CHEF DRII (BioRad) electrophoresis unit according to the manufacturer's recommendations. Briefly, 1% agarose gels (BioRad pulsed field grade) were prepared in 0.5X TBE, equilibrated for 30 minutes in the electrophoresis unit at 14°C, and electrophoresed at 6 volts/cm for 14 hrs with circulation. Switching times were ramped from 10 sec to 20 sec. Gels were stained after electrophoresis in 0.5 μg/ml ethidium bromide. Molecular weight markers included undigested lambda DNA, *Hind*III digested lambda DNA, lambda ladder PFG ladder, and low range PFG marker (all from New England Biolabs).

BAC DNA prepared either by the manual alkaline lysis or Autogen protocols were labeled for FISH analysis using a Bioprime labeling kit (BioRad) according to the manufacturer's recommendation with minor modifications. Approximately 200 ng of DNA was used for each 50 μl reaction. 3 μl were analyzed on a 2% agarose gel to determine the

extent of labeling. Reactions were purified using a Sephadex G50 spin column prior to *in situ* hybridization. Metaphase FISH was performed as described (Ma *et al.*, 1996 *Cytogenet. Cell Genet.*, 74: 266-71).

8. **BAC Endsequencing**

The sequencing of BAC insert ends utilized DNA prepared by either of the two methods described above. The DYEnamic energy transfer primers and Dynamic Direct cycle sequencing kits from Amersham were used for sequencing reactions. Ready made sequencing mix including the M13 -40 forward sequencing primer was used (Catalog # US79730) for the T7 BAC vector terminus; ready made sequencing mix (Catalog # US79530) was mixed with the M13 -28 reverse sequencing primer (Catalog # US79339) for the SP6 BAC vector terminus. The sequencing reaction mixes included one of the four fluorescently labeled dye-primers, one of the four dideoxy termination mixes, dNTPs, reaction buffer, and Thermosequenase. For each BAC DNA sample, 3 µl of the BAC DNA sample was aliquoted to 4 PCR strip tubes. 2 µl of one of the four dye primer/termination mix combinations was then added to each of the four tubes. The tubes were then sealed and centrifuged briefly prior to PCR. Thermocycling conditions involved a 1 minute denaturation at 95°C, 15 second annealing at 45°C, and extension for 1 minute at 70°C for 35 total cycles. After cycling the plates were centrifuged briefly to collect all the liquid to the bottom of the tubes. 5 µl of sterile distilled and deionized H_2O was then added into each tube, the plates sealed and centrifuged briefly again. The four samples for each BAC were then pooled together. DNA was then precipitated by adding 1.5 µl of 7.5 M NH_4OAc and 100 µl of -20°C 100% ethanol to each tube. Samples were mixed by pipetting up and down once. The plates were then sealed and incubated on ice for 10 minutes. Plates were centrifuged in a table topHaraeus centrifuge at 4000 rpm (3,290xg) for 30 minutes at 4°C to recover the DNA. The supernatant was removed and excess liquid blotted onto paper towels. Pellets were washed by adding 100 µl of -20°C 70% ethanol into each tube and re-centrifuging at 4000 rpm (3,290xg) for 10 minutes at 4°C. The supernatant was removed and excess liquid again removed by blotting on a paper towel. Remaining traces of liquid were removed by placing the plates upside down over a paper towel and centrifuging only until the centrifuge

reached 800 rpm. Samples were then air dried at room temperature for 30 min. Tubes were capped and stored dry at -20°C until electrophoresis. Immediately prior to electrophoresis the DNA was dissolved in 1.5 µl of Amersham loading dye. Plates were then sealed and centrifuged at 2000 rpm (825Xg). The plates were then vortexed on a plate shaker for 1-2 minutes. Samples were then recentrifuged at 2000 rpm (825Xg) briefly. Samples were then heated at 65°C for 2 min and immediately placed on ice. Standard gel electrophoresis was performed on ABI 377 fluorescent sequencers according to the manufacturer's recommendation.

9. Sub-cloning and Sequencing of HBM BAC DNA

The physical map of the *Zmax1* (*LRP5*) gene region provides a set of BAC clones that contain within them the *Zmax1* (*LRP5*) gene and the *HBM* gene. DNA sequencing of several of the BACs from the region has been completed. The DNA sequence data is a unique reagent that includes data that one skilled in the art can use to identify the *Zmax1* (*LRP5*) gene and the *HBM* gene, or to prepare probes to identify the gene(s), or to identify DNA sequence polymorphisms that identify the gene(s).

BAC DNA was isolated according to one of two protocols, either a Qiagen purification of BAC DNA (Qiagen, Inc. as described in the product literature) or a manual purification which is a modification of the standard alkaline lysis/Cesium Chloride preparation of plasmid DNA (see e.g., Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons (1997)). Briefly for the manual protocol, cells were pelleted, resuspended in GTE (50 mM glucose, 25 mM Tris-Cl (pH 8), 10 mM EDTA) and lysozyme (50 mg/ml solution), followed by NaOH/SDS (1% SDS/0.2 N NaOH) and then an ice-cold solution of 3 M KOAc (pH 4.5-4.8). RNaseA was added to the filtered supernatant, followed by Proteinase K and 20% SDS. The DNA was then precipitated with isopropanol, dried and resuspended in TE (10 mM Tris, 1 mM EDTA (pH 8.0)). The BAC DNA was further purified by Cesium Chloride density gradient centrifugation (Ausubel *et al.*, 1997).

Following isolation, the BAC DNA was sheared hydrodynamically using an HPLC (Hengen, 1997 *Trends in Biochem. Sci.* 22: 273-4) to an insert size of 2000-3000 bp. After shearing, the DNA was concentrated and separated on a standard 1% agarose gel. A single

fraction, corresponding to the approximate size, was excised from the gel and purified by electroelution (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring, NY (1989)).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The blunt-ended DNA was then ligated to unique *Bst*XI-linker adapters (5'- GTCTTCACCACG GGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess; SEQ ID NOS: 627 and 628 respectively). These linkers were complimentary to the *Bst*XI-cut pMPX vectors (constructed by the inventors), while the overhang was not self-complimentary. Therefore, the linkers would not concatemerize nor would the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean (BIO 101, Inc.). The linker-adapted insert was then ligated to a modified pBlueScript vector to construct a "shotgun" subclone library. The vector contained an out-of-frame lacZ gene at the cloning site which became in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their blue-color.

All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5α competent cells (Life Technologies, Bethesda, MD, DH5α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37°. DNA was purified using a silica bead DNA preparation (Ng *et al.*, 1996 *Nucl. Acids Res.* 24: 5045-7) method. In this manner, 25 μg of DNA was obtained per clone.

These purified DNA samples were then sequenced using ABI dye-terminator chemistry. The ABI dye terminator sequence reads were run on ABI377 machines and the data was directly transferred to UNIX machines following lane tracking of the gels. All reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default parameters and quality scores. The initial assembly was done at 6-fold coverage and yielded an average of 8-15 contigs. Following the initial assembly, missing mates (sequences from clones that only

gave one strand reads) were identified and sequenced with ABI technology to allow the identification of additional overlapping contigs. Primers for walking were selected using a Genome Therapeutics program Pick_primer near the ends of the clones to facilitate gap closure. These walks were sequenced using the selected clones and primers. Data were reassembled with PHRAP into sequence contigs.

10. Gene Identification by Computational Methods

Following assembly of the BAC sequences into contigs, the contigs were subjected to computational analyses to identify coding regions and regions bearing DNA sequence similarity to known genes. This protocol included the following steps.

1. Degap the contigs: the sequence contigs often contain symbols (denoted by a period symbol) that represent locations where the individual ABI sequence reads have insertions or deletions. Prior to automated computational analysis of the contigs, the periods were removed. The original data was maintained for future reference.

2. BAC vector sequences were "masked" within the sequence by using the program cross match (Phil Green, http:\\chimera.biotech.washington.edu\UWGC). Since the shotgun libraries construction detailed above leaves some BAC vector in the shotgun libraries, this program was used to compare the sequence of the BAC contigs to the BAC vector and to mask any vector sequence prior to subsequent steps. Masked sequences were marked by an "X" in the sequence files, and remained inert during subsequent analyses.

3. *E. coli* sequences contaminating the BAC sequences were masked by comparing the BAC contigs to the entire *E. coli* DNA sequence.

4. Repetitive elements known to be common in the human genome were masked using cross match. In this implementation of crossmatch, the BAC sequence was compared to a database of human repetitive elements (Jerzy Jerka, Genetic Information Research Institute, Palo Alto, CA). The masked repeats were marked by X and remained inert during subsequent analyses.

5. The location of exons within the sequence was predicted using the

MZEF computer program (Zhang, 1997 *Proc. Natl. Acad. Sci USA.* 94: 565-8).

6. The sequence was compared to the publicly available unigene database (National Center for Biotechnology Information, National Library of Medicine, 38A, 8N905, 8600 Rockville Pike, Bethesda, MD 20894; www.ncbi.nlm.nih.gov) using the blastn2 algorithm (Altschul *et al.*, 1997 *Nucl. Acids Res.* 25: 3389-3402). The parameters for this search were: E=0.05, v=50, B=50 (where E is the expected probability score cutoff, V is the number of database entries returned in the reporting of the results, and B is the number of sequence alignments returned in the reporting of the results (Altschul *et al.*, *J. Mol. Biol.*, 215:403-410 (1990)).

7. The sequence was translated into protein for all six reading frames, and the protein sequences were compared to a non-redundant protein database compiled from Genpept Swissprot PIR (National Center for Biotechnology Information, National Library of Medicine, 38A, 8N905, 8600 Rockville Pike, Bethesda, MD 20894; www.ncbi.nlm.nih.gov). The parameters for this search were E=0.05, V=50, B= 50, where E, V, and B are defined as above.

8. The BAC DNA sequence was compared to the database of the cDNA clones derived from direct selection experiments (described below) using blastn2 (Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=250, B=250, where E, V, and B are defined as above.

9. The BAC sequence was compared to the sequences of all other BACs from the HBM region on chromosome 11q12-13 using blastn2 (Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=50, B=50, where E, V, and B are defined as above.

10. The BAC sequence was compared to the sequences derived from the ends of BACs from the HBM region on chromosome 11q12-13 using blastn2 (Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=50, B=50, where E, V, and B are defined as above.

11. The BAC sequence was compared to the GenBank database (National Center for Biotechnology Information, National Library of Medicine, 38A, 8N905, 8600 Rockville Pike, Bethesda, MD 20894; www.ncbi.nlm.nih.gov) using blastn2

(Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=50, B=50, where E, V, and B are defined as above.

12. The BAC sequence was compared to the STS division of GenBank database (National Center for Biotechnology Information, National Library of Medicine, 38A, 8N905, 8600 Rockville Pike, Bethesda, MD 20894; www.ncbi.nlm.nih.gov) using blastn2 (Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=50, B= 50, where E, V, and B are defined as above.

13. The BAC sequence was compared to the Expressed Sequence (EST) Tag GenBank database (National Center for Biotechnology Information, National Library of Medicine, 38A, 8N905, 8600 Rockville Pike, Bethesda, MD 20894; www.ncbi.nlm.nih.gov) using blastn2 (Altschul *et al.*, 1997). The parameters for this search were E=0.05, V=250, B=250, where E, V, and B are defined as above.

11. Gene Identification by Direct cDNA Selection

Primary linkered cDNA pools were prepared from bone marrow, calvarial bone, femoral bone, kidney, skeletal muscle, testis and total brain. Poly (A) + RNA was prepared from calvarial and femoral bone tissue (Chomczynski *et al.*, 1987 *Anal. Biochem.* 162: 156-9; and D'Alessio *et al.*, 1987 *Focus* 9: 1-4) and the remainder of the mRNA was purchased from Clontech (Palo Alto, California). In order to generate oligo(dT) and random primed cDNA pools from the same tissue, 2.5 μg mRNA was mixed with oligo(dT) primer in one reaction and 2.5 μg mRNA was mixed with random hexamers in another reaction, and both were converted to first and second strand cDNA according to manufacturers recommendations (Life Technologies, Bethesda, MD). Paired phosphorylated cDNA linkers (see sequence below) were annealed together by mixing in a 1:1 ratio (10 μg each) incubated at 65 °C for five minutes and allowed to cool to room temperature.

Paired linkers oligo ½

OLIGO 1: 5'-CTG AGC GGA ATT CGT GAG ACC-3' (SEQ ID NO:12)

OLIGO 2: 5'-TTG GTC TCA CGT ATT CCG CTC GA-3' (SEQ ID NO:13)

Paired linkers oligo3/4

OLIGO 3: 5'-CTC GAG AAT TCT GGA TCC TC-3' (SEQ ID NO:14)

OLIGO 4: 5'-TTG AGG ATC CAG AAT TCT CGA G-3' (SEQ ID NO:15)

Paired linkers oligo5/6

OLIGO 5: 5'-TGT ATG CGA ATT CGC TGC GCG-3' (SEQ ID NO:16)

OLIGO 6: 5'-TTC GCG CAG CGA ATT CGC ATA CA-3' (SEQ ID NO:17)

Paired linkers oligo7/8

OLIGO 7: 5'-GTC CAC TGA ATT CTC AGT GAG-3' (SEQ ID NO:18)

OLIGO 8: 5'-TTG TCA CTG AGA ATT CAG TGG AC-3' (SEQ ID NO:19)

Paired linkers oligo11/12

OLIGO 11: 5'-GAA TCC GAA TTC CTG GTC AGC-3' (SEQ ID NO:20)

OLIGO 12: 5'-TTG CTG ACC AGG AAT TCG GAT TC-3' (SEQ ID NO:21)

Linkers were ligated to all oligo(dT) and random primed cDNA pools (see below) according to manufacturers instructions (Life Technologies, Bethesda, MD).

Oligo ½ was ligated to oligo(dT) and random primed cDNA pools prepared from bone marrow. Oligo 3/4 was ligated to oligo(dT) and random primed cDNA pools prepared from calvarial bone. Oligo 5/6 was ligated to oligo(dT) and random primed cDNA pools prepared from brain and skeletal muscle. Oligo 7/8 was ligated to oligo(dT) and random primed cDNA pools prepared from kidney. Oligo 11/12 was ligated to oligo(dT) and random primed cDNA pools prepared from femoral bone.

The cDNA pools were evaluated for length distribution by PCR amplification using 1 µl of a 1:1, 1:10, and 1:100 dilution of the ligation reaction, respectively. PCR reactions were performed in a Perkin Elmer 9600, each 25 µl volume reaction contained 1 µl of DNA, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.001% gelatin, 200 mM each dNTPs, 10 µM primer and 1 unit Taq DNA polymerase (Perkin Elmer) and was amplified under the following conditions: 30 seconds at 94°C, 30 seconds at 60°C and 2 minutes at 72°C for 30 cycles. The length distribution of the amplified cDNA pools were evaluated by electrophoresis on a 1% agarose gel. The PCR reaction that gave the best representation of the random primed and oligo(dT) primed cDNA pools was scaled up so that ~2-3 µg of each cDNA pool was produced. The starting cDNA for the direct selection reaction comprised of 0.5 µg of random primed cDNAs mixed with 0.5 µg of oligo(dT) primed cDNAs.

The DNA from the 54 BACs that were used in the direct cDNA selection procedure

was isolated using Nucleobond AX columns as described by the manufacturer (The Nest Group, Inc.).

The BACs were pooled in equimolar amounts and 1 µg of the isolated genomic DNA was labeled with biotin 16-UTP by nick translation in accordance with the manufacturers instructions (Boehringer Mannheim). The incorporation of the biotin was monitored by methods that could be practiced by one skilled in the art (Del Mastro *et al.*, *Methods in Molecular Biology*, Humana Press Inc., NJ (1996)).

Direct cDNA selection was performed using methods that could be practiced by one skilled in the art (Del Mastro *et al.*, 1996). Briefly, the cDNA pools were multiplexed in two separate reactions: In one reaction cDNA pools from bone marrow, calvarial bone, brain and testis were mixed, and in the other cDNA pools from skeletal muscle, kidney and femoral bone were mixed. Suppression of the repeats, yeast sequences and plasmid in the cDNA pools was performed to a Cot of 20. 100 ng of biotinylated BAC DNA was mixed with the suppressed cDNAs and hybridized in solution to a Cot of 200. The biotinylated DNA and the cognate cDNAs was captured on streptavidin-coated paramagnetic beads. The beads were washed and the primary selected cDNAs were eluted. These cDNAs were PCR amplified and a second round of direct selection was performed. The product of the second round of direct selection is referred to as the secondary selected material. A Galanin cDNA clone, previously shown to map to 11q12-13 (Evans, 1993 *Genomics* 18: 473-7), was used to monitor enrichment during the two rounds of selection.

The secondary selected material from bone marrow, calvarial bone, femoral bone, kidney, skeletal muscle, testis and total brain was PCR amplified using modified primers of oligos 1, 3, 5, 7 and 11, shown below, and cloned into the UDG vector pAMP10 (Life Technologies, Bethesda, MD), in accordance with the manufacturer's recommendations.

Modified primer sequences:

Primer	SEQ ID NO.	Sequence
Oligo 1	22	5'-CUA CUA CUA CUA CTG AGC GGA ATT CGT GAG ACC-3'
Oligo 3	23	5'-CUA CUA CUA CUA CTC GAG AAT TCT GGA TCC TC-3'
Oligo 5	24	5'-CUA CUA CUA CUA TGT ATG CGA ATT CGC TGC GCG-3'

Primer	SEQ ID NO.	Sequence
Oligo 7	25	5'-CUA CUA CUA CUA GTC CAC TGA ATT CTC AGT GAG-3'
Oligo 11	26	5'-CUA CUA CUA CUA GAA TCC GAA TTC CTG GTC AGC-3'

The cloned secondary selected material, from each tissue source, was transformed into MAX Efficiency DH5a Competent Cells (Life Technologies, Bethesda, MD) as recommended by the manufacturer. 384 colonies were picked from each transformed source and arrayed into four 96 well microtiter plates.

All secondarily selected cDNA clones were sequenced using M13 dye primer terminator cycle sequencing kit (Applied Biosystems), and the data collected by the ABI 377 automated fluorescence sequencer (Applied Biosystems).

All sequences were analyzed using the BLASTN, BLASTX and FASTA programs (Altschul *et al.*, 1990 *J. Mol. Biol.* 215: 403-410; and Altschul *et al.*, *Nucl. Acids. Res.* 25: 3389-3402). The cDNA sequences were compared to a database containing sequences derived from human repeats, mitochondrial DNA, ribosomal RNA, *E. coli* DNA to remove background clones from the dataset using the program cross_match. A further round of comparison was also performed using the program BLASTN2 against known genes (GenBank) and the BAC sequences from the HBM region. Those cDNAs that were >90% homologous to these sequences were filed according to the result and the data stored in a database for further analysis. cDNA sequences that were identified but did not have significant similarity to the BAC sequences from the HBM region or were eliminated by cross_match were hybridized to nylon membranes which contained the BACs from the HBM region, to ascertain whether they hybridized to the target.

Hybridization analysis was used to map the cDNA clones to the BAC target that selected them. The BACs that were identified from the HBM region were arrayed and grown into a 96 well microtiter plate. LB agar containing 25 μg/ml kanamycin was poured into 96 well microtiter plate lids. Once the agar had solidified, pre-cut Hybond N+ nylon membranes (Amersham) were laid on top of the agar and the BACs were stamped onto the membranes in duplicate using a hand held 96 well replica plater (V&P Scientific, Inc.). The plates were

incubated overnight at 37°C. The membranes were processed according to the manufacturers recommendations.

The cDNAs that needed to be mapped by hybridization were PCR amplified using the relevant primer (oligos 1, 3, 5, 7 and 11) that would amplify that clone. For this PCR amplification, the primers were modified to contain a linkered digoxigenin molecule at the 5' of the oligonucleotide. The PCR amplification was performed under the same conditions as described in Preparation of cDNA Pools (above). The PCR products were evaluated for quality and quantity by electrophoresis on a 1% agarose gel by loading 5 μl of the PCR reaction. The nylon membranes containing the stamped BACs were individually pre-hybridized in 50 ml conical tubes containing 10 ml of hybridization solution (5X SSPE, 0.5X Blotto, 2.5% SDS and 1 mM EDTA (pH 8.0)). The 50 ml conical tubes were placed in a rotisserie oven (Robbins Scientific) for 2 hours at 65°C. Twenty-five ng of each cDNA probe was denatured and added into individual 50 ml conical tubes containing the nylon membrane and hybridization solution. The hybridization was performed overnight at 65°C. The filters were washed for 20 minutes at 65°C in each of the following solutions: 3X SSPE, 0.1% SDS; 1X SSPE, 0.1% SDS and 0.1X SSPE, 0.1% SDS.

The membranes were removed from the 50 ml conical tubes and placed in a dish. Acetate sheets were placed between each membrane to prevent them from sticking to each other. The incubation of the membranes with the Anti-DIG-AP and CDP-Star was performed according to manufacturers recommendations (Boehringer Mannheim). The membranes were wrapped in Saran wrap and exposed to Kodak Bio-Max X-ray film for 1 hour.

12. <u>cDNA Cloning and Expression Analysis</u>

To characterize the expression of the genes identified by direct cDNA selection and genomic DNA sequencing in comparison to the publicly available databases, a series of experiments were performed to further characterize the genes in the HBM region. First, oligonucleotide primers were designed for use in the polymerase chain reaction (PCR) so that portions of a cDNA, EST, or genomic DNA could be amplified from a pool of DNA molecules (a cDNA library) or RNA population (RT-PCR and RACE). The PCR primers were used in a reaction containing genomic DNA to verify that they generated a product of

the size predicted based on the genomic (BAC) sequence. A number of cDNA libraries were then examined for the presence of the specific cDNA or EST. The presence of a fragment of a transcription unit in a particular cDNA library indicates a high probability that additional portions of the same transcription unit will be present as well.

A critical piece of data that is required when characterizing novel genes is the length, in nucleotides, of the processed transcript or messenger RNA (mRNA). One skilled in the art primarily determines the length of an mRNA by Northern blot hybridization (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor NY (1989)). Groups of ESTs and direct-selected cDNA clones that displayed significant sequence similarity to sequenced BACs in the critical region were grouped for convenience into approximately 30 kilobase units. Within each 30 kilobase unit there were from one up to fifty ESTs and direct-selected cDNA clones which comprised one or more independent transcription units. One or more ESTs or direct-selected cDNAs were used as hybridization probes to determine the length of the mRNA in a variety of tissues, using commercially available reagents (Multiple Tissue Northern blot; Clontech, Palo Alto, California) under conditions recommended by the manufacturer.

Directionally cloned cDNA libraries from femoral bone, and calvarial bone tissue were constructed by methods familiar to one skilled in the art (for example, Soares in *Automated DNA Sequencing and Analysis*, Adams, Fields and Venter, Eds., Academic Press, NY, pages 110-114 (1994)). Bones were initially broken into fragments with a hammer, and the small pieces were frozen in liquid nitrogen and reduced to a powder in a tissue pulverizer (Spectrum Laboratory Products). RNA was extracted from the powdered bone by homogenizing the powdered bone with a standard Acid Guanidinium Thiocyanate-Phenol-Chloroform extraction buffer (e.g., Chomczynski *et al.*, 1987 *Anal. Biochem.* 162: 156-9) using a polytron homogenizer (Brinkman Instruments). Additionally, human brain and lung total RNA was purchased from Clontech. PolyA RNA was isolated from total RNA using dynabeads-dT according to the manufacturer's recommendations (Dynal, Inc.). First strand cDNA synthesis was initiated using an oligonucleotide primer with the sequence: 5'-AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTT TT-3' (SEQ ID NO:27). This primer introduces a *Not*I restriction site (underlined) at the 3',

end of the cDNA. First and second strand synthesis were performed using the "one-tube" cDNA synthesis kit as described by the manufacturer (Life Technologies, Bethesda, MD). Double stranded cDNAs were treated with T4 polynucleotide kinase to ensure that the ends of the molecules were blunt (Soares in *Automated DNA Sequencing and Analysis*, Adams, Fields and Venter, Eds., Academic Press, NY, pages 110-114 (1994)), and the blunt ended cDNAs were then size selected by a Biogel column (Huynh *et al.* in *DNA Cloning*, Vol. 1, Glover, Ed., IRL Press, Oxford, pages 49-78 (1985)) or with a size-sep 400 Sepharose column (Pharmacia, catalog # 27-5105-01). Only cDNAs of 400 base pairs or longer were used in subsequent steps. *Eco*RI adapters (sequence: 5' OH-AATTCGGCACGAG-OH 3' (SEQ ID NO:28), and 5' p-CTCGTGCCG-OH 3' (SEQ ID NO:29)) were then ligated to the double stranded cDNAs by methods familiar to one skilled in the art (Soares, 1994). The *Eco*RI adapters were then removed from the 3' end of the cDNA by digestion with *Not*I (Soares, 1994). The cDNA was then ligated into the plasmid vector pBluescript® II KS+ (Stratagene, La Jolla, California), and the ligated material was transformed into *E. coli* host DH10B or DH12S by electroporation methods familiar to one skilled in the art (Soares, 1994). After growth overnight at 37°C, DNA was recovered from the *E. coli* colonies after scraping the plates by processing as directed for the Mega-prep kit (Qiagen, Chatsworth, California). The quality of the cDNA libraries was estimated by counting a portion of the total numbers of primary transformants and determining the average insert size and the percentage of plasmids with no cDNA insert. Additional cDNA libraries (human total brain, heart, kidney, leukocyte, and fetal brain) were purchased from Life Technologies, Bethesda, MD.

cDNA libraries, both oligo (dT) and random hexamer (N_6) primed, were used for isolating cDNA clones transcribed within the HBM region: human bone, human brain, human kidney and human skeletal muscle (all cDNA libraries were made by the inventors, except for skeletal muscle (dT) and kidney (dT) cDNA libraries). Four 10 x 10 arrays of each of the cDNA libraries were prepared as follows: the cDNA libraries were titered to 2.5 x 10^6 using primary transformants. The appropriate volume of frozen stock was used to inoculate 2 L of LB/ampicillin (100 mg/ml). This inoculated liquid culture was aliquoted into 400 tubes of 4 ml each. Each tube contained approximately 5000 cfu. The tubes were incubated at 30°C

overnight with gentle agitation. The cultures were grown to an OD of 0.7-0.9. Frozen stocks were prepared for each of the cultures by allocating 100 μl of culture and 300 μl of 80% glycerol. Stocks were frozen in a dry ice/ethanol bath and stored at -70°C. The remaining culture was DNA prepared using the Qiagen (Chatsworth, CA) spin miniprep kit according to the manufacturer's instructions. The DNAs from the 400 cultures were pooled to make 80 column and row pools. The cDNA libraries were determined to contain HBM cDNA clones of interest by PCR. Markers were designed to amplify putative exons. Once a standard PCR optimization was performed and specific cDNA libraries were determined to contain cDNA clones of interest, the markers were used to screen the arrayed library. Positive addresses indicating the presence of cDNA clones were confirmed by a second PCR using the same markers.

Once a cDNA library was identified as likely to contain cDNA clones corresponding to a specific transcript of interest from the HBM region, it was manipulated to isolate the clone or clones containing cDNA inserts identical to the EST or direct-selected cDNA of interest. This was accomplished by a modification of the standard "colony screening" method (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor NY (1989)). Specifically, twenty 150 mm LB+ampicillin agar plates were spread with 20,000 colony forming units (cfu) of cDNA library and the colonies allowed to grow overnight at 37°C. Colonies were transferred to nylon filters (Hybond from Amersham, or equivalent) and duplicates prepared by pressing two filters together essentially as described (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor NY (1989)). The "master" plate was then incubated an additional 6-8 hours to allow the colonies to grow back. The DNA from the bacterial colonies was then affixed to the nylon filters by treating the filters sequentially with denaturing solution (0.5 N NaOH, 1.5 M NaCl) for two minutes, neutralization solution (0.5 M Tris-Cl pH 8.0, 1.5 M NaCl) for two minutes (twice). The bacterial colonies were removed from the filters by washing in a solution of 2X SSC/0.1% SDS for one minute while rubbing with tissue paper. The filters were air dried and baked under vacuum at 80°C for 1-2 hours.

A cDNA hybridization probe was prepared by random hexamer labeling (Fineberg

and Vogelstein, *Anal. Biochem.*, 132:6-13 (1983)) or by including gene-specific primers and no random hexamers in the reaction (for small fragments). Specific activity was calculated and was >5x10^8 cpm/10^8 μg of cDNA. The colony membranes were then prewashed in 10 mM Tris-Cl pH 8.0, 1 M NaCl, 1 mM EDTA, 0.1% SDS for 30 minutes at 55°C. Following the prewash, the filters were prehybridized in > 2 ml/filter of 6X SSC, 50 % deionized formamide, 2% SDS, 5X Denhardt's solution, and 100 mg/ml denatured salmon sperm DNA, at 42°C for 30 minutes. The filters were then transferred to hybridization solution (6X SSC, 2% SDS, 5X Denhardt's, 100 mg/ml denatured salmon sperm DNA) containing denatured α^{32}P-dCTP-labeled cDNA probe and incubated at 42°C for 16-18 hours.

After the 16-18 hour incubation, the filters were washed under constant agitation in 2X SSC, 2% SDS at room temperature for 20 minutes, followed by two washes at 65°C for 15 minutes each. A second wash was performed in 0.5 X SSC, 0.5% SDS for 15 minutes at 65°C. Filters were then wrapped in plastic wrap and exposed to radiographic film for several hours to overnight. After film development, individual colonies on plates were aligned with the autoradiograph so that they could be picked into a 1 ml solution of LB Broth containing ampicillin. After shaking at 37°C for 1-2 hours, aliquots of the solution were plated on 150 mm plates for secondary screening. Secondary screening was identical to primary screening (above) except that it was performed on plates containing ~250 colonies so that individual colonies could be clearly identified for picking.

After colony screening with radiolabeled probes yielded cDNA clones, the clones were characterized by restriction endonuclease cleavage, PCR, and direct sequencing to confirm the sequence identity between the original probe and the isolated clone. To obtain the full-length cDNA, the novel sequence from the end of the clone identified was used to probe the library again. This process was repeated until the length of the cDNA cloned matches that estimated to be full-length by the northern blot analysis.

RT-PCR was used as another method to isolate full length clones. The cDNA was synthesized and amplified using a "Superscript One Step RT-PCR" kit (Life Technologies, Gaithersburg, MD). The procedure involved adding 1.5 μg of RNA to the following: 25 μl of reaction mix provided which is a proprietary buffer mix with $MgSO_4$ and dNTP's, 1 μl sense primer (10 μM) and 1 μl anti-sense primer (10 μM), 1 μl reverse transcriptase and *Taq* DNA

polymerase mix provided and autoclaved water to a total reaction mix of 50 µl. The reaction was then placed in a thermocycler for 1 cycle at 50°C for 15 to 30 minutes, then 94°C for 15 seconds, 55-60°C for 30 seconds and 68-72°C for 1 minute per kilobase of anticipated product and finally 1 cycle of 72°C for 5-10 minutes. The sample was analyzed on an agarose gel. The product was excised from the gel and purified from the gel (GeneClean, Bio 101). The purified product was cloned in pCTNR (General Contractor DNA Cloning System, 5 Prime - 3 Prime, Inc.) and sequenced to verify that the clone was specific to the gene of interest.

Rapid Amplification of cDNA ends (RACE) was performed following the manufacturer's instructions using a Marathon cDNA Amplification Kit (Clontech, Palo Alto, CA) as a method for cloning the 5' and 3' ends of candidate genes. cDNA pools were prepared from total RNA by performing first strand synthesis, where a sample of total RNA sample was mixed with a modified oligo (dT) primer, heated to 70°C, cooled on ice and followed by the addition of: 5X first strand buffer, 10 mM dNTP mix, and AMV Reverse Transcriptase (20 U/µl). The tube was incubated at 42°C for one hour and then the reaction tube was placed on ice. For second strand synthesis, the following components were added directly to the reaction tube: 5x second strand buffer, 10 mM dNTP mix, sterile water, 20X second strand enzyme cocktail and the reaction tube was incubated at 16°C for 1.5 hours. T4 DNA Polymerase was added to the reaction tube and incubated at 16°C for 45 minutes. The second-strand synthesis was terminated with the addition of an EDTA/Glycogen mix. The sample was subjected to a phenol/chloroform extraction and an ammonium acetate precipitation. The cDNA pools were checked for quality by analyzing on an agarose gel for size distribution. Marathon cDNA adapters (Clontech) were then ligated onto the cDNA ends. The specific adapters contained priming sites that allowed for amplification of either 5' or 3' ends, depending on the orientation of the gene specific primer (GSP) that was chosen. An aliquot of the double stranded cDNA was added to the following reagents: 10 µM Marathon cDNA adapter, 5x DNA ligation buffer, T4 DNA ligase. The reaction was incubated at 16°C overnight. The reaction was heat inactivated to terminate the reaction. PCR was performed by the addition of the following to the diluted double stranded cDNA pool: 10X cDNA PCR reaction buffer, 10 µM dNTP mix, 10 µM GSP, 10 µM AP1 primer

(kit), 50x Advantage cDNA Polymerase Mix. Thermal Cycling conditions were 94°C for 30 seconds, 5 cycles of 94°C for 5 seconds, 72°C for 4 minutes, 5 cycles of 94°C for 5 seconds, 70°C for 4 minutes, 23 cycles of 94°C for 5 seconds, 68°C for 4 minutes. After the first round of PCR was performed using the GSP to extend to the end of the adapter to create the adapter primer binding site, exponential amplification of the specific cDNA of interest was observed. Usually a second nested PCR is performed to confirm the specific cDNA. The RACE product was analyzed on an agarose gel and then excised and purified from the gel (GeneClean, BIO 101). The RACE product was then cloned into pCTNR (General Contractor DNA Cloning System, 5' - 3', Inc.) and the DNA sequence determined to verify that the clone is specific to the gene of interest.

13. Mutation Analysis

Comparative genes were identified using the above procedures and the exons from each gene were subjected to mutation detection analysis. Comparative DNA sequencing was used to identify polymorphisms in HBM candidate genes from chromosome 11q12-13. DNA sequences for candidate genes were amplified from patient lymphoblastoid cell lines.

The inventors developed a method based on analysis of direct DNA sequencing of PCR products amplified from candidate regions to search for the causative polymorphism. The procedure consisted of three stages that used different subsets of HBM family to find segregating polymorphisms and a population panel to assess the frequency of the polymorphisms. The family resources result from a single founder leading to the assumption that all affected individuals will share the same causative polymorphism.

Candidate regions were first screened in a subset of the HBM family consisting of the proband, daughter, and her mother, father and brother. Monochromosomal reference sequences were produced concurrently and used for comparison. The mother and daughter carried the HBM polymorphism in this nuclear family, providing the ability to monitor polymorphism transmission. The net result is that two HBM chromosomes and six non-HBM chromosomes were screened. This allowed exclusion of numerous frequent alleles. Only alleles exclusively present in the affected individuals passed to the next level of analysis.

Polymorphisms that segregated exclusively with the HBM phenotype in this original family were then re-examined in an extended portion of the HBM pedigree consisting of two additional nuclear families. These families consisted of five HBM and three unaffected individuals. The HBM individuals in this group included the two critical crossover individuals, providing the centromeric and telomeric boundaries of the critical region. Tracking the heredity of polymorphisms between these individuals and their affected parents allowed for further refining of the critical region. This group brought the total of HBM chromosomes screened to seven and the total of non-HBM chromosomes to seventeen.

When a given polymorphism continued to segregate exclusively with the HBM phenotype in the extended group, a population panel was then examined. This panel of 84 persons consisted of 42 individuals known to have normal bone mineral density and 42 individuals known to be unrelated but with untyped bone mineral density. For this purpose, normal bone mineral density is within two standard deviations of a BMD Z score of 0. The second group was from the widely used CEPH panel of individuals. Any segregating polymorphisms found to be rare in this population were subsequently examined on the entire HBM pedigree and a larger population.

Polymerase chain reaction (PCR) was used to generate sequencing templates from the HBM family's DNA and monochromosomal controls. Enzymatic amplification of genes within the HBM region on 11q12-13 was accomplished using the PCR with oligonucleotides flanking each exon as well as the putative 5' regulatory elements of each gene. The primers were chosen to amplify each exon as well as 15 or more base pairs within each intron on either side of the splice. All PCR primers were made as chimeras to facilitate dye primer sequencing. The M13-21F (5'- GTA A CGA CGG CCA GT -3') (SEQ ID NO:30) and -28REV (5'- AAC AGC TAT GAC CAT G -3') (SEQ ID NO:31) primer binding sites were built on to the 5' end of each forward and reverse PCR primer, respectively, during synthesis. 150 ng of genomic DNA was used in a 50 µl PCR with 2 U AmpliTaq, 500 nM primer and 125 µM dNTP. Buffer and cycling conditions were specific to each primer set. TaqStart antibody (Clontech) was used for hot start PCR to minimize primer dimer formation. 10% of the product was examined on an agarose gel. The appropriate samples were diluted 1:25 with deionized water before sequencing.

Each PCR product was sequenced according to the standard Energy Transfer primer (Amersham) protocol. All reactions took place in 96 well trays. 4 separate reactions, one each for A, C, G and T were performed for each template. Each reaction included 2 µl of the sequencing reaction mix and 3 µl of diluted template. The plates were then heat sealed with foil tape and placed in a thermal cycler and cycled according to the manufacturer's recommendation. After cycling, the 4 reactions were pooled. 3 µl of the pooled product was transferred to a new 96 well plate and 1 µl of the manufacturer's loading dye was added to each well. All 96 well pipetting procedures occurred on a Hydra 96 pipetting station (Robbins Scientific, USA). 1 µl of pooled material was directly loaded onto a 48 lane gel running on an ABI 377 DNA sequencer for a 10 hour, 2.4 kV run.

Polyphred (University of Washington) was used to assemble sequence sets for viewing with *Consed* (University of Washington). Sequences were assembled in groups representing all relevant family members and controls for a specified target region. This was done separately for each of the three stages. Forward and reverse reads were included for each individual along with reads from the monochromosomal templates and a color annotated reference sequence. *Polyphred* indicated potential polymorphic sites with a purple flag. Two readers independently viewed each assembly and assessed the validity of the purple-flagged sites.

A total of 23 exons present in the mature mRNA and several other portions of the primary transcript were evaluated for heterozygosity in the nuclear family of two HBM-affected and two unaffected individuals. 25 SNPs were identified, as shown in the table below.

TABLE 8

Single Nucleotide Polymorphisms in the *Zmax1* (*LRP5*) Gene and Environs

Exon Name	Location	Base Change
b200e21-h_Contig1_1.nt	69169 (309G)	C/A
b200e21-h_Contig4_12.nt	27402 (309G)	A/G
b200e21-h_Contig4_13.nt	27841 (309G)	T/C
b200e21-h_Contig4_16.nt	35600 (309G)	A/G
b200e21-h_Contig4_21.nt	45619 (309G)	G/A

Exon Name	Location	Base Change
b200e21-h_Contig4_22.nt-a	46018 (309G)	T/G
b200e21-h_Contig4_22.nt-b	46093 (309G)	T/G
b200e21-h_Contig4_22.nt-c	46190 (309G)	A/G
b200e21-h_Contig4_24.nt-a	50993 (309G)	T/C
b200e21-h_Contig4_24.nt-b	51124 (309G)	C/T
b200e21-h_Contig4_25.nt	55461 (309G)	C/T
b200e21-h_Contig4_33.nt-a	63645 (309G)	C/A
b200e21-h_Contig4_33.nt-b	63646 (309G)	A/C
b200e21-h_Contig4_61.nt	24809 (309G)	T/G
b200e21-h_Contig4_62.nt	27837 (309G)	T/C
b200e21-h_Contig4_63.nt-a	31485 (309G)	C/T
b200e21-h_Contig4_63.nt-b	31683 (309G)	A/G
b200e21-h_Contig4_9.nt	24808 (309G)	T/G
b527d12-h_Contig030g_1.nt-a	31340 (308G)	T/C
b527d12-h_Contig030g_1.nt-b	32538 (308G)	A/G
b527d12-h_Contig080C_2.nt	13224 (308G)	A/G
b527d12-h_Contig087C_1.nt	21119 (308G)	C/A
b527d12-h_Contig087C_4.nt	30497 (308G)	G/A
b527d12-h_Contig088C_4.nt	24811 (309G)	A/C
b527d12-h_Contig089_1HP.nt	68280 (309G)	G/A

In addition to the polymorphisms presented in Table 8, two additional polymorphisms can also be present in SEQ ID NO:2. These is a change at position 2002 of SEQ ID NO:2. Either a guanine or an adenine can appear at this position. This polymorphism is silent and is not associated with any change in the amino acid sequence. The second change is at position 4059 of SEQ ID NO:2 corresponding in a cytosine (C) to thymine (T) change. This polymorphism results in a corresponding amino acid change from a valine (V) to an alanine (A). Other polymorphisms were found in the candidate gene exons and adjacent intron sequences as displayed in Tables 2 and 3. Any one or combination of the polymorphisms

listed in Tables 2, 3 or 8 or the two discussed above could also have a minor effect on bone mass when present in SEQ ID NO:2. These could also be in combination with any of the other mutations discussed in Section 3 and in the Examples below.

The present invention encompasses the nucleic acid sequences having the nucleic acid sequence of SEQ ID NO: 1 with any one or more of the above-identified point mutations.

Preferably, the present invention encompasses the nucleic acid of SEQ ID NO: 2 or is a mutation in SEQ ID NO:1 that produces a phenotype like that observed with the protein encoded by SEQ ID NO:2 (HBM phenotype). Specifically, a base-pair substitution changing G to T at position 582 in the coding sequence of Zmax1 (the *HBM* gene) was identified as heterozygous in all HBM individuals, and not found in the unaffected individuals (i.e., b527d12-h_Contig087C_1.nt). Fig. 6 shows the order of the contigs in B527D12. The direction of transcription for the *HBM* gene is from left to right. The sequence of contig308G of B527D12 is the reverse complement of the coding region to the *HBM* gene. Therefore, the relative polymorphism in contig 308G shown in Table 8 as a base change substitution of C to A is the complement to the G to T substitution in the *HBM* gene. This mutation causes a substitution of glycine 171 with valine (G171V).

The HBM polymorphism was confirmed by examining the DNA sequence of different groups of individuals. In all members of the HBM pedigree (38 individuals), the HBM polymorphism was observed in the heterozygous form in affected (i.e., elevated bone mass) individuals only (N=18). In unaffected relatives (N=20) (BMDZ<2.0), the HBM polymorphism was never observed. To determine whether this polymorphism was ever observed in individuals outside of the HBM pedigree, 297 phenotyped individuals were characterized at the site of the *HBM* gene. None were heterozygous at the site of the HBM polymorphism. In an unphenotyped control group, none of 64 individuals were observed to be heterozygous at position 582. Taken together, these data prove that the polymorphism observed in the kindred displaying the high bone mass phenotype is strongly correlated with the G→T polymorphism at position 582 of Zmax1 (LRP5). Furthermore, these results coupled with the ASO results described below, establish that the HBM polymorphism genetically segregates with the HBM phenotype, and that both the HBM polymorphism and

phenotype are rare in the general population.

13. Allele Specific Oligonucleotide (ASO) Analysis

The amplicon containing the HBM polymorphism was PCR amplified using primers specific for the exon of interest. The appropriate population of individuals was PCR amplified in 96 well microtiter plates as follows. PCR reactions (20 µl) containing 1X Promega PCR buffer (Cat. # M1883 containing 1.5 mM $MgCl_2$), 100 mM dNTP, 200 nM PCR primers (1863F: 5'-CCAAGTTCTGAGAAGTCC-3' and 1864R: 5'-AATACCTGAAACCATACCTG-3'; SEQ ID NOS: 629 and 630 respectively), 1 U AmpliTaq™, and 20 ng of genomic DNA were prepared and amplified under the following PCR conditions: 94°C, 1 minute, (94°C, 30 sec.; 58°C, 30 sec.; 72°C, 1 min X35 cycles), 72°C, 5 min, 4°C, hold. Loading dye was then added and 10 µl of the products was electrophoresed on 1.5% agarose gels containing 1 µg/ml ethidium bromide at 100-150 V for 5-10 minutes. Gels were treated 20 minutes in denaturing solution (1.5 M NaCl, 0.5 N NaOH), and rinsed briefly with water. Gels were then neutralized in 1 M Tris-HCl, pH 7.5, 1.5 M NaCl, for 20 minutes and rinsed with water. Gels were soaked in 10 X SSC for 20 minutes and blotted onto nylon transfer membrane (Hybond N+- Amersham) in 10X SSC overnight. Filters were the rinsed in 6X SSC for 10 minutes and UV crosslinked.

The allele specific oligonucleotides (ASO) were designed with the polymorphism approximately in the middle. Oligonucleotides were phosphate free at the 5' end and were purchased from Gibco BRL. Sequences of the oligonucleotides are:

2326 Zmax1.ASO.g: 5'-AGACTGGGGTGAGACGC-3' (SEQ ID NO:631)

2327 Zmax1.ASO.t: 5'-CAGACTGGGTTGAGACGCC-3' (SEQ ID NO:632)

The polymorphic nucleotides are underlined. To label the oligos, 1.5 µl of 1 µg/µl ASO oligo (2326.Zmax1.ASO.g or 2327.Zmax1.ASO.t), 11 µl ddH_2O, 2 µl 10X kinase forward buffer, 5 µl γ^{32}P-ATP (6000 Ci/mMole), and 1 µl T4 polynucleotide kinase (10 U/µl) were mixed, and the reaction incubated at 37°C for 30-60 minutes. Reactions were then placed at 95°C for 2 minutes and 30 ml H_2O was added. The probes were purified using a G25 microspin column (Pharmacia).

Blots were prehybridized in 10 ml 5X SSPE, 5X Denhardt's, 2% SDS, and 100 μg/ml, denatured, sonicated salmon sperm DNA at 40°C for 2 hr. The entire reaction mix of kinased oligo was then added to 10 ml fresh hybridization buffer (5X SSPE, 5X Denhardt's, 2% SDS) and hybridized at 40°C for at least 4 hours to overnight.

All washes done in 5X SSPE, 0.1 % SDS. The first wash was at 45°C for 15 minutes; the solution was then changed and the filters washed 50°C for 15 minutes. Filters were then exposed to Kodak biomax film with 2 intensifying screens at –70°C for 15 minutes to 1 hr. If necessary the filters were washed at 55°C for 15 minutes and exposed to film again. Filters were stripped by washing in boiling 0.1X SSC, 0.1% SDS for 10 minutes at least 3 times.

The two films that best captured the allele specific assay with the 2 ASOs were converted into digital images by scanning them into Adobe PhotoShop. These images were overlaid against each other in Graphic Converter and then scored and stored in FileMaker Pro 4.0 (see Fig. 9).

In order to determine the HBM allele frequency in ethnically diverse populations, 672 random individuals from various ethnic groups were typed by the allele specific oligonucleotide (ASO) method. This population included 96 CEPH grandparents (primarily Caucasian), 192 Caucasian, 192 African-American, 96 Hispanic, and 96 Asian individuals. No evidence was obtained for the presence of the HBM polymorphism in any of these individuals. Overall, a total of 911 individuals were typed either by direct sequencing or ASO hybridization; all were homozygous GG at the site of the HBM polymorphism (Fig. 14). This information illustrates that the HBM allele is rare in various ethnic populations.

Thus this invention provides a rapid method of identifying individuals with the HBM allele. This method could be used in the area of diagnostics and screening of an individual for susceptibility to osteoporosis or other bone disorder. The assay could also be used to identify additional individuals with the HBM allele or the additional polymorphisms described herein.

14. Cellular Localization of Zmax1 (LRP5)

14.1 Gene Expression in rat tibia by non isotopic *in situ* Hybridization

In situ hybridization was conducted by Pathology Associates International (PAI), Frederick, MD. This study was undertaken to determine the specific cell types that express the *Zmax1* (*LRP5*) gene in rat bone with particular emphasis on areas of bone growth and remodeling. Zmax1 (LRP5) probes used in this study were generated from both human (HuZmax1) and mouse (MsZmax1) cDNAs, which share an 87% sequence identity. The homology of human and mouse Zmax1 (LRP5) with rat Zmax1 (LRP5) is unknown.

For example, gene expression by non-isotopic *in situ* hybridization was performed as follows, but other methods would be known to the skilled artisan. Tibias were collected from two 6 to 8 week old female Sprague Dawley rats euthanized by carbon dioxide asphyxiation. Distal ends were removed and proximal tibias were snap frozen in OCT embedding medium with liquid nitrogen immediately following death. Tissues were stored in a –80°C freezer.

Probes for amplifying PCR products from cDNA were prepared as follows. The primers to amplify PCR products from a cDNA clone were chosen using published sequences of both human LRP5 (GenBank Accession No. ABO17498) and mouse LRP5 (GenBank Accession No. AF064984). In order to minimize cross reactivity with other genes in the LDL receptor family, the PCR products were derived from an intracellular portion of the protein coding region. PCR was performed in a 50 µl reaction volume using cDNA clone as template. PCR reactions contained 1.5 mM $MgCl_2$, 1 unit AmpliTaq, 200 µM dNTPs and 2 µM each primer. PCR cycling conditions were 94°C for 1 min., followed by 35 cycles of 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 30 seconds; followed by a 5 minute extension at 72°C. The reactions were then run on a 1.5% agarose Tris-Acetate gel. DNA was eluted from the agarose, ethanol precipitated and resuspended in 10 mM Tris, pH 8.0. Gel purified PCR products were prepared for both mouse and human cDNAs and supplied to

Pathology Associates International for *in situ* hybridizations.

The sequence of the human and mouse PCR primers and products were as follows:

Human Zmax1 (LRP5) sense primer (HBM253)

5'-CCCGTGTGCTCCGCCGCCCAGTTC-3' (SEQ ID NO:633)

Human Zmax1 (LRP5) antisense primer (HBM465)

5'-GGCTCACGGAGCTCATCATGGACTT-3' (SEQ ID NO:634)

Human Zmax1 PCR product

5'-CCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCT
GCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGG
ACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGT
CCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAG
CTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGT
GCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTA
TTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTC
CCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGG
GCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGA
GCTCCGTGAGCC-3' (SEQ ID NO:635)

Mouse Zmax1 (LRP5) Sense primer (HBM655)

5'-AGCGAGGCCACCATCCACAGG-3' (SEQ ID NO:636)

Mouse Zmax1 (LRP5) antisense primer (HBM656)

5'-TCGCTGGTCGGCATAATCAAT-3' (SEQ ID NO:637)

Mouse (LRP5) 1 PCR product

5'-AGCAGAGCCACCATCCACAGGATCTCCCTGGAGACTAACAACAACGATGTGG
CTATCCCACTCACGGGTGTCAAAGAGGCCTCTGCACTGGACTTTGATGTGTCCAA

CAATCACATCTACTGGACTGATGTTAGCCTCAAGACGATCAGCCGAGCCTTCATG
AATGGGAGCTCAGTGGAGCACGTGATTGAGTTTGGCCTCGACTACCCTGAAGGA
ATGGCTGTGGACTGGATGGGCAAGAACCTCTATTGGGCGGACACAGGGACCAAC
AGGATTGAGGTGGCCCGGCTGGATGGGCAGTTCCGGCAGGTGCTTGTGTGGAGA
GACCTTGACAACCCCAGGTCTCTGGCTCTGGATCCTACTAAAGGCTACATCTACT
GGACTGAGTGGGGTGGCAAGCCAAGGATTGTGCGGGCCTTCATGGATGGGACCA
ATTGTATGACACTGGTAGACAAGGTGGGCCGGGCCAACGACCTCACCATTGATT
ATGCCGACCAGCGA-3′ (SEQ ID NO:638)

Riboprobes were synthesized as follows. The PCR products were reamplified with chimeric primers designed to incorporate either a T3 promoter upstream, or a T7 promoter downstream of the reamplification products. The resulting PCR products were used as template to synthesize digoxigenin-labeled riboprobes by *in vitro* transcription (IVT). Antisense and sense riboprobes were synthesized using T7 and T3 RNA polymerases, respectively, in the presence of digoxigenin-11-UTP (Boehringer-Mannheim) using a MAXIscript IVT kit (Ambion) according to the manufacturer. The DNA was then degraded with Dnase-1, and unincorporated digoxigenin was removed by ultrafiltration. Riboprobe integrity was assessed by electrophoresis through a denaturing polyacrylamide gel. Molecular size was compared with the electrophoretic mobility of a 100–1000 base pair (bp) RNA ladder (Ambion). Probe yield and labeling was evaluated by blot immunochemistry. Riboprobes were stored in 5 μl aliquots at –80°C.

The *in situ* hybridization was performed as follows. Frozen rat bone was cut into 5 μM sections on a Jung CM3000 cryostat (Leica) and mounted on adhesive slides (Instrumedics). Sections were kept in the cryostat at –20°C until all the slides were prepared in order to prevent mRNA degradation prior to post-fixation for 15 minutes in 4% paraformaldehyde. Following post-fixation, sections were incubated with 1 ng/μl of either

antisense or sense riboprobe in Pathology Associates International (PAI) customized hybridization buffer for approximately 40 hours at 58°C. Following hybridization, slides were subjected to a series of post-hybridization stringency washes to reduce nonspecific probe binding. Hybridization was visualized by immunohistochemistry with an anti-digoxigenin antibody (FAB fragment) conjugated to alkaline phosphatase. Nitroblue tetrazolium chloride/bromochloroindolyl phosphate (Boehringer-Mannheim), a precipitating alkaline phosphatase substrate, was used as the chromogen to stain hybridizing cells purple to nearly black, depending on the degree of staining. Tissue sections were counter-stained with nuclear fast red. Assay controls included omission of the probe, omission of probe and anti-digoxigenin antibody.

Specific cell types were assessed for demonstration of hybridization with antisense probes by visualizing a purple to black cytoplasmic and/or peri-nuclear staining indicating a positive hybridization signal for mRNA. Each cell type was compared to the replicate sections, which were hybridized with the respective sense probe. Results were considered positive if staining was observed with the antisense probe and no staining or weak background with the sense probe.

The cellular localization of the hybridization signal for each of the study probes is summarized in Table 9. Hybridization for Zmax1 (LRP5) was primarily detected in areas of bone involved in remodeling, including the endosteum and trabecular bone within the metaphysis. Hybridization in selected bone lining cells of the periosteum and epiphysis were also observed. Positive signal was also noted in chondrocytes within the growth plate, particularly in the proliferating chondrocytes. See Figs. 10, 11 and 12 for representative photomicrographs of *in situ* hybridization results.

TABLE 9

Summary of Zmax1 (LRP5) *in situ* hybridization in rat tibia

PROBE	SITE	ISH SIGNAL
Hu Zmax1	Epiphysis	
	Osteoblasts	+
	Osteoclasts	-
	Growth Plate	
	resting chondrocytes	-
	proliferating chondrocytes	+
	hypertrophic chondrocytes	-
	Metaphysis	
	osteoblasts	+
	osteoclasts	+
	Diaphysis	-
	Endosteum	
	osteoblasts	+
	osteoclasts	+
	Periosteum	-
MsZmax1	Epiphysis	
	Osteoblasts	+
	Osteoclasts	-
	Growth Plate	
	resting chondrocytes	-
	proliferating chondrocytes	+
	hypertrophic chondrocytes	+
	Metaphysis	
	osteoblasts	+
	osteoclasts	+
	Diaphysis	-
	Endosteum	
	osteoblasts	+
	osteoclasts	+
	Periosteum	+

Legend: "+" = hybridization signal detected "-" = no hybridization signal detected

"ISH" – *In situ* hybridization

These studies confirm the positional expression of Zmax1 (LRP5) in cells involved in bone remodeling and bone formation. Zmax1 (LRP5) expression in the zone of proliferation

and in the osteoblasts and osteoclasts of the proximal metaphysis, suggests that the *Zmax1* (*LRP5*) gene is involved in the process of bone growth and mineralization. The activity and differentiation of osteoblasts and osteoclasts are closely coordinated during development as bone is formed and during growth as well as in adult life as bone undergoes continuous remodeling. The formation of internal bone structures and bone remodeling result from the coupling of bone resorption by activated osteoclasts with subsequent deposition of new material by osteoblasts. Zmax1 (LRP5) is related to the LDL receptor gene, and thus may be a receptor involved in mechanosensation and subsequent signaling in the process of bone remodeling. Therefore, changes in the level of expression of this gene could impact on the rate of remodeling and degree of mineralization of bone.

15. Antisense

Antisense oligonucleotides are short synthetic nucleic acids that contain complementary base sequences to a targeted RNA. Hybridization of the RNA in living cells with the antisense oligonucleotide interferes with RNA function and ultimately blocks protein expression. Therefore, any gene for which the partial sequence is known can be targeted by an antisense oligonucleotide.

Antisense technology is becoming a widely used research tool and will play an increasingly important role in the validation and elucidation of therapeutic targets identified by genomic sequencing efforts.

Antisense technology was developed to inhibit gene expression by utilizing an oligonucleotide complementary to the mRNA that encodes the target gene. There are several possible mechanisms for the inhibitory effects of antisense oligonucleotides. Among them, degradation of mRNA by RNase H is considered to be the major mechanism of inhibition of protein function. This technique was originally used to elucidate the function of a target gene, but may also have therapeutic applications, provided it is designed carefully and properly.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed

using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethlaminomethyluracil, dihydrouracil, β-D-galactosylqueosine, inosine, N6-isopentenyladenine, I-methylguanine, I-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), t-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In addition, the use of morpholino oligonucleotides could be employed. Morpholinos are oligomers with modification of the ribose moiety to a morpholino group. This technology is covered by U.S. Patent No. 5,185,444 and is described in Summerton *et al.*, 1997 *Antisense Nucleic Acid Drug Dev.* 7(3): 187-95. The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an HBM or Zmax1 (LRP5) protein or a protein which interacts with Zmax1 (LRP5) and/or HBM to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration

of an antisense nucleic acid molecule of the invention includes direct injection at a tissue site. Alternatively, an antisense nucleic acid molecule can be modified to target selected cells and then administered systemically. For example, for systemic administration, an antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An μ-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual γ-units, the strands run parallel to each other (Gaultier *et al.,* 1987 *Nucl. Acids Res.* 15: 6625-41). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987 *Nucl. Acids Res.* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987 *FEBS Lett.* 215: 327-330). In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff *et al.*, 1988 *Nature* 334: 585-591) can be used to catalytically cleave Zmax1 (LRP5) or HBM mRNA transcripts to thereby inhibit translation of Zmax1 (LRP5) or HBM mRNA. A ribozyme having specificity for a Zmax1- or HBM-encoding nucleic acid can be designed based upon the nucleotide sequence of a Zmax1 (LRP5) or HBM cDNA disclosed herein (i.e., SEQ ID NOS:1 or 3). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an HBM or Zmax1-encoding mRNA. See, e.g., Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742 both incorporated herein by reference. Alternatively, Zmax1 (LRP5) or HBM mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, 1993 *Science* 261: 1411-1418. Alternatively, *Zmax1* (*LRP5*) or *HBM* gene expression can be inhibited by targeting nucleotide sequences

complementary to the regulatory region of the *Zmax1* (*LRP5*)or *HBM* gene (e.g., the *Zmax1* or *HBM* gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the *Zmax1* (*LRP5*) or *HBM* genes in target cells. See generally, Helene, 1991 *Anticancer Drug Des.* 6(6):569-84; Helene *et al.*, 1992 *Ann. N.Y. Acad Sci.* 660:27-36; and Maher, 1992 *Bioassays* 14(12):807-15.

Zmax1 (*LRP5*), LRP6, HBM-like and *HBM* gene expression can also be inhibited using RNA interference (RNAi) caused by small inhibitory RNAs (siRNAs). This is a technique for post-transcriptional gene silencing (PTGS), in which target gene activity is specifically abolished with cognate double-stranded RNA (dsRNA). siRNAs resemble in many aspects PTGS in plants and has been detected in many invertebrates including trypanosome, hydra, planaria, nematode and fruit fly (*Drosophila melanogaster*). It may be involved in the modulation of transposable element mobilization and antiviral state formation. RNAi in mammalian systems is disclosed in PCT application WO 00/63364 which is incorporated by reference herein in its entirety. See also, Elbashir *et al.*, 2001 *Nature* 411: 494-98. Basically, dsRNA, homologous to the target (Zmax1 or HBM) is introduced into the cell and a sequence specific reduction in gene activity is observed.

Another embodiment contemplates the use of small hairpin RNAs (shRNAs). These compounds are described further in Yu *et al.*, 2002 *Proc. Natl. Acad. Sci. USA* 99: 6047-52; and Paddison *et al.*, 2002 *Genes & Devel.* 16: 948-58.

As an example, preparing antisense oligonucleotides can be performed as follows. Studies have been undertaken using antisense technology in the osteoblast-like murine cell line, MC3T3. These cells can be triggered to develop along the bone differentiation sequence. An initial proliferation period is characterized by minimal expression of differentiation markers and initial synthesis of collagenous extracellular matrix. Collagen matrix synthesis is required for subsequent induction of differentiation markers. Once the matrix synthesis begins, osteoblast marker genes are activated in a clear temporal sequence: alkaline phosphatase is induced at early times while bone sialoprotein and osteocalcin appear later in the differentiation process. This temporal sequence of gene expression is useful in monitoring the maturation and mineralization process. Matrix mineralization, which does not

begin until several days after maturation has started, involves deposition of mineral on and within collagen fibrils deep within the matrix near the cell layer-culture plate interface. The collagen fibril–associated mineral formed by cultured osteoblasts resembles that found in woven bone *in vivo* and therefore is used frequently as a study reagent.

MC3T3 cells were transfected with antisense oligonucleotides for the first week of the differentiation, according to the manufacturer's specifications (U.S. Patent No. 5,849,902).

The oligonucleotides designed for Zmax1 (LRP5) are given below:

10875: 5'-AGUACAGCUUCUUGCCAACCCAGUC-3' (SEQ ID NO:639)

10876: 5'-UCCUCCAGGUCGAUGGUCAGCCCAU-3' (SEQ ID NO:640)

10877: 5'-GUCUGAGUCCGAGUUCAAAUCCAGG-3' (SEQ ID NO:641)

Fig. 13 shows the results of antisense inhibition of (LRP5) 1 in MC3T3 cells. The three oligonucleotides shown above were transfected into MC3T3 and RNA was isolated according to standard procedures. Northern analysis clearly shows markedly lower steady state levels of the Zmax1 (LRP5) transcript while the control gene GAPDH remained unchanged. Thus, antisense technology using the primers described above allows for the study of the role of Zmax1 (LRP5) expression on bone biology.

16. Yeast Two Hybrid

In order to identify the signaling pathway that Zmax1 (LRP5) participates in to modulate bone density, the yeast two hybrid protein interaction technology was utilized. This technique facilitates the identification of proteins that interact with one another by coupling tester proteins to components of a yeast transcription system (Fields *et al.*, 1989 *Nature* 340: 245-246; U.S. Pat. No. 5,283,173 by Fields *et al.*; Johnston, 1987 *Microbiol. Rev.* 51: 458-476; Keegan *et al.*, 1986 *Science* 231: 699-704; Durfee *et al.*, 1993, *Genes Dev.* 7: 555-569; Chien *et al.*, 1991 *Proc. Natl. Acad. Sci USA* 88: 9578-9582; Fields *et al.*, 1994 *Trends in Genetics* 10: 286-292; and Gyuris *et al.*, 1993 *Cell* 75: 791-803). First a "bait" protein, the protein for which one seeks interacting proteins, is fused to the DNA binding domain of a yeast transcription factor. Second, a cDNA library is constructed that contains cDNAs fused to the transcriptional activation domain of the same yeast transcription factor;

this is termed the prey library. The bait construct and prey library are transformed into yeast cells and then mated to produce diploid cells. If the bait interacts with a specific prey from the cDNA library, the activation domain is brought into the vicinity of the promoter via this interaction. Transcription is then driven through selectable marker genes and growth on selective media indicates the presence of interacting proteins.

The amino acid sequence used in the yeast two hybrid experiments discussed herein consisted of the entire cytoplasmic domain and a portion of the transmembrane domain and is shown below (amino to carboxy orientation):

RVVCQRYAGA NGPFPHEYVS GTPHVPLNFI APGGSQHGPF TGIACGKSMM
SSVSLMGGRG GVPLYDRNHV TGASSSSSSS TKATLYPPI<u>L NPPPSPA</u>TDP
SLYNMDMFYS SNIPATVRPY RPYIIRG<u>MAP PTTP</u>CSTDVC DSDYSASRWK
ASKYYLDLNS DSDP<u>YPPPPT PH</u>SQYLSAE<u>D SCPPSP</u>ATER SYFHL<u>PPPPP</u>
<u>SPC</u>TDSS (SEQ ID NO: 765)

The last 6 amino acids of the putative transmembrane domain are indicated in bold. Putative SH3 domains are underlined. Additional amino acid sequences of 50 amino acids or greater in either the proteins encoded by the Zmax1 (LRP5) or HBM alleles can also be used as bait. The upper size of the polypeptide used as bait is limited only by the presence of a complete transmembrane domain (see Fig. 4), which will render the bait to be nonfunctional in a yeast two hybrid system. These additional bait proteins can be used to identify additional proteins which interact with the proteins encoded by HBM or Zmax1 (LRP5) in the focal adhesion signaling pathway or in other pathways in which these HBM or Zmax1 (LRP5) proteins may act. Once identified, methods of identifying agents which regulate the proteins in the focal adhesion signaling pathway or other pathways in which HBM acts can be performed as described herein for the HBM and Zmax1 (LRP5) proteins.

In order to identify cytoplasmic Zmax1 (LRP5) signaling pathways, the cytoplasmic domain of Zmax1 (LRP5) was subcloned into two bait vectors. The first vector was pDBleu, which was used to screen a brain, and Hela prey cDNA library cloned into the vector pPC86 (Clontech). The second bait vector used was pDBtrp, which was used to screen a cDNA prey library derived from the TE85 osteosarcoma cell line in vector pOP46. Another suitable vector which is widely available, is p86 (Gibco, iest™ System). Standard techniques known

to those skilled in the art were used as described in Fields and Song, 1989 *Nature* 340: 245-246; U.S. Pat. No. 5,283,173 by Fields and Song; Johnston, 1987 *Microbiol. Rev.* 51: 458-476; Keegan *et al.*, 1986 *Science* 231: 699-704; Durfee *et al.*, 1993 *Genes Dev.* 7: 555-569; Chien *et al.*, 1991 *Proc. Natl. Acad. Sci USA* 88: 9578-9582; Fields *et al.*, 1994 *Trends in Genetics* 10: 286-292; and Gyuris *et al.*, 1993 *Cell* 75: 791-803. The bait construct and prey cDNA libraries were transformed into yeast using standard procedures.

To perform the protein interaction screen, an overnight culture of the bait yeast strain was grown in 20 ml SD selective medium with 2% glucose (pDBLeu, SD -Leu medium, pDBtrp, SD –trp medium). The cultures were shaken vigorously at 30°C overnight. The cultures were diluted 1:10 with complete medium (YEPD with 2% glucose) and the cultures then incubated with shaking for 2 hrs at 30°C.

The frozen prey library was thawed, and the yeast cells reactivated by growing them in 150 ml YEPD medium with 2% glucose for 2 hrs at 30°C. A filter unit was sterilized with 70% ethanol and washed with sterile water to remove the ethanol. The cell densities of both bait and prey cultures were measured by determining the OD at 600 nm. An appropriate volume of yeast cells that corresponded to a cell number of 1 ml of OD 600 = 4 of each yeast strain, bait and prey (library) was placed in a 50 ml Falcon tube. The mixture was then filtered through the sterilized filter unit. The filter was then transferred onto a prewarmed YEPD agar plate with the cell side up, removing all air bubbles underneath the filter. Plates were then incubated at 30°C for 6 hrs. One filter was transferred into a 50 ml Falcon tube, and 10 ml of SD with 2% Glucose was added; cells were resuspended by vortexing for 10 sec.

The number of primary diploid cells (growth on SD -Leu, -Trp plates) versus the numbers of colony forming units growing on SD -Trp and SD -Leu plates only was then titered. Different dilutions were plated and incubated at 30°C for two days. The number of colony forming units was then counted. The number of diploid colonies (colonies on SD -Leu -Trp plates) permits the calculation of whether or not the whole library of prey constructs was mated to the yeast expressing the bait. This information is important to judge the quality of the screen.

16.1 Indirect selection

Resuspended cells from 5 filter-matings were then pooled and the cells sedimented by centrifugation in a 50 ml Falcon tube. Cells were then resuspended in 16 ml SD medium with 2% Glc. Two ml of this cell suspension was plated onto 8 square plates each (SD -Leu, -Trp) with sterile glass beads and selected for diploid cells by incubating at 30°C for 18 - 20 hrs.

Cells were then scraped off the square plates, the cells centrifuged and combined into one 50 ml Falcon tube. The cell pellet was then resuspended in 25 ml of SD medium with 2% glucose. The cell number was then determined by counting of an appropriate dilution (usually 1:100 to 1:1000) with a Neugebauer chamber. Approximately 5×10^7 diploid cells were plated onto the selective medium. The observations about the growth of the bait strain together with irrelevant prey vectors helps to determine which selective plates will have to be chosen for the library screen. Generally, all screens were plated on one square plate each with SD -Leu, -Trp, -His; SD -Leu, -Trp, His, 5 mM 3AT, and SD -Leu, -Trp, -His, -Ade is recommended.

The yeast cells were then spread homogeneously with sterile glass beads and incubated at 30°C for 4 days. The number of colony forming yeast cells was titered by plating different dilutions of the scraped cell suspension onto SD -Leu, -Trp plates. Usually, plating of 100 µl of a 10^{-3} and 10^{-4} dilution gave 100 - 1000 colonies per plate.

16.2 Direct selection

Five filters with the mated yeast cells were each transferred into separate 50 ml Falcon tubes and the cells resuspended with 10 ml SD medium with 2% Glc, each, followed by vortexing for 10 sec. The resuspended cells were combined and centrifuged in a Beckman centrifuge at 3000 rpm. The supernatant was discarded and the cells resuspended in 6 ml of SD medium with 2% Glc. Two ml of the suspension was spread onto each selective square plate and incubated at 30°C for 4 - 5 days.

16.3 Isolation of Single Colonies

Yeast cells from an isolated colony were picked with a sterile tooth pick and transferred into individual wells of a 96 well plate. The cells were resuspended in 50 µl of SD -Leu, -Trp, -His medium and incubated at 30°C for one day. The yeast cells were then stamped onto a SD -Leu, -Trp, -His plate in 96 well format and incubated at 30°C for 2 days. Yeast cells were also stamped onto a Nylon filter covering a YEPD plate and incubated at 30°C for one day. The cells on the Nylon filter were used for the analysis of the ß - Gal reporter activity.

Yeast colonies were scraped from the SD -Leu, -Trp, -His plate with a sterile tooth pick, and reconfigured, if necessary, according to the ß-Gal activity and then resuspended in 20 % glycerol. This served as a master plate for storage at -80°C.

For DNA preparation, yeast cells from the glycerol stock were stamped onto a SD - Trp plate and incubated at 30°C for 2 days. After two days of incubation, the yeast colonies were ready for colony PCR and sequencing. Standard colony PCR conditions were used to amplify inserts from preys recovered from the interaction screen. Sequencing was done using standard sequencing reactions and ABI377 (Perkin Elmer) fluorescent sequencing machines.

16.4 Verification of bait/prey interaction

Glycerol stocks of the prey of interest were thawed and inoculated in a 10 ml overnight culture of SD with glucose -Trp. After overnight growth, plasmid DNA preparation was performed using the BIO 101 RPM Yeast Plasmid Isolation Kit with 10 ml of culture. The culture was centrifuged and transferred to a 1.5 ml microcentrifuge tube. Yeast Lysis Matrix was then added to the pellet followed by 250 µl of Alkaline Lysis Solution. Samples were then vortexed for 5 minutes. 250 µl Neutralizing Solution was added and the sample mixed briefly. Samples were centrifuged for 2 minutes at room temperature in a microcentrifuge. The supernatant was transferred to a Spin Filter avoiding debris and Lysis Matrix. 250 µl of Glassmilk Spin Buffer was added, and the tubes inverted to mix. Samples were centrifuged for 1 min and the liquid in the Catch Tube was discarded.

500 µl of Wash Solution was added, the samples were centrifuged for 1 min, and the wash solution was discarded. The wash step was repeated once followed by a 1 min dry centrifugation to drive the remaining liquid out of the Spin Filter. The filter was transferred to a new Catch Tube and 100 µl of sterile H_2O was added; samples were then vortexed briefly to resuspend and centrifuged for 30 seconds to collect the DNA in the bottom of the Catch Tube.

Five µl of DNA was then transformed into DH10B Electromax cells using standard procedures and glycerol stocks prepared. Miniprep DNA was prepared using the Qiagen QIAprep Spin Miniprep Kit. DNA was finally eluted with 30 µl of Qiagen EB buffer. One µl of the plasmid DNA samples was then used to transform yeast cells using standard procedures. After 2 days of growth on SD –trp media, colonies were picked and patched onto fresh media. Similarly, bait colonies were patched onto SD –Leu media. Both were grown overnight at 30°C.

For mating, cells from bait and prey patches were spread together on YAPD media and incubated at 30°C for 12 hr. This plate was then replica plated onto an SD Agar-Leu-Trp plate and grown for 2 days at 30°C. To test the strength of interaction these plates were replica plated onto SD Agar-Leu-Trp-His, SD Agar-Leu-Trp-His with 5 mM 3AT and 10 mM 3AT, SD Agar-Leu-Trp-His-Ade, and SD Agar-Leu-Trp-Ura media and grown for 2 days at 30°C.

16.5 Galacton Star β-Galactosidase Activity Assay

After streaking and replica plating positive interactors on selection plates, colonies were placed in a 96 well dish with 200 µl of SD-medium, leaving wells 1 and 96 blank. Ten microliters from the first 96 well dish was plated into another flat bottom 96 well dish containing 100 µl of SD-medium. Controls consisted of a negative control and a very weak positive control. The cell density was measured at OD_{600} (a value of 1 corresponds to 1×10^7 cells utilizing a 96 well spectrophotometer). The OD was usually between 0.03 and 0.10. Using microplates specifically for the luminometer, 50 µl of reaction mixture were pipetted into each well. Fifty microliters of culture were then added and mixed by pipetting up and

down twice. The reaction was incubated for 30 minutes at room temperature followed by measurement of Relative Light Units using a luminometer.

Table 9 lists the genes identified in the yeast two hybrid screens from the 3 prey libraries tested. Two genes, zyxin and axin, were found to interact with the cytoplasmic domain of (LRP5) 1 in all three screens. Three genes, alpha-actinin, TCB and S1-5 interacted in two of the three screens.

A variety of proteins found at sites of cell-cell and cell-matrix contact (focal contacts/adesion plaques) were shown to interact with the cytoplasmic domain of Zmax1 (LRP5). These include α-actinin, Trio, Pinch-like protein, and Zyxin. PINCH is a LIM domain-containing protein that is known to interact with integrin-linked kinase, an early signaler in integrin and growth factor signaling pathways. The finding of a closely related gene in the yeast two hybrid screen raises the possibility of a novel pathway linked to integrin signaling from extracellular matrix signals. Trio, also known to localize to focal adhesions, is thought to play a key role in coordinating cell-matrix interactions and cytoskeletal rearrangements involved in cell movement. Zyxin, another LIM domain-containing protein, is also localized to adhesion plaques and is thought to be involved in reorganization of the cytoskeleton when triggers are transmitted via integrin signaling pathways. Zyxin also interacts with alpha actinin, which we identified as interacting with Zmax1 (LRP5). Other LIM domain containing proteins identified include the human homologue of mouse ajuba, LIMD1, and a novel LIMD1-like protein.

Axin was also identified from the two hybrid experiments. This protein is involved in inhibition of the Wnt signaling pathway and interacts with the tumor suppressor APC. There is a link here with the focal adhesion signaling described above: one common step in the two pathways involves inhibition of glycogen synthase kinase 3, which in turn results in the activation of ß-catenin/Lef-1 and AP-1 transcription factors. Axin/APC are involved in this as well as integrin linked kinase. The Wnt pathway has a role in determining cell fates during embryogenesis. If inappropriately activated, the Wnt pathway may also lead to cancer. The Wnt pathway also seems to have a role in cytoskeletal rearrangements. In a *Xenopus* embryo assay, the combination of HBM and Wnt5a proteins stimulated the Wnt pathway to a much

greater extent than the combination of Zmax1 (LRP5) and Wnt5a, which was modestly above the control and Wnt5a alone scores. The HBM and Zmax1 (LRP5) extracellular domains (ECD) caused a modest stimulation of Wnt signaling in the absence of Wnt5a which was slightly increased by the presence of Wnt5a in the presence of HBM ECD. A model depicting Zmax1 (LRP5) involvement in focal adhesion signaling is depicted in Fig. 15.

This data coupled with other studies suggest that integrin signaling pathways have a role in cellular responses to mechanical stress and adhesion. This provides an attractive model for the mechanism of action of Zmax1 (LRP5) in bone biology. It is possible that Zmax1 (LRP5) is involved in sensing either mechanical stress directly or binding a molecule in the extracellular matrix that is related to mechanical sensation. Signaling through subsequent pathways may be involved in bone remodeling due to effects on cell morphology, cell adhesion, migration, proliferation, differentiation, and apoptosis in bone cells.

TABLE 10: Yeast Two Hybrid Results

Gene Symbol	Gene	Genbank Accession #	NT SEQ ID NO:	AA SEQ ID NO:
ACTN1	alpha-actinin	NM_001102	642	
AES	amino-terminal enhancer of	NM_001130.3	643	
AIP4	atrophin-1 interacting protein	AF038564.1	644	
Novel	Ajuba		645	
AXIN	Wnt signaling	AF009674.1	646	
CDC23	cell division cycle 23, yeast, homolog	NM_004661.1	647	
HSM800944	Similar to TRIO	AL117435.1	748	
HSM800936		AL117427.1	649	
Novel	Similar to LIM domains containing protein 1		650	
DEEPEST	mitotic spindle coiled-coil related protein	NM_006461.1	651	
ECM1	extracellular matrix protein 1	U65932.1	652	
EF1A	elongation factor 1-alpha	X16869.1	653	
FN	fibronectin	X02761.1	654	

Gene Symbol	Gene	Genbank Accession #	NT SEQ ID NO:	AA SEQ ID NO:
HOXB13	homeodomain protein	U81599.1	655	
Novel	Glu-Lys Rich protein		656	
LIMD1	LIM domains containing 1	NM_014240.1	657	
Novel	PINCH-like		658	
RANBPM	centrosomal protein	NM_005493.1	659	
S1-5	extracellular protein	U03877.1	660	
TCB	gene encoding cytosolic thyroid hormone-binding	M26252.1	661	
TID	tumorous imaginal discs	NM_005147.1	662	
ZYX	Zyxin	NM_003461.1	663	
TRIO	GTPase	U42390.1	664	
HUMPITPB	phosphatidylinositol transfer protein	D30037.1	665	
ACTN1	alpha-actinin	NP_001093.1		666
AES	amino-terminal enhancer of	NP_001121.2		667
AIP4	atrophin-1 interacting protein	AAC04845.1		668
Novel	Ajuba			669
AXIN	Wnt signaling	AAC51624.1		670
CDC23	cell division cycle 23, yeast homolog	NP_004652.1		671
Novel	Similar to TRIO CAB55923.1			672
Novel	Similar to LIM domains containing protein 1			673
DEEPEST	mitotic spindle coiled-coil related protein	NP_006452.1		674
ECM1	extracellular matrix protein 1	AAB05933.1		675
EF1A	elongation factor 1-alpha	CAA34756.1		676
FN	fibronectin	CAA26536.1		677
Novel	Glu-Lys rich protein			678
HOXB13	homeodomain protein B13	AAB39863.1		679
LIMD1	LIM domains containing 1	NP_055055.1		680
Novel	PINCH-like			681
RANBPM	centrosomal protein	NP_005484.1		682
S1-5	extracellular protein	AAA65590.1		683

Gene Symbol	Gene	Genbank Accession #	NT SEQ ID NO:	AA SEQ ID NO:
TCB	cytosolic thyroid hormone-binding protein	AAA36672.1		684
TID	tumorous imaginal discs	NP_005138.1		685
ZYX	Zyxin	NP_003452.1		686
TRIO	GTPase	AAC34245.1		687
PTDINSTP	phosphatidylinositol transfer protein beta isoform	P48739		688

In light of the model depicted in Fig. 15 and the results shown in Table 10, another aspect contemplated by the invention would be to regulate bone density and bone mass disorders by the regulating focal adhesion signaling. The regulation can occur by regulating the DNA, mRNA transcript or protein encoded by any of the members involved in the focal adhesion signaling pathway as identified by the yeast two hybrid system.

Also contemplated are the novel nucleic acids and proteins identified by the HBM yeast two hybrid system. These include but are not limited to SEQ ID NO: 645 (Ajuba), SEQ ID NO: 651 (a gene similar to a gene encoding LIM domains containing protein 1), SEQ ID NO: 656 (Glu-Lys Rich protein), SEQ ID NO: 658 (PINCH-like gene), SEQ ID NO: 669 (Ajuba protein), SEQ ID NO: 672 (protein similar to TRIO), SEQ ID NO: 673, SEQ ID NO: 678 (Glu-Lys rich protein) and SEQ ID NO: 681 (PINCH-like protein).

17. Potential Function

The protein encoded by Zmax1 (LRP5) and LRP6 are related to the Low Density Lipoprotein receptor (LDL receptor). *See*, Goldstein *et al.*, 1985 *Ann. Rev. Cell Biology*, 1: 1-39; Brown *et al.*, 1986 *Science*, 232:34-47. The LDL receptor is responsible for uptake of low density lipoprotein, a lipid-protein aggregate that includes cholesterol. Individuals with a defect in the LDL receptor are deficient in cholesterol removal and tend to develop artherosclerosis. In addition, cells with a defective LDL receptor show increased production of cholesterol, in part because of altered feedback regulation of cholesterol synthetic enzymes

and in part because of increased transcription of the genes for these enzymes. In some cell types, cholesterol is a precursor for the formation of steroid hormones.

Thus, the LDL receptor may, directly or indirectly, function as a signal transduction protein and may regulate gene expression. Because Zmax1 (LRP5) and LRP6 are related to the LDL receptor, this protein may also be involved in signaling between cells in a way that affects bone remodeling.

The glycine 171 amino acid is likely to be important for the function of Zmax1 (LRP5) because this amino acid is also found in the mouse homologue of Zmax1 (LRP5). The closely related LRP6 (Genbank Accession No. JE0272) protein also contains glycine at the corresponding position (Brown *et al.*, 1988 *Biochem. Biophys. Res. Comm.* 248: 879-88). Amino acids that are important in a protein's structure or function tend to be conserved between species, because natural selection prevents mutations with altered amino acids at important positions from arising.

In addition, the extracellular domain of Zmax1 (LRP5) contains four repeats consisting of five YWTD motifs followed by an EFG motif. This 5YWTD+EGF repeat is likely to form a distinct folded protein domain, as this repeat is also found in the LDL receptor and other LDL receptor-related proteins. The first three 5YWTD+EGF repeats are very similar in their structure, while the fourth is highly divergent. Glycine 171 occurs in the central YWTD motif of the first 5YWTD+EGF repeat in Zmax1 (LRP5). The other two similar 5YWTD+EGF repeats of Zmax1 (LRP5) also contain glycine at the corresponding position, as does the 5YWTD+EGF repeat in the LDL receptor protein. However, only 17.6% of the amino acids are identical among the first three 5YWTD+EGF repeats in Zmax1 (LRP5) and the single repeat in the LDL receptor. These observations indicate that glycine 171 is essential to the function of this repeat, and mutation of glycine 171 causes a functional alteration of Zmax1 (LRP5). The cDNA and peptide sequences are shown in Figs. 6A-6J. The critical base at nucleotide position 582 is indicated in bold and is underlined.

Northern blot analysis (Figs. 7A-B) reveals that Zmax1 (LRP5) is expressed in human bone tissue as well as numerous other tissues. A multiple-tissue Northern blot (Clontech, Palo Alto, CA) was probed with exons from Zmax1 (LRP5). As shown in Fig. 7A, the 5.5 kb

Zmax1 (LRP5) transcript was highly expressed in heart, kidney, lung, liver and pancreas and is expressed at lower levels in skeletal muscle and brain. A second northern blot, shown in Fig. 7B, confirmed the transcript size at 5.5 kb, and indicated that Zmax1 (LRP5) is expressed in bone, bone marrow, calvaria and human osteoblastic cell lines.

Taken together, these results coupled with the yeast two hybrid results indicate that the HBM polymorphism in the *Zmax1* (*LRP5*) gene is responsible for the HBM phenotype, and that the *Zmax1* gene is important in bone development. In addition, because mutation of Zmax1 can alter bone mineralization and development, it is likely that molecules that bind to Zmax1 may usefully alter bone development. Such molecules may include, for example, small molecules, proteins, RNA aptamers, peptide aptamers, and the like.

18. Preparation of Nucleic Acids, Vectors, Transformations and Host Cells

Large amounts of the nucleic acids of the present invention may be produced by replication in a suitable host cell. Natural or synthetic nucleic acid fragments coding for a desired fragment will be incorporated into recombinant nucleic acid constructs, usually DNA constructs, capable of introduction into and replication in a prokaryotic or eukaryotic cell. Usually the nucleic acid constructs will be suitable for replication in a unicellular host, such as yeast or bacteria, but may also be intended for introduction to (with and without integration within the genome) cultured mammalian or plant or other eukaryotic cell lines. The purification of nucleic acids produced by the methods of the present invention is described, for example, in Sambrook *et al.*, *Molecular Cloning. A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) or Ausubel *et al.*, *Current Protocols in Molecular Biology*, J. Wiley and Sons, NY (1992).

The nucleic acids of the present invention may also be produced by chemical synthesis, e.g., by the phosphoramidite method described by Beaucage *et al.*, 1981 *Tetra. Lett.* 22: 1859-62 or the triester method according to Matteucci,*et al.*, 1981 *J. Am. Chem. Soc.* 103: 3185, and may be performed on commercial, automated oligonucleotide synthesizers. A double-stranded fragment may be obtained from the single-stranded product of chemical synthesis either by synthesizing the complementary strand and annealing the strands together

under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Nucleic acid constructs prepared for introduction into a prokaryotic or eukaryotic host may comprise a replication system recognized by the host, including the intended nucleic acid fragment encoding the desired protein, and will preferably also include transcription and translational initiation regulatory sequences operably linked to the protein encoding segment. Expression vectors may include, for example, an origin of replication or autonomously replicating sequence (ARS) and expression control sequences, a promoter, an enhancer and necessary processing information sites, such as ribosome-binding sites, RNA splice sites, polyadenylation sites, transcriptional terminator sequences, and mRNA stabilizing sequences. Secretion signals may also be included where appropriate, whether from a native HBM or Zmax1 (LRP5) protein or from other receptors or from secreted proteins of the same or related species, which allow the protein to cross and/or lodge in cell membranes, and thus attain its functional topology, or be secreted from the cell. Such vectors may be prepared by means of standard recombinant techniques well known in the art and discussed, for example, in Sambrook *et al.*, (1989) or Ausubel *et al.*, (1992).

An appropriate promoter and other necessary vector sequences will be selected so as to be functional in the host, and may include, when appropriate, those naturally associated with *Zmax1* (*LRP5*) or *HBM* genes. Examples of workable combinations of cell lines and expression vectors are described in Sambrook *et al.*, (1989) or Ausubel *et al.*, (1992). Many useful vectors are known in the art and may be obtained from such vendors as Stratagene, New England BioLabs, Promega Biotech, and others. Promoters such as the trp, lac and phage promoters, tRNA promoters and glycolytic enzyme promoters may be used in prokaryotic hosts. Useful yeast promoters include promoter regions for metallothionein, 3-phosphoglycerate kinase or other glycolytic enzymes such as enolase or glyceraldehyde-3-phosphate dehydrogenase, enzymes responsible for maltose and galactose utilization, and others. Vectors and promoters suitable for use in yeast expression are further described in EP 73,675A. Appropriate non-native mammalian promoters might include the early and late promoters from SV40 (Fiers *et al.*, 1978 *Nature* 273: 113) or promoters derived from murine

Moloney leukemia virus, mouse tumor virus, avian sarcoma viruses, adenovirus II, bovine papilloma virus or polyoma. In addition, the construct may be joined to an amplifiable gene (e.g., DHFR) so that multiple copies of the gene may be made. For appropriate enhancer and other expression control sequences, see also *Enhancers and Eukaryotic Gene Expression*, Cold Spring Harbor Press, Cold Spring Harbor, NY (1983).

While such expression vectors may replicate autonomously, they may also replicate by being inserted into the genome of the host cell, by methods well known in the art.

Expression and cloning vectors will likely contain a selectable marker, a gene encoding a protein necessary for survival or growth of a host cell transformed with the vector. The presence of this gene ensures growth of only those host cells which express the inserts. Typical selection genes encode proteins that a) confer resistance to antibiotics or other toxic substances, e.g. ampicillin, neomycin, methotrexate, etc.; b) complement auxotrophic deficiencies, or c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for Bacilli. The choice of the proper selectable marker will depend on the host cell, and appropriate markers for different hosts are well known in the art.

The vectors containing the nucleic acids of interest can be transcribed *in vitro*, and the resulting RNA introduced into the host cell by well-known methods, e.g., by injection (see, Kubo *et al.*, *FEBS Letts*. 241: 119 (1988)), or the vectors can be introduced directly into host cells by methods well known in the art, which vary depending on the type of cellular host, including electroporation; transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; infection (where the vector is an infectious agent, such as a retroviral genome); and other methods. See generally, Sambrook *et al.*, 1989 and Ausubel *et al.*, 1992. The introduction of the nucleic acids into the host cell by any method known in the art, including those described above, will be referred to herein as "transformation." The cells into which have been introduced nucleic acids described above are meant to also include the progeny of such cells.

Large quantities of the nucleic acids and proteins of the present invention may be prepared by expressing the Zmax1(LRP5), LRP6, HBM or HBM-like nucleic acids or

portions thereof in vectors or other expression vehicles in compatible prokaryotic or eukaryotic host cells. The most commonly used prokaryotic hosts are strains of *Escherichia coli*, although other prokaryotes, such as *Bacillus subtilis* or *Pseudomonas* may also be used.

Mammalian or other eukaryotic host cells, such as those of yeast, filamentous fungi, plant, insect, or amphibian or avian species, may also be useful for production of the proteins of the present invention. Propagation of mammalian cells in culture is per se well known. See, Jakoby and Pastan (eds.), *Cell Culture. Methods in Enzymology*, volume 58, Academic Press, Inc., Harcourt Brace Jovanovich, NY, (1979). Examples of commonly used mammalian host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cells, and WI38, BHK, and COS cell lines, although it will be appreciated by the skilled practitioner that other cell lines may be appropriate, e.g., to provide higher expression desirable glycosylation patterns, or other features.

Clones are selected by using markers depending on the mode of the vector construction. The marker may be on the same or a different DNA molecule, preferably the same DNA molecule. In prokaryotic hosts, the transformant may be selected, e.g., by resistance to ampicillin, tetracycline or other antibiotics. Production of a particular product based on temperature sensitivity may also serve as an appropriate marker.

Prokaryotic or eukaryotic cells transformed with the nucleic acids of the present invention will be useful not only for the production of the nucleic acids and proteins of the present invention, but also, for example, in studying the characteristics of Zmax1 (LRP5), LRP6, HBM or HBM-like proteins.

Antisense nucleic acid sequences are useful in preventing or diminishing the expression of Zmax1(LRP5), LRP6, HBM or HBM-like molecules, as will be appreciated by one skilled in the art. For example, nucleic acid vectors containing all or a portion of the Zmax1(LRP5), LRP6, HBM or HBM-like nucleic acid may be placed under the control of a promoter in an antisense orientation and introduced into a cell. Expression of such an antisense construct within a cell will interfere with Zmax1(LRP5), LRP6, HBM or HBM-like transcription and/or translation and/or replication.

The probes and primers based on the *Zmax1(LRP5)*, *LRP6*, *HBM* or *HBM*-like gene

sequences disclosed herein are used to identify homologous gene sequences and proteins in other species. The gene sequences and proteins can also be used in the diagnostic/prognostic, therapeutic and drug screening methods described herein for the species from which they have been isolated.

19. Protein Expression and Purification

Expression and purification of the Zmax1 (LRP5), LRP6, HBM or HBM-like proteins of the invention can be performed essentially as outlined below (LRP5, LRP6 and HBM-like proteins are also included when referring only to HBM). To facilitate the cloning, expression and purification of membrane and secreted protein from the *HBM* gene, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli* was selected. Also, a DNA sequence encoding a peptide tag, the His-Tap, was fused to the 3' end of DNA sequences of interest to facilitate purification of the recombinant protein products. The 3' end was selected for fusion to avoid alteration of any 5' terminal signal sequence.

Nucleic acids chosen, for example, from the nucleic acids set forth in SEQ ID NOS: 1, 3 and 5-12 for cloning HBM were prepared by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5' and 3' ends of the HBM nucleotide sequence were designed and purchased from Life Technologies (Gaithersburg, MD). All forward primers (specific for the 5' end of the sequence) were designed to include an *Nco*I cloning site at the 5' terminus. These primers were designed to permit initiation of protein translation at the methionine residue encoded within the *Nco*I site followed by a valine residue and the protein encoded by the HBM DNA sequence. All reverse primers (specific for the 3' end of the sequence) included an *Eco*RI site at the 5' terminus to permit cloning of the HBM sequence into the reading frame of the pET-28b. The pET-28b vector provided a sequence encoding an additional 20 carboxyl-terminal amino acids including six histidine residues (at the C-terminus), which comprised the histidine affinity tag.

Genomic DNA prepared from the *HBM* gene was used as the source of template DNA for PCR amplification (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley

& Sons (1994)). To amplify a DNA sequence containing the HBM nucleotide sequence, genomic DNA (50 ng) was introduced into a reaction vial containing 2 mM $MgCl_2$, 1 μM synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined HBM, 0.2 mM of each of deoxynucleotide triphosphate, dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (AmpliTaq™, Roche Molecular Systems, Inc., Branchburg, NJ) in a final volume of 100 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA was purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD). All amplified DNA samples were subjected to digestion with the restriction endonucleases, e.g., *Nco*I and *Eco*RI (New England BioLabs, Beverly, MA) (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994)). DNA samples were then subjected to electrophoresis on 1.0% NuSeive (FMC BioProducts, Rockland, ME) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave UV irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101, Vista, CA).

The pET-28b vector was prepared for cloning by digestion with restriction endonucleases, e.g., *Nco*I and *Eco*RI (New England BioLabs, Beverly, MA) (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994)). The pET-28a vector, which encodes the histidine affinity tag that can be fused to the 5' end of an inserted gene, was prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts were cloned (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994)) into the previously digested pET-28b expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* (Ausubel *et al.*, 1994) as described below.

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21 (DE3), were transformed with recombinant pET expression plasmids carrying the cloned HBM sequence according to standard methods (Ausubel *et al.*, 1994). Briefly, 1 μl of ligation reaction was mixed with 50 μl of electrocompetent cells and subjected to a high voltage pulse, after which samples were incubated in 0.45 ml SOC medium (0.5% yeast extract, 2.0% tryptone, 10 mM

NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 μg/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts, as described below.

Individual BL21 clones transformed with recombinant pET-28b HBM nucleotide sequences were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers specific for the HBM sequences that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the HBM sequence in the expression vector (Ausubel *et al.*, 1994).

Individual clones of recombinant pET-28b vectors carrying properly cloned HBM nucleotide sequences were picked and incubated in 5 ml of LB broth plus 25 μg/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA).

The pET vector can be propagated in any *E. coli* K-12 strain, e.g., HMS174, HB101, JM109, DH5 and the like, for purposes of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts were lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase was induced by addition of isopropyl-β-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid containing a functional T7 promoter, such as pET-28b, carrying its gene of interest. Strains include, for example, BL21(DE3) (Studier *et al.*, 1990 *Meth. Enzymol.*, 185: 60-89).

To express the recombinant HBM sequence, 50 ng of plasmid DNA are isolated as described above to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression kit). The lacZ gene (β-galactosidase) is expressed in the pET-System as described for the HBM recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour, and the culture was then plated on LB plates containing 25 μg/ml kanamycin sulfate. The following day, the bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 μg/ml) to an optical

density at 600 nM of 0.5 to 1.0 O.D. units, at which point 1 mM IPTG was added to the culture for 3 hours to induce gene expression of the HBM recombinant DNA constructions.

After induction of gene expression with IPTG, bacteria were collected by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 ml of cold mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 minutes at 4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

19.1 Chinese Hamster Ovary (CHO) Expression System

Alternatively, HBM and Zmax1 (LRP5) may be expressed in eukaryotic cells. Eukaryotic cells, such as mammalian derived cell lines, are more capable of expressing properly folded proteins containing cystine rich domains such as the EGF and LDLR modules.

19.2 Development of Constructs

HBM and Zmax1 (LRP5) extracellular domain fusions (ECD) to IgG-Fc were prepared. These ECD fusions to the IgG-Fc domain remove the endogenous transmembrane and cytoplasmic portion of the Zmax1/HBM receptor and should produce a secreted fusion protein. The Fc region is separated from the Zmax1/HBM ECD by an enterokinase recognition site so that purified Zmax1 or HBM ECD protein can be obtained without the Fc domain present. The vector used for this construct was pHTop, a derivative of pED (Kaufman *et al.*, 1991 *Nuc. Acids Res.* 19: 4485-90) in which the majority of the adenomajor late promoter was replaced by six repeats of the tet operator (Gossen *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89: 5547-51). This vector contains the dihydrofolate reductase (*dhfr*) gene, and when introduced in the cell line CHO/A2 (see description below), functions very efficiently. Clones with high expression can be selected by isolating cells which survive in high methotrexate (MTX) concentrations.

The CHO expression vector pHTOP-Fc was digested with *Sal*I and *Not*I. The intervening sequence was purified away from the rest of the vector by electroelution from an

acrylamide gel slice. *Sal*I cuts 5' to the intrinsic honey bee mellitin signal sequence in pHTOP-Fc, and *Not*I cuts just 5' to the coding sequence IgG1-Fc. The resulting *Sal*I-*Not*I pHTOP-Fc vector has the signal sequence removed and the *Not*I cloning site is amenable to creating a 5' fusion to IgG-Fc. Full-length Zmax1 (LRP5) in pCMVSPORT6 and full-length HBM in pCMVSPORT6 were digested individually with *Xma*1 which cuts within the region of the ORF that encodes the signal sequence) and *Bam*HI (that cuts internally in the ORF) to generate a 2286 bp 5' fragment of Zmax1 and HBM. The mutation which distinguishes Zmax1 from HBM lies on this fragment. Separately, the Zmax1 DNA was digested with *Bam*HI and *Sac*I to isolate an 1800 bp 3' fragment which is common to both the *Zmax1* and the *HBM* genes. Together, these two fragments constitute the coding sequence for the HBM and Zmax1 extracellular domains, less the coding sequence for the first 6 amino acids of the signal sequence and ending 18 amino acids prior to the end of the extracellular domain, which we estimated from Kyte-Doolittle plots to end at the sequence "SPAHSS" (SEQ ID NO:698).

A synthetic duplex was designed to recreate the coding sequence of the Zmax1/HBM signal sequence 5' of the native *Xma*I site, which included the initiator methionine and Kozak sequence. This duplex was designed to contain *Sal*I (5') and *Xma*I (3') cohesive ends to adapt ends to adapt the gene fragments described above to the pHTOP-Fc vector. This synthetic duplex was constructed from two partially complementary oligonucleotides as given below:

5'-TCGACCACCATGGAGGCAGCGCCGC-3' (SEQ ID NO:699)

3'-GGTGGTACCTCCGTCGCGGCGGGCC-5' (SEQ ID NO:700)

A second synthetic duplex was designed to recreate the 3' coding sequence from a native *Sac*I site to the estimated end of the extracellular domain following the serine in the sequence ". . .SPAHSS", and to also encode a cloning site to allow in-frame fusion to the downstream IgG-Fc. This duplex was designed to contain *Sac*I (5') and *Not*I (3') cohesive ends to adapt the gene fragments described above to the pHTOP-Fc vector. This synthetic duplex was constructed from two partially complementary oligonucleotides whose sequences are given below:

5'-CATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAG

CAGTGGC-3' (SEQ ID NO:701)

3'-TCGAGTACACACTTTAGTGGTTCGGCGGGAGTCTGCTGTC GGGCCGGGT GTCGTCACCGCCGG-5' (SEQ ID NO:702)

The fragments, synthetic duplexes, and vector were ligated together in a single reaction. Separate reactions were performed for Zmax (LRP5) 1 and HBM. The ligation mixtures were used to transform electrocompetent *E. coli* DH10B cells, and the resulting colonies were screened by radioactive colony hybridization using the common *Sac*I-*Bam*HI 3' fragment as a probe. Colonies containing plasmids with the Zmax1 or HBM fragment inserted were identified, and plasmids were isolated from multiple candidates and their sequences were verified by DNA sequencing. Verified constructs were then used for transfection into CHO cells.

19.2.1 Establishment of CHO stable cell lines

The CHO/A2 cell line is derived from CHO DUKX B11 (Urlaub *et al.*, 1980 *Proc. Natl. Acad. Sci. USA* 77: 4216-20) by stably integrating a transcriptional activator (tTA), a fusion protein, between the Tet repressor and the herpes virus VP16 transcriptional domain (Gossen *et al.*) CHO cell lines expressing extracellular HBM-1.Fc and Zmax1.Fc were established by transfecting (using lipofection) pHTopHBM-1.Fc into CHO/A2 cells and pHTopZmax1.Fc into CHO/A2 cells. Clones were selected using by culturing the cells in 0.02 μM methotrexate. Clones were later amplified step-wise to a final concentration of 0.5 μM methotrexate.

19.2.2 Screening of CHO stable cell lines

Multiple clones were screened by a variety of techniques. Clones were screened by Western blot assay using a (mouse) anti-human IgG.Fc horseradish peroxidase (HRP) antibody. The same clones were also metabolically labeled with ^{35}S-Met/Cys) for a 6 hour pulse, or a 15 minute pulse, followed by a 1 hour, 4 hour, or 24 hour chase in media without radiolabeled Met/Cys. Immunoprecipitations were performed on proteins obtained from conditioned media, as well as from cell extracts. Purification is then performed followed by

sequencing of the proteins using N-terminal sequencing as known in the art.

19.2.3 Fusion Protein Purification

Zmax1-IgG or HBM-IgG fusion protein can be purified from conditioned media or cell extracts of CHO stable cells. The fusion protein is isolated by affinity binding to protein A (for example using protein A coated beads or columns). The IgG-FC domain can then subsequently be cleaved from the Zmax/HBM1 ECD protein by enterokinase digestion.

19.2.4 Potential uses for cell lines and protein

Stable cell lines may be used for generation of purified protein for use in ligand hunting, antibody generation, determination of crystal structure, and competitive binding assays.

A variety of methodologies known in the art can be used to purify the isolated proteins (Coligan *et al.*, *Current Protocols in Protein Science,* John Wiley & Sons (1995)). For example, the frozen cells can be thawed, resuspended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corp., Newton, MA). The resultant homogenate is centrifuged to yield a clear supernatant (crude extract) and, following filtration, the crude extract is fractioned over columns. Fractions are monitored by absorbance at OD_{280} nm and peak fractions may be analyzed by SDS-PAGE.

The concentrations of purified protein preparations are quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, 1986 *Eur. J. Biochem.* 157:169-180). Protein concentrations are also measured by the method of Bradford, 1976 *Anal. Biochem.* 72: 248-54 and Lowry *et al.*, 1951 *J. Biol. Chem.* 193: 265-275 using bovine serum albumin as a standard.

SDS-polyacrylamide gels of various concentrations were purchased from BioRad (Hercules, CA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* β-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4

kDa) and bovine aprotinin (6.5 kDa).

Once a sufficient quantity of the desired protein has been obtained, it may be used for various purposes. A typical use is the production of antibodies specific for binding. These antibodies may be either polyclonal or monoclonal, and may be produced by *in vitro* or *in vivo* techniques well known in the art. Monoclonal antibodies to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas (Kohler, 1975 *Nature*, 256: 495). In summary, a mouse is inoculated with a few micrograms of HBM protein over a period of two weeks. The mouse is then sacrificed. The cells that produce antibodies are then removed from the mouse's spleen. The spleen cells are then fused with polyethylene glycol with mouse myeloma cells. The successfully fused cells are diluted in a microtiter plate and growth of the culture is continued. The amount of antibody per well is measured by immunoassay methods such as ELISA (Engvall, 1980 Meth. *Enzymol.* 70: 419). Clones producing antibody can be expanded and further propagated to produce HBM antibodies. Other suitable techniques involve *in vitro* exposure of lymphocytes to the antigenic polypeptides, or alternatively, to selection of libraries of antibodies in phage or similar vectors. See Huse *et al.*, 1989 *Science* 246: 1275-81. For additional information on antibody production see Davis *et al.*, Basic Methods in Molecular Biology, Elsevier, NY, Section 21-2 (1989).

Additional uses for purified or isolated protein includes use in X-ray crystallography, binding assays, and so forth as described in greater detail *infra*.

19.3 Zmax1, LRP6, and Variant Antibodies

Polyclonal antibodies were developed to both human Zmax1 (LRP5) (SEQ ID NO:3) and LRP6 (GenBank Accession No. AF074264). Antibodies can similarly be prepared against HBM and HBM like proteins and polypeptides. Peptides from the Zmax1 amino acid sequence were selected as immunogens based on five goals. 1) Maximize differences between Zmax1 and LRP6 amino acid sequences (71% amino acid identity). See Fig. 27. For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference

sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s), relative to the reference sequence, based on the designated program parameters. 2) Minimize potential cross reactivity with other known genes by performing sequence alignment and similarity searches. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith *et al.*, 1981 *Adv. Appl. Math.* 2: 482, by the homology alignment algorithm of Needleman *et al.*, 1970 *J. Mol. Biol.* 48: 443, by the search for similarity method of Pearson *et al.*, 1988 *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms and others in programs contained in the Wisconsin genetics software package, Genetics Computer Group, 585 Science Dr., Madison, WI, or by visual inspection (see generally Ausubel *et al., Current Protocols in Molecular Biology,* John Wiley & Sons (1997). Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, 1990 *J. Mol. Biol.* 215: 403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. 3) Obtain peptides with the highest antigenicity index as possible as determined by PeptideStructure protein analysis using software programs contained in the Wisconsin Genetics software package, Genetics Computer Group, 575 Science Dr., Madison, WI. 4) Locating peptides relative to highly homologous domains (*e.g.*, EGF-like domains and LDL receptor repeats) within the gene family and the location relative to the extracellular and cytoplasmic regions of the gene. 5) And, for human Zmax1 specific antibodies, the human amino acid sequence (SEQ ID NO: 3) was compared to the mouse Zmax1 sequence (GenBank Accession No. AF064984) and peptides were selected based on the above criteria in addition to minimizing the sequence similarity between the two species (See Figure 26).

Using the same criteria above, LRP6 specific peptides were selected for polyclonal antibody production. Table 11 lists the amino acid sequences that were chosen, the amino acid differences within the peptide between the human and mouse sequences. All the peptide sequences (ranging from 12-18 amino acids) were provided to Sigma/Genosys (St. Louis,

MO) for peptide synthesis and subsequent polyclonal antibody production in New Zealand White Rabbits. The IgG fraction from the serum of each immunized rabbit was isolated using Protein G Sepharose (Amersham). Polyclonal antibody generation using these peptides may be done in other species as well, for example, chickens. This is often advantageous when there is a high degree of similarity between the human (reference) and murine/rodent sequence.

TABLE 11

Amino Acids	Amino Acids	SEQ ID NO	H/M* Differences	Comments
171-187	VETPRIERAGMDGSTRK	703	5	Contains HBM polymorphism
264-278	NKRTGGKRKEILSAL	704	3	Extracellular
290-301	ERQPFFHTRCEE	705	2	Adjacent to EGF-I, extracellular
532-546	VDGTKRRTLLEDKLP	706	5	Extracellular
901-915	DGLNDCMHNNGQCGQ	707	2	In EGF-III, extracellular
1010-1021	PFVLTSLSQGQN	708	6	Extracellular, human specific
1415-1429	YAGANGPFPHEYVSG	709	3	Cytoplasmic
1452-1464	ACGKSMMSSVSLM	710	5	Cytoplasmic, human specific
1556-1573	RWKASKYYLDLNSDSDPY	711	1	Cytoplasmic
888-902	SGWNECASSNGHCSH	712		LRP6 specific
1308-1321	NGDANCQDKSDEKN	713		LRP6 specific

* H/M-differences between human and mouse sequences

Antibodies towards variants of LRP6, HBM and LRP5 are also contemplated. Based on the analysis of the structural model of the LRP5 beta propeller 1 (discussed in more detail in the Examples), interior regions of the propeller were analysed. Since the site-directed mutagenesis experiments had confirmed that modulation of propeller 1, particularly in the interior regions of beta propeller 1, could result in an HBM effect, a strategy was employed to generate antibodies with epitopes specific to these regions. Such antibodies to the wild type

LRP5 receptor could serve, for examples, as an HBM mimetic, by altering ligand/receptor interactions, protein-protein interactions, or by modulating Wnt or Dkk activity. Such antibodies could be used as therapies to treat, for example osteoporosis.

One set of preferred antibodies includes:

LRP5 Amino Acids	Sequence
208-223	KLYWADAKLSFIHRAN
277-291	ALYSPMDIQVLSQER
61-73	GLEDAAAVDFQFSKGA
234-247	EGSLTHPFALTLSG
249-264	TLYWTDWQTRSIHACN
144-156	VLFWQDLDQPRAI
194-210	IYWPNGLTIDLEEQKLY
34-47	LLLFANRRDVRLVD
75-89	GAVYWTDVSEEAIKQ
121-135	KLYWTDSETNRIEVA

Similar peptides can be used to prepare antibodies based on the LRP6 or HBM structures and the proposed mutations in their propellers. Other antibodies could easily be prepared based on the structural model discussed in the Examples, as would be readily appreciated by the skilled artisan.

Another series of antibodies could be prepared which target the domains on HBM, LRP5, LRP6 and their variants which interact Dkk. Such antibodies could again serve as HBM mimetics, for example by displacing Dkk binding and thereby could be used as an osteoporosis therapeutic. Preferred peptides for preparing antibodies include but are not limited to:

LRP5 Amino Acids	Sequence
969-993	LILPLHGLRNVKAIDYDPLDKFIYW
989-1013	KFIYWVDGRQNIKRAKDDGTQPFVL

LRP5 Amino Acids	Sequence
1009-1033	QPFVLTSLSQGQNPDRQPHDLSIDI
1029-1053	LSIDIYSRTLFWTCEATNTINVHRL
10491073	NVHRLSGEAMGVVLRGDRDKPRAIV
1253-1266	CGEPPTCSPDQFAC
1278-1295	WRCDGFPECDDQSDEEGC
1316-1332	RCDGEADCQDRSDEADC
1370-1383	CEITKPPSDDSPAH

Additional peptides would be readily apparent to the artisan of ordinary skill.

19.3.1 Single chain Fv molecules developed by phage display

Peptides were chosen from the Zmax1 (LRP5) sequence (SEQ ID NO: 3) to screen for single chain Fv (scFv) molecules by phage display. Similar peptides can be chosen for LRP6, HBM and HBM-like proteins to screen for scFv molecules. As discussed below, all mention of LRP5 is also meant to include these other proteins.

A total of 17 peptides from the Zmax1 sequence were selected for synthesis and subsequent phage display screen for scFv molecules. All peptide synthesis and phage display work was performed at Cambridge Antibody Technology (CaT) in Cambridge, UK. Peptides were selected based on criteria as described above.

TABLE 12

Protein Domain	Zmax1 Residues	LRP6 Residues	% Identity
Spacer 1 (+G171V)	161-181	148-168	76%
Spacer 1 (-G171V)	161-181	148-168	76%
EGF 1	301-321	288-308	76%
Spacer 2	401-421	388-408	52%
EGF 2	611-631	598-618	62%
Spacer 3	781-801	768-788	62%

Protein Domain	Zmax1 Residues	LRP6 Residues	% Identity
EGF 3	921-941	908-928	10%
Spacer 4	1000-1021	988-1008	26%
EGF 4	1229-1249	1219-1239	76%
LDLR 1	1261-1282	1252-1272	81%
LDLR 2	1300-1320	1290-1310	57%
LDLR 3	1338-1358	1328-1348	48%
Cytosolic 1	1418-1438	1405-1425	14%
Cytosolic 1	1516-1536	1503-1525	52%
Cytosolic 1	1535-1555	1524-1544	81%
Cytosolic 1	1595-1615	1592-1613	82%
Spacer 2 (cross reactive)	421-441	408-428	100%

Note that a number of these regions (e.g., 401-421, 421-441, 781-801, and 1229-1249) share 100% identity with mouse LRP5 (see Fig. 26). Therefore, these may be used against both mouse and human forms of the protein. The peptide 421-441 was included to facilitate the generation of an antibody that would recognize both Zmax1 (LRP5) and LRP6 (see Figure 27). Two peptides were synthesized spanning the HBM mutation site (Zmax1 residues 161-181), one with the Zmax1 sequence and the other containing the HBM sequence.

Once scFv molecules were isolated, they were used as reagents in immunochemistry to detect Zmax1 (LRP5) protein expression in a variety of human normal and diseased tissues. The details of the scFV antibody immunohistochemical analysis of three phage clones against peptide 1000-1021 (i.e., IKRAKDDGTQPFVLTSLSQGQN; SEQ ID NO: 714) of the extracellular domain of Zmax1 showed positive staining with cardiac muscle, kidney, lung and liver.. Expression was also detected in prostate carcinoma. These results are consistent with mRNA tissue distribution profiles as well as with the published reports of LRP5 mRNA localization (Kim *et al.*, 1998 *J. Biochem.* 124: 1072-6). The resulting phage clones arise from pools and will be sequenced to identify potential variants in the Fv

region of the molecules. Once identified, the suitable scFVs can then be subcloned into variable heavy chain and variable light chain DNA constructs for cotransfection into COS cells for final assembly of an intact and functional immunoglobulin gamma (IgG) molecule. The IgG that is expressed by the cells can then be further characterized for specificity and reactivity as would be known in the art.

19.3.2 Monoclonal antibody development

Monoclonal antibodies can be developed to Zmax1 (LRP5), LRP6, HBM and HBM-like proteins/polypeptides by complete cell and adenovirus immunization of, for example, Balb/c mice (antibodies to all forms are contemplated even when only a few examples are discussed in detail). Dendritic cells can be isolated from spleens of Balb/c mice, for example, and the cells expanded *in vitro* in the presence of growth factors IL-4 and GM-CSF. The dendritic cells can then be infected with HBM or Zmax1 adenovirus particles. The cells are then cultured for 24 hours prior to intravenous injection into Balb/c mice. Dendritic cells (1×10^6 cells/mouse) are injected 2-3 times every 3-4 weeks over a three month period.

Alternatively, purified HBM and Zmax DNAs in, for example, the pcDNA3.1 expression vector, can be coated on colloidal gold particles. These particles can then be injected subcutaneously into the desired mouse using gene gun technology. Approximately, 5 μg cDNA/mouse can be injected. Injections are performed 4-6 times every 2 weeks over approximately a 3 month period.

Another option is that cells (any species of animal, but preferably Balb/c mouse strain or the same species as the mouse strain being used which is related to limit antigen response to non-specific protein) over expressing HBM and Zmax1 (LRP5) and their respective adenovirus will be injected into the mice every 2-3 weeks for a period of about 1.5 to 3 months, as necessary. The bleeds from the mice can be tested for reactivity with the native and denatured protein by ELISA (using purified protein or protein-fusions), cell based ELISA, immunohistochemical staining and Western blotting. Serum samples from

the animals can be screened by FACS (fluorescent activated cell sorting) using cells infected with Zmax1 or HBM adenovirus. The spleen cells (antibody producing cells) from the mice with the strongest reactivity can then be fused with a myeloma to generate the hybridoma cells. The conditioned media from the hybridoma is then screened for the positive cell colonies for subsequent cloning. These cloned cells can then be injected into the intraperitoneal space in mice for ascites production.

19.3.3 Polyclonal Antibody Applications

Polyclonal antibodies directed against Zmax1 (LRP5) and LRP6 were developed to determine the function of these proteins, analyze the expressed pattern and levels in various tissues, cells or any biological sample. Similar antibodies could be prepared which distinguish the wild type forms from the HBM and HBM-like variants.

Uses for polyclonal antibodies against Zmax1, HBM, HBM-like polypeptides, and LRP6 include but are not limited to: analysis of bone cross-sectional mounts, tissue distribution, evaluation of expression of the protein from bone biopsy samples of affected/non-affected family members (e.g., bone cell digests, explants of bone marrow stromal cell cultures), evaluation of protein expression levels in transiently or stably transfected cells, evaluating protein concentration in tissues, serum or body fluid, purification of full length or fragments of these proteins for ligand hunting and functional assay development, identification of ligands or proteins which interact with these proteins, and elucidations of the signaling pathways of LRP6, Zmax1 (LRP5) and HBM, and related variants.

For example, Zmax1 cloned in pcDNA3.1 (Invitrogen, Carlsbad, CA). This was used to generate ^{35}S-labeled *in vitro* translated (Promega, Madison, WI) Zmax1. Antibody (10 μg/ml) 3109 and 3110, which are directed against peptide immunogen, RWKASKYYLDLNSDSDPY (SEQ ID NO:711), was combined with 20 µl of the *in vitro* translated product in the presence of either 10 µg/ml specific peptide (*i.e.*, RWKASKYYLDLNSDSDPY; SEQ ID NO: 711) or non-specific peptide (*i.e.*,

SGWNECASSNGHCSH; SEQ ID NO: 712) or no peptide and incubated for 1.5 hr at 4°C. Protein A Sepharose was then added to the samples (previously blocked for about 1.5 hr with reticulocyte lysate), and the samples were shaken for 1 hour at 4°C. The protein A Sepharose was washed 3 times with 0.5 ml of PBS. The bound protein was subsequently separated on a 4-12% gradient NuPAGE gel (Invitrogen) according to manufacturer's instructions. The gel was dried at 80°C for 30 min and then exposed to Kodak X-OMAT-AR film for 24 to 48 hr. The specific peptide was observed to significantly compete for the ^{35}S-labeled Zmax1 immunoprecipitated protein with either antibody. The competition was not observed with a non-specific peptide.

These antibodies can also be used for immunohistochemistry. For example, HBM transgenic and wild-type mice were sacrificed using CO_2 narcosis. Mouse calvariae were removed intact, and the soft tissues gently dissected. The bones were fixed in 10% phosphate buffered formalin for 24 hours for further processing and analysis. After fixation, calvariae were decalcified in TBD-2 decalcifying agent (Shandon, Pittsburgh, PA) for about 7-8 hours and then dehydrated in graded alcohol. Calvariae were then bisected perpendicular to the sagittal suture through the central portion of the parietal bones parallel to the lambdoidal and coronal sutures and embedded in paraffin. Four to six 5 μm thick representative sections were cut.

For example, the rabbit polyclonal antibody, Zmax1/HBM (i.e., antibody 3109 and 3110) recognize Zmax1 (LRP5) in both HBM transgenic and wild-type mouse calvariae. An anti-Zmax1 or anti-HBM antibody can be used to detect Zmax1 or HBM protein in order to evaluate its abundance and pattern of protein expression. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, P-galactosidase, or acetylcholinesterase; example of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine

fluorescein, dansyl chloride or phycoerythrin; and example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin and acquorien; and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S, and ^{3}H. Alternatively, a secondary antibody can be employed that detects the presence of the primary Zmax1 polyclonal antibody. An example would be an antibody that recognized all rabbit immunoglobulins. This secondary antibody could be coupled in an identical manner as described above to facilitate detection. Controls comprised samples with the avidin peroxidase, but without antibody. Intensive positive staining of stroma cells and mesenchymal cells was observed in the suture area. Pre-osteoblasts and osteoblasts were observed to stain within the periosteum and some osteocytes with antibody 3109 and 3110 in the calvariae of the HBM compared to wild-type mice. High magnification of tissue calvaria sections of the HBM transgenic mice showed a pronounced cell membrane staining of the osteocytes and the cells within the suture area.

Similar antibodies could be prepared to HBM-like proteins and polypeptides, as would be readily appreciated by the artisan of ordinary skill.

20. Methods of Use: Gene Therapy

In recent years, significant technological advances have been made in the area of gene therapy for both genetic and acquired diseases (Kay *et al.*, 1997 *Proc. Natl. Acad. Sci. USA*, 94: 12744-6). Gene therapy can be characterized as the deliberate transfer of DNA for therapeutic purposes. Improvement in gene transfer methods has allowed for development of gene therapy protocols for the treatment of diverse types of diseases. Gene therapy has also taken advantage of recent advances in the identification of new therapeutic genes, improvement in both viral and nonviral gene delivery systems, better understanding of gene regulation, and improvement in cell isolation and transplantation.

The preceding experiments identify the *HBM* gene as a dominant mutation conferring elevated bone mass. Additional HBM-like genes are identifiable based on the model and data presented herein regarding the propellers and structure of the HBM protein. The fact that this mutation is dominant indicates that expression of the HBM protein causes elevated bone

mass. Older individuals carrying the *HBM* gene, and, therefore expressing the HBM protein, do not suffer from osteoporosis. These individuals are equivalent to individuals being treated with the HBM protein. These observations are a strong experimental indication that therapeutic treatment with the HBM protein prevents osteoporosis. The bone mass elevating activity of the *HBM* gene is termed "HBM function" or "HBM like phenotype" in the instance of other HBM variants.

Therefore, according to the present invention, a method is also provided of supplying HBM function to mesenchymal stem cells (Onyia *et al.*, 1998 *J. Bone Miner. Res.* 13: 20-30; Ko *et al.*, 1996 *Cancer Res.* 56: 4614-9). Supplying such a function provides protection against osteoporosis. The *HBM* gene or a part of the gene or other *HBM*-like gene may be introduced into the cell in a vector such that the gene remains extrachromosomal. In such a situation, the gene will be expressed by the cell from the extrachromosomal location.

Vectors for introduction of genes both for recombination and for extrachromosomal maintenance are known in the art, and any suitable vector may be used. Methods for introducing DNA into cells such as electroporation, calcium phosphate co-precipitation, and viral transduction are known in the art, and the choice of method is within the competence of one skilled in the art (Robbins, ed., Gene Therapy Protocols, Human Press, NJ (1997)). Cells transformed with the *HBM* gene (or HBM-like gene) can be used as model systems to study osteoporosis and drug treatments that promote bone growth.

As generally discussed above, the *HBM* or HBM-like gene or biologically active fragment thereof, where applicable, may be used in gene therapy methods in order to increase the amount of the expression products of such genes in mesenchymal stem cells (in all instances where discussing HBM gene and its cognate product, the HBM-like gene and cognate protein is also contemplated). It may be useful also to increase the level of expression of a given HBM protein, or a fragment thereof, even in those cells in which the wild type gene is expressed normally. Gene therapy would be carried out according to generally accepted methods as described by, for example, Friedman, Therapy for Genetic Diseases, Friedman, Ed., Oxford University Press, pages 105-121 (1991).

A virus or plasmid vector containing a copy of the *HBM* gene linked to expression

control elements and capable of replicating inside mesenchymal stem cells, is prepared. Suitable vectors are known and described, for example, in U.S. Patent No. 5,252,479 and WO 93/07282, the disclosures of which are incorporated by reference herein in their entirety. The vector is then injected into the patient, either locally into the bone marrow or systemically (in order to reach any mesenchymal stem cells located at other sites, i.e., in the blood). If the transfected gene is not permanently incorporated into the genome of each of the targeted cells, the treatment may have to be repeated periodically.

Gene transfer systems known in the art may be useful in the practice of the gene therapy methods of the present invention. These include viral and non-viral transfer methods. A number of viruses have been used as gene transfer vectors, including polyoma, i.e., SV40 (Madzak *et al.*, 1992 *J. Gen. Virol.* 73: 1533-6), adenovirus (Berkner, 1992 *Curr. Top. Microbiol. Immunol.* 158: 39-61; Berkner *et al.*, 1988 *BioTechniques*, 6: 616-629; Gorziglia *et al.*, 1992 *J. Virol.* 66: 4407-12; Quantin *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89: 2581-2584; Rosenfeld *et al.*, 1992 *Cell* 68: 143-155; Wilkinson *et al.*, 1992 *Nucl. Acids Res.* 20: 2233-39; Stratford-Perricaudet *et al.*, 1990 *Hum. Gene Ther.* 1: 241-256), vaccinia virus (Mackett *et al.*, 1992 *Biotechnology* 24: 495-499), adeno-associated virus (Muzyczka, 1992 *Curr. Top. Microbiol. Immunol.* 158: 91-123; Ohi *et al.*, 1990 *Gene* 89: 279-282), herpes viruses including HSV and EBV (Margolskee, 1992 *Curr. Top. Microbiol. Immunol.* 158: 67-90; Johnson *et al.*, 1992 *J. Virol.*, 66: 2952-65; Fink *et al.*, 1992 *Hum. Gene Ther.* 3: 11-9; Breakfield *et al.*, 1987 *Mol. Neurobiol.* 1: 337-371; Fresse *et al.*, 1990 *Biochem. Pharmacol.*, 40: 2189-2199), and retroviruses of avian (Brandyopadhyay *et al.*, 1984 *Mol. Cell Biol.*, 4: 749-754; Petropouplos *et al.*, 1992 *J. Virol.* 66: 3391-3397), murine (Miller, 1992 *Curr. Top. Microbiol. Immunol.* 158: 1-24; Miller *et al.*, 1985 *Mol. Cell Biol.* 5: 431-437; Sorge *et al.*, 1984 *Mol. Cell Biol.* 4: 1730-7; Mann *et al.*, 1985 *J. Virol.* 54: 401-7), and human origin (Page *et al.*, 1990 *J. Virol.* 64: 5370-6; Buchschalcher *et al.*, 1992 *J. Virol.* 66: 2731-9). Most human gene therapy protocols have been based on disabled murine retroviruses.

Non-viral gene transfer methods known in the art include chemical techniques such as calcium phosphate coprecipitation (Graham *et al.*, 1973 *Virology* 52: 456-67; Pellicer *et al.*, 1980 *Science* 209: 1414-22), mechanical techniques, for example microinjection (Anderson

et al., 1980 *Proc. Natl. Acad. Sci. USA*, 77: 5399-5403; Gordon *et al.*, 1980 *Proc. Natl. Acad. Sci. USA*, 77: 7380-4; Brinster *et al.*, 1981 *Cell* 27: 223-231; Constantini *et al.*, 1981 *Nature* 294: 92-94), membrane fusion-mediated transfer via liposomes (Felgner *et al.*, 1987 *Proc. Natl. Acad. Sci. USA* 84: 7413-7; Wang *et al.*, 1989 *Biochemistry* 28: 9508-14; Kaneda *et al.*, 1989 *J. Biol. Chem.* 264: 12126-9; Stewart *et al.*, 1992 *Hum. Gene Ther.* 3: 267-275; Nabel *et al.*, 1990 *Science* 249: 1285-8; Lim *et al.*, 1992 *Circulation* 83: 2007-11), and direct DNA uptake and receptor-mediated DNA transfer (Wolff *et al., 1990 Science* 247: 1465-8; Wu *et al.*, 1991 *BioTechniques* 11: 474-85; Zenke *et al.*, 1990 *Proc. Natl. Acad. Sci. USA* 87: 3655-9; Wu *et al.*, 1989 *J. Biol. Chem.* 264: 16985-7; Wolff *et al.*, 1991 *BioTechniques* 11: 474-45; Wagner *et al.*, 1990; Wagner *et al.*, 1991 *Proc. Natl. Acad. Sci. USA*, 88: 4255-9; Cotten *et al.*, 1990 *Proc. Natl. Acad. Sci. USA*, 87: 4033-7; Curiel *et al.*, 1991 *Proc. Natl. Acad. Sci. USA*, 88: 8850-4; Curiel *et al.*, 1991 *Hum. Gene Ther.* 3: 147-54). Viral-mediated gene transfer can be combined with direct *in vivo* vectors to the mesenchymal stem cells and not into the surrounding cells (Romano *et al.*, 1998 *In Vivo*, 12: 59-67; Gonez *et al.*, 1998 *Hum. Mol. Genetics* 7:1913-9). Alternatively, the retroviral vector producer cell line can be injected into the bone marrow (Culver *et al., 1992 Science* 256: 1550-2). Injection of producer cells would then provide a continuous source of vector particles. This technique has been approved for use in humans with inoperable brain tumors.

In an approach which combines biological and physical gene transfer methods, plasmid DNA of any size is combined with a polylysine-conjugated antibody specific to the adenovirus hexon protein, and the resulting complex is bound to an adenovirus vector. The trimolecular complex is then used to infect cells. The adenovirus vector permits efficient binding, internalization, and degradation of the endosome before the coupled DNA is damaged.

Liposome/DNA complexes have been shown to be capable of mediating direct *in vivo* gene transfer. While in standard liposome preparations the gene transfer process is non-specific, localized *in vivo* uptake and expression have been reported in tumor deposits, for example, following direct *in situ* administration (Nabel, *Hum. Gene Ther.*, 3:399-410 (1992)).

21. Methods of Use: Transformed Hosts and Transgenic Animals as Research Tools and for the Development of Pharmaceuticals

Cells and animals that carry the *HBM, HBM*-like, *Zmax1* (*LRP5*), or *LRP6* genes, used as model systems, are valuable research tools to study and test for substances that have potential as therapeutic agents (Onyia *et al.*, 1998 *J. Bone Miner. Res.*, 13: 20-30; Broder *et al.*, 1997 *Bone*, 21: 225-35). Discussion of one of these is meant to include the others, e.g., discussion of HBM is meant to include HBM-like variants, and so forth.

Cells for this purpose are typically cultured mesenchymal stem cells. These may be isolated from individuals with somatic or germline *HBM* genes. Alternatively, the cell line can be engineered to carry the *HBM* or HBM-like gene, as described above. After a test substance is applied to the cells, the transformed phenotype of the cell is determined. Any trait of transformed cells can be assessed, including, for example, formation of bone matrix in culture (Broder *et al.*, 1997 *Bone*, 21: 225-235), mechanical properties (Kizer *et al.*, 1997 *Proc. Natl. Acad. Sci. USA* 94: 1013-8), expression of marker genes and response to application of putative therapeutic agents.

Transgenic modified animals and cell lines may be used to test therapeutic agents. Transgenic modifications include, for example, insertion of the *Zmax1* (*LRP5*) gene, *LRP6*, *HBM* gene or *HBM*-like gene and disrupted homologous genes. Alternatively, the inserted *Zmax1, LRP6, HBM,* and/or HBM-like gene of the animals may be disrupted by insertion or deletion mutation of other genetic alterations using conventional techniques, such as those described by, for example, Capecchi, 1989 *Science* 244: 1288; Valancuis *et al.*, 1991 *Mol. Cell Biol.* 11: 1402; Hasty *et al.*, 1991 *Nature* 350: 243; Shinkai *et al.*, *Cell*, 68:855 (1992); Mombaerts *et al.*, *Cell*, 68:869 (1992); Philpott *et al.*, 1992 *Science* 256: 1448; Snouwaert *et al.*, 1992 *Science* 257: 1083; Donehower *et al.*, 1992 *Nature* 356: 215. After test substances have been administered to the animals, the growth of bone must be assessed. If the test substance modulates (e.g., enhances) the growth of bone, then the test substance is a candidate therapeutic agent. These animal models provide an extremely important vehicle for potential therapeutic products.

The present invention also provides animals and cell lines wherein the expression of

endogenous genes are activated, and may be further amplified, which does not require *in vitro* manipulation and transfection of exogenous DNA encoding Zmax1 (LRP5) or HBM proteins. These methods are described for example in PCT Application WO 94/12650 and U.S. Patent No. 5,968,502, both of which are herein incorporated in their entirety by reference. In addition, the present invention includes methods wherein endogenous activation or over-expression is achieved by *in situ* homologous recombination, non-homologous recombination, or illegitimate recombination methods. These methods are described for example in PCT Applications WO 99/15659 and WO 00/49162, both of which are incorporated herein in their entirety.

21.1 Creating transgenic and gene-targeted animals

The present invention provides genetically modified animals that recapitulate the human HBM or a HBM-like phenotype. The approaches taken involve the creation of both transgenic and gene-targeted animals that have the human G to T nucleotide substitution incorporated into the genome, express human Zmax1 (LRP5) or express a variant with a bone mass altering phenotype. These approaches can be used with any gene, such as HBM, HBM-like, LRP5 and LRP6 systems.

21.1.1 Transgenic mice over-expressing the HBM polymorphism

Plasmid constructs were prepared that utilized either the CMVbActin or type I collagen promoters to drive expression of the human HBM cDNA. The most commonly-used promoters for mammalian expression are from cytomegalovirus (CMV), Rous sarcoma virus (RSV), Simian virus 40 (SV40), and EF-1a (human elongation factor 1a-subunit). CMV is derived from the human cytomegalovirus immediate-early viral promoter. CMV is a stronger promoter in most cell lines than either RSV or SV40. The RSV promoter is derived from an avian virus and tends to be a strong promoter in avian cell lines. The SV40 promoter expresses well in cell lines that carry the large T antigen, such as COS-1. In these cell lines, the plasmid is replicated to higher copy numbers. EF-1a is beginning to be more widely used for recombinant protein expression. EF-1a is the promoter from the human

elongation factor 1a-subunit, a gene that is highly expressed and conserved in mammalian cell lines.

The chimeric CMVbActin promoter is a strong promoter that has been shown to produce ubiquitous gene expression in transgenic mice including bone. This promoter was chosen to drive expression of HBM in a manner consistent with the reported widespread expression of the endogenous mouse *Zmax1* (*LRP5*) gene. Although the HBM phenotype is observed in bone, the *HBM* gene may have direct or indirect effects in other tissues. Therefore, other strong ubiquitous promoters may be utilized as would be known to those skilled in the art.

Type I collagen promoters provide tissue-restricted gene expression wherein expression is primarily limited to bone. Other bone-specific promoters are available that could result in expression of HBM in bone. For example, promoters associated with proliferation of osteoblasts include histone, type I collagen, TGFβ1, MSX2, cfos/cJun and Cbfa1 may be used. Promoters associated with bone matrix maturation including alkaline phosphatase, MGP, Cbfa1, Fra/Jun and Dlx5 also can be used. Promoters associated with bone mineralization such as osteocalcin, osteopontin, bone sialoprotein and collagenase also can be used. The promoter chosen would be determined by, for example, the tissue expression, the degree of regulatable control and the like as would be known to the skilled artisan. For example, the type I collagen promoters were chosen to insure that HBM would be expressed in bone in a temporal, spatial and bone cell-specific pattern resembling the endogenous pattern of Zmax1 (LRP5) expression in bone.

21.1.2 <u>Transgenic mice over-expressing the wild-type (*LRP5*) *Zmax1* gene</u>

Plasmid constructs were prepared using the CMVbActin and type I collagen promoters driving expression of Zmax1 (LRP5). These animals can serve as a control animal model for the HBM, HBM-like and LRP6 transgenic mice (all of which are contemplated when discussing LRP5/Zmax1). Additional controls include non-transgenic littermates and wild-type animals of an identical genetic background. Methods for preparing these animals would be similar to what is discussed for mice which over express the HBM polymorphism.

21.1.3 *LRP6 gene targeted knock out mice*

LRP6 knock-out mice were generated using Omnibank embryonic stem (ES) cells carrying a gene trap vector which inserted into the first intron of the *LRP6* gene. The insert location was determined to be the LRP6 gene by an Omnibank Sequence Tag (OST) generated by reverse transcription PCR (RT-PCR) of a fusion transcript comprised of 5' gene trap vector sequence spliced to the host gene transcript 3' of the insertion site. The gene trap vector functionally knocks out the mouse LRP6 gene by forced spicing of LRP6 exon 1 to the IRES-LacZ-PolyA element of the gene trap, preventing transcription of LRP.

Chimeric mice were generated with ES cells, identified as OST38808, by injection into C57BL/6 albino host blastocysts which were then transferred to pseudopregnant females and allowed to develop through birth. Germ line chimeras were backcrossed to 129SvEVBrd strain mice to maintain the knockout allele of LRP6 on an inbred 1298SvEvBrd genetic background. Germ line transmission of the LRP6-KO allele was identified by PCR amplification of a gene trap specific sequence. Heterozygous LRP6-KO mating pairs were used for continued breeding. The genotype of wt and LRP6-KO progeny is determined by tail DNA PCR.

Measurements of bone density at 9 weeks of age in female heterozygous knock-out mice has shown significant ($p<0.05$) decreases in bone volume, trabecular number, and trabecular thickness as measured by uCT. These results are consistent with the hypothesis that LRP6 is also involved in modulating bone density and is a target for development of therapies and drugs. Accordingly, LRP6 transgenic animals and transgenic animals expressing bone modulating variants of LRP6 are contemplated within the scope of the invention.

21.1.4 Gene-targeted mice expressing the HBM polymorphism

A gene-targeting construct was prepared that could be used to create animals containing a HBM or HBM-like knock-in (KI) allele and a Zmax1 (LRP5) knock-out (KO) allele. The gene-targeting construct contained the HBM polymorphism in exon 3 and included a neomycin selection cassette that was linked to a transcriptional stop sequence and

was flanked with lox P sites. The HBM polymorphism in mouse Zmax1 results in a glycine to valine change in the amino acid sequence at position 170 of the mouse LRP5 homolog (Genbank Accession No. AF064984). Homologous recombination is used to stably introduce the construct into the mouse genome. If the transcriptional stop sequence functioned to completely block transcription of the modified *Zmax1* allele, then a functional *Zmax1* knock-out allele would be generated. This would facilitate production of a homozygous knock-out animal for the *Zmax1* gene.

To create the knock-in allele, Cre recombinase could be used to excise the neomycin selection cassette leaving behind the modified exon 3 and one copy of the loxP site. Cre could be introduced into single-cell fertilized embryos to facilitate ubiquitous expression of HBM or by crossing animals with transgenic mice to obtain bone-specific HBM expression. Homozygous animals could be made for the HBM knock-in allele. Alternatively, animals could be created by nuclear transfer techniques, wherein nuclei from homozygous animals is transferred into a prepared oocyte (e.g., enucleated) as is known in the art. See, e.g., Campbell *et al..*, *Nature* 380: 64-68 (1996). Additional methods of creating knock out mice include engineering a homologous recombination vector wherein the ATG start codon is deleted or mutated, engineering a frame-shift mutation into the vector, engineering deletions of critical portions of the promoter region, and/ or engineering a vector to delete critical regions of the gene.

The methods used for the LRP5, LRP6 and HBM mice can similarly be used for other variants of these genes.

21.2 Materials and Methods

21.2.1 Construction of the Zmax1 (LRP5) plasmid Zmax1GI_3AS

The full-length *Zmax1* cDNA construct has been engineered into the *Xba*I-*Not*I sites of the pCMVSPORT6.0 vector from Life Technologies (part of the Gateway cloning system) to create Zmax1GI_3AS. The insert (5,278 bp) can be released from the vector by digestion with either *Hind*III or *Xba*I on the 5' side together with either *Eco*RV or *Eco*RI on the 3' end. A similar construct can be prepared for LRP6 and HBM-like nucleic acids as would be

apparent to one of ordinary skill and is contemplated as well in the discussion of this section.

The Zmax1 (LRP5) construct was generated from four independent partial clones. These clones were isolated from a Zmax1 specific primed cDNA library. A partial Zmax1 cDNA clone existed in the internal survey sequencing clone set as L236B_P0049E08 isolated from an oligo-dT primed HeLa cell cDNA library. This clone was truncated at the 5-primed end. In order to isolate more 5-prime containing fragments necessary to generate a full length cDNA, a *Zmax1* gene-specific cDNA library was generated from Clontech human liver poly-A mRNA (catalog #6510-1, lot# 9060032) and Life Technologies SuperScript® Plasmid System for cDNA Synthesis and Plasmid Cloning kit (catalog no. 18248-013). This library was designated as L401. The manufacturer's protocol was carried out with the following modifications. 1)In both first and second strand synthesis reactions, DEPC-treated water was substituted for α-^{32}P-dCTP. 2)Reverse transcription was primed using oligonucleotides that were selected to be specific for the *Zmax1* gene at approximately 1 kb intervals. These sequences were checked using the program BLAST against the public databases to ensure *Zmax1* specificity. 3)Two separate reverse transcription reactions were performed. The first reaction, (A), was primed with oligonucleotides which annealed to the more 3' regions of *Zmax1* (LRP5) as follows:

47114: 5'-CGTACGTAAAGCGGCCGCTTGGCAATACAGATGTGGGA-3' (SEQ ID NO: 715)

47116: 5'-CGTACGTAAAGCGGCCGCAGTAGCTCCTCTCGGTGGC-3' (SEQ ID NO: 716)

47118: 5'-CGTACGTAAAGCGGCCGCGCTCATCATGGACTTTCCG-3' (SEQ ID NO: 717)

47120: 5'-CGTACGTAAAGCGGCCGCGCACTGCTGTTTGATGAGG-3' (SEQ ID NO: 718)

The second reaction, (B), used the previously mentioned four oligonucleotides, as well as

47108: 5'-CGTACGTAAAGCGGCCGCGAGTGTGGAAGAAAGGCTGC-3' (SEQ ID NO: 719)

47110: 5'-CGTACGTAAAGCGGCCGCAGTAGAGCTTCCCCTCCTGC-3' (SEQ ID NO: 720)

47112: 5'-CGTACGTAAAGCGGCCGCGTCCATCACGAAGTCCAGGT-3' (SEQ ID NO: 721)

All oligonucleotides contained a *Not*I linker sequence and were used at a concentration of 0.02 ug/ul. 4)The *Sal*I-adapted cDNA from both reverse transcription reactions was size-fractionated by electrophoresis on 1% agarose, 0.1 ug/ml ethidium bromide, 1x TAE gels.

The ethidium bromide-stained cDNA between 0.6 and 8.0 kb was excised from the gel. The cDNA was purified from the agarose gel by electroelution (ISCO Little Blue Tank Electroelutor®) using the manufacturer's protocol. The purified cDNA from reactions A and B were then pooled together. 5) The size-fractionated *Sal*I-adapted cDNA was ligated to *Not*I-*Sal*I digested pBluescript® (Stratagene, La Jolla, CA).

Ligated library cDNA (3 ml) was used to transform electrocompetent *E. coli* cells (ElectroMAX® DH10B cells and protocol, Life Technologies catalog no. 18290-015, BioRad *E. coli* pulser, voltage 1.8 KV, 3-5 msec pulse). The transformed cells were plated on LB-ampicillin (100 μg/ml) agar plates and incubated overnight at 37°C. Approximately 10^6 colony forming units (cfu) were plated at a density of 50,000 cfu/150 mm plate. Cells were washed off the plates with LB media, and collected by centrifugation. Plasmid DNA was purified from the cells using the QIAGEN Plasmid Giga Kit and protocol (catalog no. 12191) at a final concentration of 2.05 μg/μl.

Two probes for use in library screening were generated by the polymerase chain reaction (PCR) using 100 ng of library L401 as template. Standard PCR techniques were used. A reaction mixture contained 10 pmol of each oligo primer; 0.2 mM each dATP, dTTP, dCTP and dGTP (PE Applied Biosystems catalog no. N808-0260); 1.5 units Expand™ High Fidelity Taq DNA polymerase and 1x PCR reaction buffer (Roche Molecular Biochemicals, catalog no. 732-641; 10 mM Tris-HCl, 1.5 mM $MgCl^2$, 50 mM KCl, pH 8.3). The mixture was incubated at 99°C for one minute, followed by 30 cycles of 96° C for 15 seconds, 50° C for 30 seconds, 72° C for 1 minute with a final incubation at 72° C for 7 minutes (MJResearch DNA Engine® Tetrat PTC-225). The first was generated using oligos

107335: 5'-CAGCGGCCTGGAGGATGC-3' (SEQ ID NO: 722)

107338: 5'-CGGTCCAGTAGAGGTTTCG-3' (SEQ ID NO: 723)

which amplify a *Not*I-*Sal*I fragment of the *Zmax1* gene. The second was generated using oligos

107341: 5'-CATCAGCCGCGCCTTCATG-3' (SEQ ID NO: 724)

107342: 5'-CCTGCATGTTGGTGAAGTAC-3' (SEQ ID NO: 725)

which amplify a *Sac*I-*Kpn*I fragment of the *Zmax1* gene. Both PCR products were purified

using the Qiaquick® kit and the manufacturer's protocol (Qiagen catalog 28106) then subcloned into the vector pCRII-TOPO® (Invitrogen catalog no. K4600) following the manufacturer's protocol. Positive subclones were identified by restriction digestion of purified plasmid DNA (using standard molecular biology techniques) and subsequent DNA sequence analysis (ABI Prism BigDye Terminator Cycle® sequencing, catalog no. 4303154, ABI 377 instruments). Probe DNA was isolated by *Eco*RI restriction digestion (New England Biolabs, catalog no. R0101L) of the respective sequence-verified pCRII-TOPO® clone. Restriction fragments were size-fractionated by gel electrophoresis on 1% agarose, 0.1 ug/ml ethidium bromide, 1x TAE gels. Insert DNA was excised from the gel and purified using the Clontech NucleoSpin® Nucleic Acid Purification Kit (catalog no. K3051-2) following the manufacturer's protocol. The purified DNA fragment (25-50 ng) was labeled with Redivue ® (α^{32}P)-dCTP (Amersham Pharmacia, catalog no. AA0005) using the Prime-It II® Random Primer labeling Kit and protocol (Stratagene, catalog no. 300385). Unincorporated dCTP was removed with Amersham's NICK® column and protocol (catalog no. 17-0855-02).

Two rounds of screening library L401 were initiated to isolate fragments of the *Zmax1* (*LRP5*) gene. In the first, forty-three 150 cm LB -100 μg/ml ampicillin agar plates were plated with primary transformants from L401 at a density of about 3,000-4,000 colonies per plate. This library was screened using the ^{32}P-labeled probe (*Not*I-*Sal*I fragment) as described above at 500,000-1,000,000 cpm/ml hybridization buffer, using standard molecular biology protocols. From this primary screen, 13 single colonies were identified based on positive hybridization to the Zmax1 probe. Plasmid DNA, prepared using the QIAprep Spin Miniprep Kit and protocol (Qiagen Inc., catalog no. 27106), was analyzed by restriction digestion and sequence analysis as described above. cDNA clone # 44 was isolated from this screen and sequence verified to contain a partial Zmax1 clone.

In the second library screen, one hundred-and-four 150 cm LB ampicillin 100 ug/ml agar plates were plated with primary transformants from L401 at a density of 3000-4000 colonies per plate. This library was screened using the ^{32}P-labeled probe (*Sac*I-*Kpn*I) exactly as previously described. From this primary screen, 48 colonies were identified based on

positive hybridization to the *Zmax1* (*LRP5*) probe. Since these colonies were not single colony isolates, a secondary screen was initiated where each of the 48 primary isolates was plated at a density of approximately 500 colonies per plate. These colonies were then screened exactly as the primaries using the labeled *Sac*I-*Kpn*I fragment as probe. Thirty-four of the 48 primary clones resulted in positive hybridization to the *Zmax1* probe and were isolated as single colonies. Plasmid DNA was prepared and analyzed as described above. cDNA isolate #71_2 was isolated from this screen and sequence verified to contain a partial *Zmax1* clone.

In all cases, the sequence of any Zmax1 (LRP5) isolate was compared to a reference sequence (i.e., the sequence of the wild-type *Zmax1* allele from an affected member of the HBM kindred). This analysis was important since DNA polymorphisms had been reported for this gene in the literature. This reference sequence is predicted to encode a polypeptide of Genbank Accession No. AF077820.

The four independent partial clones used to prepare ZmaxIGI_3AS are as follows:

1). Bases 1-1366: A *Xba*I-*Sal*I fragment was obtained from a Zmax1 cDNA construct, GTC.Zmax1_13. GTC.Zmax1_13 contains a 5075 BP insert containing the entire ORF of LRP5. The clone was blunt end cloned in the *Eco*RV site of pSTBlue-1. This clone was generated by fusing a 5' clone derived from screening a bone random primed cDNA library in a pBluescript™ II derivative with a 3' clone derived from a PCR product from a bone dT primed cDNA library in pBluescript™ II. PCR was performed using LRP5 specific forward primer 5'-GCCCGAAACCTCTACTGG ACCGAC-3' (SEQ ID NO: 726) and reverse primer 5'-GCCCACCCCATCACAGTTCA CATT-3' (SEQ ID NO: 727) using DNAzyme polymerase. The resultant 3.7 kb PCR product was cloned into PCR-XL-TOPO. To generate the full length clone the 5' and 3' plasmids were transformed into DM1 (dam-) from Gibco/BRL. The 5' plasmid was digested with *Xba*I and the 3' plasmid was digested with *Hind*III. The digested plasmids were filled in with T4 polymerase to generate blunt ends and cut with *Bcl*I. the 1.7 kb 5' fragment and 3.5 kb 3' fragments were gel purified, ligated together, and cloned in the *Eco*RV site of pSTBlue-1. It provides a short 5'UTR, with coding

sequence beginning at base 100. Furthermore, it carries some additional restriction sites at the 5′ multiple cloning site. This fragment also contains a DNA polymorphism relative to the Genbank Accession No. AF077820 sequence at position 558 resulting in an A (AF077820) to a G change; this mutation does not result in an amino acid difference (Pro).

2). Bases 1367-2403: This clone was obtained from a *Zmax1*-gene primed cDNA library made from commercial human liver RNA described above. This fragment is a *SalI-BamHI* piece of DNA obtained from isolate #44. The sequence is identical to Genbank Accession No. AF077820.

3). Bases 2404-4013: This *BamHI-Bss*HII fragment was obtained from isolate #71-2 from the same library as described above. At position 3456, there is a DNA polymorphism resulting in a G (AF077820) to an A. This nucleotide difference does not change the encoded amino acid (Val).

4). Bases 4014-5278: This *Bss*HII-*Not*I fragment came from an internal clone, L236B_P0049E08. It was obtained from an oligo-dT primed HeLa cell cDNA library. The stop codon occurs at base 4947. The clone contains 331 bp of 3′ UTR sequence, including a 120 bp poly-A tail followed by the *Not*I site. The 3′ *Not*I site used in this subcloning step is a result of an added linker that was introduced at the end of the poly-A tail during library construction. A DNA polymorphism is present at base 4515 resulting in a G (AF077820) to C change that is silent at the amino acid level (Leu).

To generate the 5' section of the *Zmax1* (*LRP5*) gene, the *Xba*I-*Sal*I fragment and *Sal*I-*Bam*HI fragment were ligated into the *Xba*I-*Bam*HI sites of pBluescript® (Stratagene). The 3' section of the gene was obtained by ligating the 1.61 kb *Bam*HI-*Bss*HII fragment from Zmax1 isolate #71_2 to the 1.26 kb *Bss*HII-*Not*I fragment from L236B_P0049E08. These two fragments were ligated into the *Bam*HI-*Not*I sites of pBluescript®. The full length *Zmax1* cDNA was engineered into the *Xba*I-*Not*I sites of the vector pCMVSPORT6.0 (Life Technologies) by ligation of the *Xba*I-*Bam*HI 5' section and the *Bam*HI-*Not*I 3' section. The resulting plasmid, ZmaxGI_3AS, contains an insert of 5278 bp from the *Xba*I site to the *Not*I

site of the vector's multiple cloning site. This clone is in the antisense orientation with respect to the CMV promoter present in the vector. *Zmax1* coding sequence begins at base 100 and ends at base 4947, followed by 331 bp of 3-primed UTR sequence including a 120 bp poly-A tail. This full length cDNA contains three DNA polymorphisms from the reference sequence (GenBank Accession No. AF077820) that do not alter the predicted amino acid sequence. These polymorphisms are at position 558 resulting in an A to G that maintains the proline residue; at position 3456 resulting in a G to A that maintains the valine residue; and, at position 4515 resulting in a G to C that maintains the leucine residue.

The sequence of Zmax1GI_3AS (Figure 25) also contains a DNA polymorphism relative to SEQ ID NO. 1 at base 4088 resulting in a C (SEQ ID NO: 1 and Genbank Accession No: AB017498) to T change that results in an amino acid change at position 1330 of alanine to valine. This is consistent with the sequence determined in the wild-type allele from an affected member of the HBM kindred as well as with the published sequence of Genbank Accession No. AF077820. Zmax1GI_3AS also has 29 additional bases at the 5' end relative to SEQ ID NO: 1, as well as 129 bases at the 3' end consisting of an extra G, 120 bases of poly-A tract, and the *Not*I site.

21.2.2 Creation of the HBM mutation G171V

The HBM mutation that results in a predicted amino acid change from glycine to valine at amino acid 171 was introduced into the full length human Zmax1 (LRP5) cDNA (plasmid Zmax1GI_3AS) using PCR to change the G at position 611 to a T. Introduction of the HBM mutation was done using oligos 107335: (5'-CAGCGGCCTGGA GGATGC-3'; SEQ ID NO: 728) and 49513: (5'-CGGGTACATGTACTGGACAGC TGATTAGC-3'; SEQ ID NO: 729), which flank the endogenous *Not*I site of the *Zmax1* (*LRP5*) gene. This method creates a new *PvuII* site at the 3' end of the PCR product. A second PCR reaction was completed using oligos which introduce a *Sca*I site at the 5′ end of the product and contains the endogenous *Sal*I site of *Zmax1* in the 3-primed end. PCR products were purified using the QiaQuick® procedure (Qiagen Inc.); subcloned into the vector pCRII-TOPO (Invitrogen) as described above. Plasmid DNA was purified from single bacterial colonies and analyzed

by restriction digest and subsequent sequence analysis, all as described above. The sequence-verified pCRII-TOPO clones were restriction digested with *Not*I-*Pvu*II and *Sca*I-*Sal*I, respectively. The resulting DNA fragments were size fractionated and purified as described above. These two fragments were then subcloned into the vector, pBluescript® that had been prepared by *Not*I-*Sal*I digestion. Both *Pvu*II and *Sca*I produce blunt ends when used to digest double stranded nucleic acids. Thus, the resulting ligated fragment fails to recreate either the *Pvu*II or *Sca*I site and contains only the consensus Zmax1 sequence, with the exception of the newly introduced HBM mutation. To introduce the mutation into the full length *Zmax1* gene, this resulting plasmid was digested with *Msc*I and *Sal*I, while the 5' region of *Zmax1* was obtained by *Xba*I-*Msc*I digestion of Zmax1 plasmid GTC.Zmax1_13. These two fragments were ligated together into *Xba*I-*Sal*I digested pBluescript®, in effect creating a similar 1.366 kb *Xba*I-*Sal*I fragment. The only difference being that this construct contains the HBM mutation described above. The full length HBM cDNA then was assembled into pCMVSPORT6.0 exactly as described above for the *Zmax1* gene, with the substitution of this newly created *Xba*I-*Sal*I fragment containing the HBM mutation. The entire cDNA insert was verified by DNA sequence analysis and the introduction of the HBM mutation was confirmed.

The resulting plasmid, HBMGI_2AS (Fig. 24), contains an insert of 5,278 bp from the *Xba*I site to the *Not*I site of the vector's multiple cloning site. This clone is in the antisense orientation with respect to the CMV promoter in the vector. HBM coding sequence begins at base 100 and ends at base 4947, followed by 331 bp of 3-primed UTR sequence which includes a 120 bp poly-A tail. This full length cDNA contains three DNA polymorphisms from the reference sequence, which do not alter the amino acid sequence. These polymorphisms occur at position 558, resulting in an A to G change that maintains the proline residue; at position 3456 resulting in a G to A change that maintains the valine residue; and, at position 4515 resulting in a G to C change that maintains the leucine residue. Additionally, the HBM mutation is present at position 611 (G in Zmax1 to T in HBM) which results in a predicted amino acid change of glycine to valine at amino acid position 171, as found in affected members of the HBM kindred. This insert sequence was used to generate

the construct used for HBM over-expressing transgenic mice.

21.3 Transgene preparation

The examples provided herein are illustrations of how transgenic animals can be prepared. Additional transgenic animals can be prepared as would be known in the art. See, for example, Glenn Monastersley *et al.*., ed, Strategies in Transgenic Animal Studies (Amer. Soc. Microbiology 1995) and the references cited therein.

21.3.1 CMVbActin promoter-HBM cDNA (HBMMCBA)

To prepare the CMV*b*actin–HBM construct, pCX-EGFP, a plasmid containing the chimeric CMV*b*actin promoter, was purified as a 4778 bp *Eco*RI fragment. Subsequently, the HBM cDNA was excised from HBMGI_2AS as a 4994 bp *Xba*I/*Dra*I fragment, treated with Klenow fragment of DNA polymerase, ligated to *Eco*RI linkers, and digested with *Eco*RI. This fragment was then inserted into the *Eco*RI site of pCX-EGFP. A *Spe*I/*Hind*III 7265 bp CMV*b*actin–HBM fragment was purified for microinjection into mouse embryos.

21.3.2 Type I collagen promoter–HBM cDNA (HBMMTIC)

The rat type I collagen promoter–HBM construct was created by first replacing the pBS(SK-) (Stratagene) polylinker with another polylinker (i.e., comprising *Kpn*1 – *Spe*I – *Hind*III - *Bgl*II – *Nde*I – *Sal*I – *Sma*I – *Eco*RI – *Pst*I – *Bam*HI – *Xba*I – *Sca*I – *Nco*I – *Cla*I – *Not*I – *Sac*II - *Sac*I), that is referred to as BS(SK-)A/D. The SV40 splice and poly $(A)_n$ *Xba*I-*Nco*I region (750 bp) from pcDNA I (Invitrogen, Inc.) was directionally cloned into BS(SK-)A/D. Next, a 4994 bp *Eco*RI HBM cDNA fragment (above) was cloned into the EcoRI site. A 3640 bp *Xba*I, type I collagen promoter fragment was subcloned into the *Xba*I site of BS(SK-) (Stratagene). The promoter fragment was then excised from BS(SK-) with *Sac*II, blunt-ended with T4 DNA polymerase, digested with *Spe*I, and ligated into the HBM BS(SK-) A/D construct, which was digested with *Nde* I, blunted with T4 DNA polymerase, and digested with *Spe*I. A *Spe*I/*Cla*I 9435 bp type I collagen–HBM fragment was purified for microinjection into mouse embryos.

21.3.3 CMVbActin promoter–Zmax1 cDNA (Zmax1WTCBA)

The CMV*b*Actin promoter-HBM cDNA construct from above was used to generate the final plasmid. The following three fragments were ligated together: 1) a 6.34 kb *Xba*I-*Kpn*I backbone fragment from HBMMCBA; 2) a 0.64 kb *Xba*I-*Sap*I fragment from HBMMCBA containing the 3' end of the bActin promoter and the 5' end of the HBM cDNA; and 3) a 2.8 kb *Sap*I-*Kpn*I fragment derived from the Zmax1 cDNA that contains the wild-type sequence. A 7.2 kb *Spe*I – *Hind*III CMV*b*Actin – Zmax1 fragment was purified for micro-injection into mouse embryos.

21.3.4 Type I collagen promoter–Zmax1 cDNA (Zmax1WTTIC)

The type I collagen – HBM cDNA construct from above was used to generate the final plasmid. The HBMMTIC plasmid was linearized with *Hind*III and cut with either *Sal*I to yield a 8.52 kb *Hind*III – *Sal*I fragment or *Sap*I to yield a 2.98 kb *Sap*I – *Hind*III fragment. A 2.8kb *Sap*I – *Sal*I fragment from the Zmax1 (LRP5) cDNA containing the wild-type sequence was then ligated to the above two fragments to yield the final plasmid. A 9.4 kb *Spe*I – *Cla*I type I collagen – Zmax1 fragment was purified for micro-injection into mouse embryos.

21.4 Confirmation of transgene expression *in vitro*

Plasmid constructs for HBMMCBA, HBMMTIC, Zmax1WTCBA and Zmax1WTTIC were transiently transfected into human osteoblast (HOB) cells to measure mRNA expression as a test for functionality.

21.4.1 Transient Transfections

HOB-02-02 cells are a clonal, post-senescent, cell line derived from the HOB-02-C1 cells (Bodine et. al, 1996, *J. Bone Miner. Res.* 11: 806-819). Like the parental cell line, the HOB-02-02 cells express the temperature-sensitive SV40 large T-antigen mutant, *tsA*209. Consequently, these cells proliferate at the permissive temperature of 34°C, but stop dividing at non-permissive temperatures of 37 °C or above. Also like the parental cell line, the HOB-

02-02 cells are cultured with Growth Medium (D-MEM/F-12 containing 10% heat inactivated fetal bovine serum, 1% penicillin-streptomycin and 2 mM GlutaMAX-1) at 34°C in a 5% CO_2/95% humidified air incubator (Forma Scientific, Marietta, OH).

For the transient transfections, the HOB-02-02 cells were seeded with Growth Medium at 400,000 cells/well into 6-well plates and incubated overnight at 34°C. The cells were transfected with 0.3 mg/well of either the CMVβActin-HBM expression plasmid, the Type I Collagen-HBM expression plasmid or the corresponding empty vectors using LipofectAMINE 2000 transfection reagent according to the manufacturer's instructions (Life Technologies, Rockville, Md). After a 24 hr incubation at 34°C, the medium was changed, and the cells were incubated for an additional 24 hr at 39°C. At the end of this last incubation, the cells were rinsed with Hank's buffered salt solution. Total cellular RNA was then isolated using TRIzol® according to the manufacturer's instructions (GibcoBRL, Grand Island, NY). The RNA was treated with RNase-free DNase in order to remove contaminating DNA as previously described (Bodine *et al.*, 1997, *J. Cell. Biochem.* 65: 368-387).

21.4.2 <u>TaqMan® assay for mRNA expression</u>

TaqMan® primers and probes were chosen based on human and mouse Zmax1 (LRP5) cDNA sequences. The selected sequences were designed to be gene-specific by analysis of an alignment of human and mouse Zmax1 (LRP5) sequences as illustrated in Fig. 26.

TaqMan® quantitative reverse transcriptase-polymerase chain reaction (RT-PCR) analysis of RNA isolated from human cells was performed as described by the manufacturer (PE Applied Biosystems, Foster City, CA) using the following primers and probe set:

Human Zmax1-1/HBM-1:

Forward Primer: 5'-GTCAGCCTGGAGGAGTTCTCA-3' (SEQ ID NO: 730)

Reverse Primer: 5'-TCACCCTTGGCAATACAGATGT-3' (SEQ ID NO:731)

Probe: 6-FAM-5'-CCCACCCATGTGCCCGTGACA-3' (SEQ ID NO:732)

Results from the experimental primers/probe set were normalized to human GAPDH

levels using the multiplex protocol with the human GAPDH control kit from PE Applied Biosystems. Species-specific TaqMan® quantitative RT-PCR analysis of RNA isolated from murine cells and tissues was performed as described by the manufacturer (PE Applied Biosystems, Foster City, CA) using the following primers and probes sets:

Human Zmax-1/HBM-1:

Forward Primer: 5'-CGTGATTGCCGACGATCTC-3' (SEQ ID NO:733)

Reverse Primer: 5'-TTCCGGCCGCTAGTCTTGT-3' (SEQ ID NO:734)

Probe: 6-FAM-5'-CGCACCCGTTCGGTCTGACGCAGTAC-3' (SEQ ID NO:735)

Mouse Zmax-1/HBM-1:

Forward Primer: 5'-CTTTCCCCACGAGTATGTTGGT-3' (SEQ ID NO:736)

Reverse Primer: 5'-AAGGGACCGTGCTGTGAGC-3' (SEQ ID NO:737)

Probe: 6-FAM-5'-AGCCCCTCATGTGCCTCTCAACTTCATAG-3' (SEQ ID NO:738)

Results from the experimental primers/probe sets were normalized to 18S ribosomal RNA levels using the multiplex protocol with the 18S ribosomal RNA control kit from PE Applied Biosystems. A summary of these results is presented in Figures 17-20.

21.5 Production of transgenic mice

21.5.1 DNA microinjection

Transgene fragments for micro-injection were first purified on 1% agarose gels according to the GELase protocol from Epicentre Technologies. Fragments were then further purified on cesium chloride density gradients and extensively dialyzed against 5 mM Tris (pH 7.4), and 0.1 mM EDTA.

Linearized DNA was microinjected into mouse embryos according to standard procedures. DNA was injected into primarily the male pronucleus of fertilized C57BL/6T mouse embryos. Injected embryos (n=20-35) were transferred to the oviduct (unilaterally) of day 0.5 post coitum pseudopregnant Swiss Webster embryo recipients. Offspring were tail-biopsied and genotyped at age 10-14 days.

21.6 Production of gene-targeted transgenic mice

21.6.1 Gene targeting vectors and probes

Two gene-targeting vectors were constructed for modification of the *Zmax1* (*LRP5*) gene in embryonic stem (ES) cells. The two constructs, illustrated in Figure 16, designated as Zmax1-KI/KO A&B were designed to generate two types of mutations, a knock-out (KO) of the *Zmax1* gene and a Cre recombinase dependent knock-in (KI) of a nucleotide substitution in order to create a mouse model (i.e., glycine 170 to valine amino acid substitution in mouse Zmax1, of the HBM kindred.

Both gene-targeting vectors were constructed using genomic DNA of the mouse genomic DNA BAC clone 473P5 (Genbank Accession No. AZ095413) containing the first five exons of the mouse *Zmax1* gene. This clone was isolated by Research Genetics (Huntsville, AL) from their mouse 129SvJ genomic BAC library using a polymerase chain reaction (PCR) screen for exon 3. A forward and reverse primers of

Forward: 5'-GAGCGGGCAGGGATGGATGG-3' (SEQ ID NO: 739)

Reverse: 5'-AGGTTGGCACGGTGGATGAAGC-3' (SEQ ID NO: 740)

were used to amplify exon 3 by PCR; the following thermal cycling conditions were employed: for thirty cycles, 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. Identity of this clone with mouse *Zmax1* was confirmed by sequencing exon 3 using the BAC clone DNA as template. PCR products were cloned using the pGEM-T-easy T/A cloning kit.

21.6.2 Zmax1 (LRP5) knock-in/knock-out vector

The organization of the genomic BAC clone 473P5 was characterized by Southern blot analysis using subcloned exon 1, exon 2 and exon 3 as probes and by sequencing the region spanning exon 1 through exon 5. Two different constructs were prepared for the *Zmax1* KI/KO targeting. These constructs (A and B) differ only in flanking arms of homology. Construct (A) contains a 6.5 kb *Bst*EII-*Xba*I 5' arm of homology and a 1 kb *Xba*I-*Eco*RI 3' arm of homology; whereas, construct (B) contains a 1 kb 5' arm of homology and a 6.0 kb 3' arm of homology. The constructs were prepared by ligating short and long arms of homology to a LoxP flanked cassette containing the neomycin resistance gene (MC1-

Neo, Stratagene) and a synthetic transcriptional pause sequence (Promega).

Both *Zmax1*-KI/KO- targeting vectors (A and B) were modified to a G-to-T nucleotide substitution, encoding the G170V amino acid substitution, in exon 3. These modifications were introduced into by overlapping PCR mutagenesis using the wild type sequence of the short arm of homology as template. In addition, the 1 kb short arm of the *Zmax1*-KI/KO (B) targeting vector was modified to include a 5' terminal *Pme*I restriction recognition site. The 5' overlapping fragment was made using the following forward primer and reverse mutagenic primer:

Forward: 5'-AAGCTTGTTTAAACTGGGCATGGTGGCACATGGTTGTAAT-3' (SEQ ID NO: 741)

Reverse: 5'-GGGCTTCCACCCAGTCAGTCCAGTACATGTACCT-3' (SEQ ID NO: 742).

The thermal cycling conditions utilized for thirty cycles are 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. The 3' fragment was made using the following forward and reverse primers:

Forward: 5'-CTGACTGGGTGGAAGCACCCCGGATCGAGC-3' (SEQ ID NO: 743)

Reverse (mutagenic): 5'-GAATTCATCGGTACCTGTGCGGCCGCTTCATTG -3' (SEQ ID NO: 744).

The thermal cycling conditions utilized for thirty cycles are 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. The final overlapping PCR used 1 ml each of the 5' fragment and 3' fragment PCR reactions as template and amplification was performed using the forward and reverse primers of the 5' and 3' fragments respectively and the same thermal cycling parameters. The final PCR product was cloned using the pGEM-T-easy T/A cloning kit. The mutagenized exon 3 was excised from *Zmax1*-KI/KO (B) and transferred to *Zmax1*-KI/KO (A) as a 600 bp *Bsm*BI-*Xba*I fragment.

Probes for screening for and characterization of *Zmax1*-KI/KO (A) gene targeted ES cell clones are prepared by subcloning restriction fragments of BAC clone 473P5. The 5' outside probe is a 400 bp *Nde*-*Bst*EII fragment, and the 3' outside probe is a 500 bp *Eco*RI-*Bst*XI fragment.

The outside probes for *Zmax1*-KI/KO (B) are prepared by PCR cloning genomic fragments flanking and immediately adjacent to the targeting vector region of homology. The 5' outside probe used for *Zmax1*-KI/KO (B) is a 498 bp fragment generated using the forward primer of the sequence (5'-TGAGATGTCCTGTCTGTGGC-3'; SEQ ID NO: 745) and a reverse primer of the sequence (5'-TCCTTCCTTCCCTACAGTTG-3'; SEQ ID NO: 746). The thermal cycling conditions utilized with these probes for thirty cycles are: 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. The 3' outside probe is a 600 bp fragment generated using the forward primer of the sequence (5'-CCTAAGGATCTCCTTGT GTCTGTGG-3'; SEQ ID NO: 747) and a reverse primer of the sequence (5'-CTGCAGCAG GTCAGTAGCCTGC-3'; SEQ ID NO: 748). The thermal cycling conditions utilized with these probes for thirty cycles were: 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. Both probes are specific for the *Zmax1* gene in genomic southern analysis. PCR products are cloned using the pGEM-T-easy T/A cloning kit.

A probe for ribonuclease protection analysis of *Zmax1* mRNA structure and transcription levels was prepared by PCR cloning a cDNA fragment containing exon 3 through exon 4. The PCR reaction used a complete cDNA as template, a forward primer of the sequence (5'-TGAGATGTCCTGTCTGTGGC-3'; SEQ ID NO: 749), a reverse primer of the sequence (5'-TCCTTCCTTCCCTACAGTTG-3'; SEQ ID NO: 750) and the following thermal cycling conditions for thirty cycles; 95°C for 0.5 minute, 55°C for 1 minute and 72°C for 1 minute. The PCR product is cloned using the pGEM-T-easy T/A cloning kit.

One skilled in the art could use similar protocols to generate other engineered KI-alleles to produce transgenic animals with an HBM-like phenotype.

21.6.3 Gene targeting in ES cells

For gene targeting, embryonic stem (ES) cells are electroporated with 50 mg of linearized targeting vector and selected in 200 mg/ml G418 for 7-10 days beginning the day after electroporation. G418 resistant clones are picked, expanded and cryopreserved. Resistant clones were screened for homologous recombination by an *Eco*RI genomic Southern restriction fragment length analysis using the 5' outside probe, which detects the

wild type and targeted alleles of Zmax1 as 4 kb and 5 kb fragments, respectively. Gene targeted ES cell clones are thawed, expanded, and characterized by *Sca*I genomic restriction fragment length analysis using the 3' outside probe, which detects the wild type and targeted alleles of Zmax1 as 9 kb and 8 kb fragments, respectively. Gene targeted clones are also characterized by sequence analysis of Zmax1 exon 3 to ensure that the G to T substitution was included in homologous recombination.

21.6.4 Production of gene targeted mice by blastocyst injection

To generate chimeric mice, gene targeted ES cell clones are thawed, expanded and 9-14 ES cells injected into the blastocoel of 3.5 post coitum (p.c.) host C57BL/6 blastocysts. Injected blastocysts (12-17) are then transferred unilaterally into the uterus of 2.5 p.c. pseudopregnant Swiss Webster embryo recipients and allowed to develop to term. Chimeric males are back-crossed to 129SvEv females and tested for transmission of the targeted allele by PCR geneotyping with primers specific to the neomycin resistance gene.

21.6.5 *In vitro* deletion of the Neomycin resistance cassette via Cre recombinase

To generate Zmax1 (LRP5) KI mice from the Zmax1 KI/KO mice the Neomycin resistance (KO) cassette was deleted by micro injection of a Cre expressing plasmid (2 mg/ml) into the male pronucleus of Zmax1 KI/KO pre-fusion zygotes. Deletion of the KO cassette was confirmed by PCR analysis of the cassette insertion site.

21.6.6 Genotyping transgenic mice

Genomic DNA was isolated from mouse tail snips by digestion in 500 ul buffer containing 50 mM Tris-HCl, (pH 7.2), 50 mM EDTA, (pH 8.0), 0.5% SDS and 0.8 mg/ml proteinase K. Samples are incubated at 55°C with shaking overnight. A 10 μl aliquot was heat-inactivated at 99°C for 5 minutes and diluted 1:20 in water. For PCR, 1 μl of the diluted DNA was amplified under the following conditions: Denature: 96°C for 4.5 min; 45 cycles: 96°C for 30 sec; 63°C for 1 min; 72°C for 1 min; Extension: 72°C for 5 min; 4°C hold.

The following primer sets are used for genotyping:

HBMMCBA:

5' primers: 296 bp fragment (SEQ ID NOS: 751-752 respectively)

Forward: 5′-GCT TCT GGC GTG TGA CCG GCG-3′

Reverse: 5′-GCC GCACAG CGC CAG CAG CAG C-3′

3' primers: 400 bp fragment (SEQ ID NOS: 753-754 respectively)

Forward: 5′-CAC CCA CGC CCC ACA GCC AGT A-3′

Reverse: 5′-ATT TGC CCT CCC ATA TGT CCT TCC-3′

HBMMTIC:

5' primers: 382 bp fragment (SEQ ID NOS: 755-756 respectively)

Forward: 5′-TTC CTC CCA GCC CTC CTC CAT CAG-3′

Reverse: 5′-GCC GCA CAG CGC CAG CAG CAG C-3′

3' primers: 524 bp fragment (SEQ ID NOS: 757-758 respectively)

Forward: 5′-GAA TGG CGC CCC CGA CGA C-3′

Reverse: 5′-GCT CCC ATT CAT CAG TTC CAT AGG-3′

21.6.7 Confirmation of genotype by Southern analysis

Mouse genomic DNA was digested with *Eco*RI and probed with a 1.0 kb *Sal*I-*Bam*HI restriction fragment from the *Zmax1* cDNA. The probe hybridizes to a 5 kb fragment in transgene positive animals.

21.7 Phenotyping

Both *in vivo* and *ex vivo* assays are used to evaluate the phenotype in transgenic mice. Two strains of wild-type mice, namely C57BL/6 and 129 SvEv, are studied to provide control data for phenotypic evaluation in transgenic and gene-targeted mice. In addition, non-transgenic littermate animals are used as controls.

21.7.1 *In vivo* analysis

Spinal bone mineral content (BMC) and bone mineral density (BMD) measurements performed at Creighton University (Omaha, Nebraska) were made by DXA using a Norland

Instruments densitometer (Norland XR2600 Densitometer, Dual Energy X-ray Absorptiometry, DXA). Spinal BMC and BMD at other locations used the machinery available. There are estimated to be 800 DXA machines currently operating in the U.S. Most larger cities have offices or imaging centers which have DXA capabilities, usually a Lunar or Hologic machine. Each location that provided spine BMC and BMD data included copies of the printouts from their machines to provide verification that the regions of interest for measurement of BMD have been chosen appropriately. Complete clinical histories and skeletal radiographs were obtained.

The HBM phenotype (and HBM like phenotype which is also included when discussing the HBM phenotype) in human and animal subjects, preferably humans, can be described using criteria such as: very high spinal BMD; a clinical history devoid of any known high bone mass syndrome; and skeletal radiographs showing a normal shape of the appendicular skeleton.

pDXA: Wild-type and transgenic mice are anesthetized, weighed and whole-body X-ray scans of the skeleton generated using the LUNAR small animal PIXImus device. Scans are begun when the mice are weaned (i.e., at 3 weeks of age) and repeated at 2 week intervals. Wild-type animals are scanned at 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 27, and 29 weeks. Scanning of transgenic animals would be performed for periods up to 17 weeks. Scans are analysed for BMD (bone mineral density), BMC (bone mineral content), TTM (total tissue mass), and % fat for various body regions.

Faxitron radiographs: Following pDXA scanning of anesthetized animals, an additional X-ray was taken using a Faxitron device allowing measurement of bone size.

Calcein labeling: Animals are dosed with 15 mg/kg calcein intraperitoneally on two consecutive occasions. The first dose was given 9 days before euthanasia and the second given 2 days before euthanasia allowing measurement of bone formation rate.

21.7.2 *Ex vivo analysis*

RNA isolation: Total RNA was isolated from tibia and other tissues using TRIzol® to determine mRNA expression.

pQCT: The right femur was cleaned of soft tissue and stored in 70% ethanol for determination of total and trabecular density of the distal metaphysis and cortical density of the mid-shaft.

MicroCT: The right femur was used to determine trabecular indices of the distal metaphysis.

Histology: The right femur was used to determine bone area and static and dynamic parameters of the distal metaphysis.

Bending strength: The left femur was cleaned of soft tissue and stored at –20°C prior to analysis of 3-point bending strength of the mid-shaft.

Compressive strength of vertebra: The entire spine was removed from T10-L6-7. Soft tissue was left on and the spine frozen at -20°C until analysis. Compressive strength was measured at the L5 vertebra.

Serum: Animals are euthanized and serum prepared from blood to measure total cholesterol, triglycerides, osteocalcin and other biochemical markers.

Lysis: Examples include immunocytochemistry, such as *in situ* hybridization of osteogenic markers and TUNEL staining of cells undergoing apoptosis.

21.8 Results

21.8.1 Confirmation of expression from transgenic plasmid constructs

The HBM (HBMMCBA and HBMMTIC) and wild-type (Zmax1WTCBA and Zmax1WTTIC) plasmid constructs were transiently transfected into HOB-02-02 cells, which have a very low endogenous level of Zmax1 (LRP5) expression. Two days after transfection, RNA was isolated and TaqMan® quantitative RT-PCR was performed to determine the mRNA levels of Zmax1/HBM in the cells. To control for contaminating plasmid DNA, PCR was performed with or without the prior RT step, in the absence of the RT step, only very low levels of Zmax1/HBM mRNA were detected. However, with the RT step, a 1000-fold increase in HBM and Zmax1 mRNA was observed in cells transfected with CMV*b*Actin-promoter constructs as compared to those transfected with the CMV-b-Galactosidase control. The type I collagen promoter constructs showed approximately 10-fold increases in HBM

and Zmax1 mRNAs, which is consistent with the weaker nature of this promoter compared to the CMVβActin promoter. See Fig. 17.

21.8.2 <u>Species specific TaqMan® reagents for HBM/Zmax1 expression</u>

Species specific TaqMan® primer and probe sets for Zmax1/HBM were developed. In a series of experiments using HOB cells and mouse MC-3T3-E1 osteoblastic cells, Zmax1/HBM mRNA was measured in a mouse background, and vise versa. These reagents useful for the detection and quantization of species-specific expression. As demonstrated in Fig. 18, the primer sets are species specific in the mouse and human cell lines. Further, Fig. 19 demonstrates the quantitative measurement of human Zmax1 RNA in a background of mouse RNA. These TaqMan® sets can be used to determine the levels of human or mouse HBM or Zmax1 (or other HBM-like variant) message that are being expressed in the mouse transgenic lines.

The species-specific TaqMan® reagents are novel tools for the characterization of both endogenous Zmax1 mRNA levels and human Zmax1/HBM mRNA levels in the transgenic mouse tissues. These tools have several advantages over other conventional methods, such as Northern hybridization and standard RT-PCR. Some of these advantages are as follows: (1) specificity, since only a small region (<100 bps) is amplified primers and probes are chosen to sequence regions predicted to have no or minimal cross-reactivity; (2) speed, since the procedure is less labor intensive; (3) accuracy, since it is truly quantitative; and (4) sensitivity, since it requires only small amounts of starting material (i.e., RNA) and the signal-to-noise ratio is high. These advantages are especially important for analyzing mRNA levels in bone, because it is difficult to obtain large amounts of RNA from bone. Thus, the primer sets developed for TaqMan® analysis of a HBM and Zmax1 expression are important embodiments of the present invention. One skilled in the art will recognize that the primers described here are preferred embodiments; modifications such as extension or truncation of a primer or base substitution are encompassed by the present invention so long as the resultant nucleic acid continues to perform substantially the same function.

21.8.3 HBM expression in transgenic mice

Eight transgenic founder animals were produced for the CMV*b*Actin (HBMMCBA) construct and a breeding program initiated to establish lines. Expression of mRNA determined by TaqMan® analysis, shown in Fig. 20, showed variable levels of bone expression in 4 lines. In tibia, expression levels (relative to endogenous Zmax1 (LRP5) in HOB-03-C5 cells) showed the following range: line 18 (x10-11 fold); line 2 (x7-10 fold); line 13 (x1-2 fold) and line 28 (x1 fold). Expression was also detected in other tissues as expected based on the known activity of the promoter. For lines 2 and 13, the highest levels of HBM expression were found in the heart. A TaqMan® genotyping assay will screen for potential homozygous animals.

Six transgenic founder animals were produced for the type I collagen (HBMMTIC) construct, and a breeding program initiated to establish lines. Expression of mRNA was found in two lines initially tested. In line 19, expression was 7-8 fold and 19-20 fold greater than Zmax1 in HOB-03-C5 cells in tibia and femur, respectively. In line 35, a low level of expression was detected in tibia and femur.

21.9 *In vivo* pDXA in HBM transgenic mice

21.9.1 HBMMCBA construct

Initial analysis of limited numbers of mice, illustrated in Fig. 21 (A-C), at the 5 week and 9 week time-points showed that one line tested to date had greater BMD values compared to control. At 5 weeks, HBMMCBA line 2 (n=11) BMD in femur, spine and total body was 21%, 24% and 10% greater respectively, than wild-type control. At 9 weeks (n=3), these increases in BMD amounted to 19%, 32% and 12%, respectively.

21.9.2 HBMMTIC construct

Analysis of limited numbers of mice, illustrated in Fig. 21 (D-F), at the 5 week and 9 week time points showed that two lines tested to date had greater BMD values as compared to control. At 5 weeks, HBMMTIC line 19 (n=5) BMD in femur, spine and total body was 63%, 70% and 41% greater respectively than the wild-type control. At 9 weeks (n=2), these

increases in BMD amounted to 52%, 64% and 37% respectively.

At 5 weeks, HBMMTIC line 35 (n=1) BMD in femur, spine and total body was 4%, 47% and 6% greater, respectively than the wild-type control. At 9 weeks (n=3), these increases in BMD amounted to 32%, 43% and 18% respectively.

These results indicate that three lines analyzed to date show evidence for a high bone mass phenotype. There appeared to be no obvious correlation between levels of mRNA expression and BMD phenotype from the limited numbers of lines and animals studied to date. For example, HBMMCBA line 2 and HBMMTIC line 19 have similar levels of HBM mRNA in tibia, but the phenotype is more evident in line 19. Also, HBMMTIC line 35 shows a very low level of expression when compared to HBMMCBA line 2, but HBMMTIC line 35 appears to have a stronger phenotype. These observations point to possible differences in cellular expression that may impact the phenotype.

Overall, the BMD results from the transgenic mice show similarities in magnitude to the phenotype observed in the HBM affected kindred (Johnson *et al.*, 1997, *Am. J. Hum. Genetics*, 60:1326-1332). For example, spinal BMD measured in affected individuals is approximately 34-63% greater than non-affected family members. The data for spinal BMD from the transgenic animals ranges from ~30-70% greater than normal at 9 weeks of age.

21.9.3 *Ex vivo* analysis of transgenic mice

In order to further examine increases in bone density that were detected in select transgenic lines through monitoring of the animals by non-invasive bone imaging, necropsies were performed on animals of these lines at 5 and 9 weeks of age for direct bone densitometric and histologic analysis. The left femur was isolated, cleaned and positioned in an XCT Research peripheral Quantitative Computed Tomograph (pQCT; Stradtec Medizintechnik, Pforzheim, Germany). The distal end of the femur was located and pQCT scanning was initiated 2.5 mm proximal from this point for total and trabecular measurements. The pQCT scan for cortical measurements was initiated 3.5 mm proximal from the first scan (i.e., 6 mm proximal from the distal end). The pQCT scans were 0.5 mm thick, had a voxel (i.e., three dimensional pixel) size of 0.07 mm, and consisted of 360

projections through the slice. After the scans were completed, the images were displayed on the monitor and a region of interest, including the entire femur for each scan, was outlined. The soft tissue was automatically removed using an iterative algorithm, and the density of the remaining bone (total density) in the first slice was determined. The outer 55% of the bone was then peeled away in a concentric spiral and the density of the remaining bone (trabecular density) of the first slice was reported in mg/cm^3. In the second slice, the boundary between cortical and trabecular bone was determined using an iterative algorithm, and the density of the cortical bone was determined.

Analysis of Line 2 F1 CMV*b*Actin-HBM 5 week old transgenic animals revealed that total density, trabecular density and cortical density, were 20%, 37% and 4% higher, respectively, in the transgenic male mice versus the non-transgenic males. In 5 week old Line 19 type I collagen-HBM transgenic males, an even more dramatic increase in bone density over their non-transgenic littermates was evident. Total density, trabecular density and cortical density were 53%, 104 % and 5% higher, respectively. In the Line 19 animals, the phenotype was found to be maintained at 9 weeks of age with total, trabecular and cortical bone density being 44%, 101% and 6% higher than the non-transgenic littermates. At 17 weeks, total and trabecular density were increased 46%, 202%, respectively. The effects on the total trabecullar parameters in line 19 at all three time points were statistically significantly higher ($p<0.001$). A somewhat different pattern of bone phenotypic expression was evident from males of type I collagen-HBM transgenic Line 35. At 5 weeks of age total, trabecular and cortical density were only marginally higher (7%, 4% and 4%, respectively). However, at 9 weeks of age a clear and statistically significant ($P < 0.05$, 0.005, and 0.001 respectively) increase in these parameters became evident (i.e., 25%, 37% and 4%, respectively). The occurrence of different patterns of age-related expression of the phenotype is not unexpected, particularly with the "bone specific" type I collagen transgene, which is influenced by stage of bone cell differentiation. Both Line 2 and Line 19 animals at 5 weeks of age express comparable levels of HBM mRNA in tibia samples, and these levels are significantly greater (>7-8-fold) than other lines that show no apparent bone phenotype at this age. Line 19, which is driven by the type I collagen promoter, unlike line 2, shows very low

expression of the transgene in tissues other than bone. At 5 weeks of age, Line 35 animals show low level expression in bone and none in other tissues. Immunohistochemistry of calvarial bone sections using an HBM/Zmax1 specific antibody reveals much more intense staining in bone cells of transgenic animals from Lines 2 and 19 at 5 weeks of age and from Line 35 at 9 weeks of age versus their non-transgenic littermates.

The findings revealed by pQCT analysis were further examined under greater resolution using μCT instrumentation (Scanco). The femur was positioned such that the region being imaged includes the distal end of the femur extending approximately 4 mm proximally with the view being perpendicular to the axis of the articulating cartilage. The reference line for beginning the μCT measurement was placed to minimally overlap the growth plate and extends proximally for 200 scan slices (9 mm thickness). After completing the μCT measurement, the first slice in which the condyles have fully merged was identified. A region of interest was outlined to include a maximum amount of the trabecular space, while excluding the cortex. For the first thirty slices, regions of interest were drawn every five slices and merged. For the remaining 105 slices, regions of interest were drawn every 10-20 slices. The more regular the trabecular space, the less frequently a region of interest needed to be drawn. Each region of interest was merged with its predecessor after it was drawn. After regions of interest had been established for all 135 slices, three dimensional evaluation was performed using a threshold setting of 350.

The increased bone densities identified by pQCT were confirmed and extended by μCT to include elements of bone architecture. In the Line 2 transgenic animals, μCT bone volume/total volume, connectivity density and trabecular thickness were 50%, 83% and 12% higher, respectively. Both the connectivity density and trabecular thickness indices suggest that the increased density is also associated with increased structural strength. Bone surface/ bone volume was lower by 17% in the transgenic males, which may suggest that there may be fewer resorptive surfaces and pits. The trabecular bone response was further confirmed by histological evaluation of non-decalcified, Goldner's stained sections, which revealed 36% greater bone mineral area in the distal femoral metaphysis of the transgenic males. Dynamic histomorphometric analysis revealed that a substantial increase in bone mineral apposition

rate (+100%), as determined by calcein double labeling, may be partially responsible for the increased bone in the transgenics. The dramatic effects evident by pQCT on trabecular bone in Line 19 were supported by μCT evaluation where bone volume/total volume, trabecular number, trabecular thickness and connectivity density were found to be 130%, 45%, 30% and 121% higher, respectively, in the transgenic males. As seen in Line 2, the bone surface/ bone volume was lower in the transgenic males (-36%). All of these effects were statistically significant with $p < 0.01$. The bone phenotype seen at 5 weeks of age in Line 19 was maintained in 9 week-old animals where bone volume/total volume, trabecular number and connectivity density were 125%, 38% and 110% higher than in the non-transgenic littermates.

μCT analysis of the Line 35 transgenics revealed a somewhat different pattern than the other two lines. In contrast to only modestly increased density indicated by pQCT in 5 week-old females from Line 35, a statistically significant effect ($p < 0.01$) was seen with mCT, which has greater image resolution and encompasses a larger volumetric sample. Bone volume/total volume, trabecular thickness and connectivity density were 35%, 9% and 27% higher. A similar result was seen in 5 week-old males from Line 35 where bone volume/total volume and connectivity density increases of 37% and 45%, respectively, were evident by μCT analysis, where only slight increases were revealed by pQCT. The differences between the Line 35 transgenic males and their non-transgenic littermates appeared to increase with age such that statistically significant increases in total density (25%) and trabecular density (37%) were evident by pQCT at 9 weeks of age. The μCT results support an age-related divergence in bone phenotype in this line and show that differences between transgenic and non-transgenic animals, in terms of bone volume/total volume and connectivity density, had nearly doubled those seen at 5 weeks to 70% and 83%, respectively. The bone volume increases seen in the transgenic animals is in agreement with a significant increase in this parameter that was detected in a bone biopsy sample from an adult male affected member of the HBM kindred. The other parameters that were found to be affected in the transgenic lines may reflect changes that lead to an increased peak/adult bone mass, which in this strain of mice occurs between the ages of 17-20 weeks

The bone density and bone architectural changes seen in the over-expressing transgenic lines would suggest potentially greater bio-mechanical strength. This was tested directly by evaluating 3-point bending strength of femurs from 5 week old Line 19 males. The femora were cleaned of soft tissue and the femoral length measured using a digital caliper. Periosteal and endosteal circumferences, as well as cortical thickness, were measured 6 mm from the distal end of the bone using pQCT. The femur was then placed on a fixture so that the center of mid-shaft was at an equal distance from fixed supports located 5 mm apart. The cross bar of an Instron 5543 load device was placed over the mid-shaft and a force applied at a speed of 1 mm/minute until fracture occurred. A force vs. displacement curve was generated and peak load determined using Instron Merlin software. There was a 75% increase ($p<0.01$) in strength that appears to be due to an increase in periosteal circumference leading to an increase in cortical thickness. Thus, it appears that the changes in bone density and bone geometry, as seen in the HBM transgenic animals, do translate into increases in biomechanical strength.

In view of the association of HBM/Zmax1 within the class of LDL related receptor proteins, it was of interest to determine whether the mutation might affect lipid profiles. Indeed, lipid studies in the HBM kindred (i.e., 8 affected and 7 unaffected members) have revealed that triglyceride and VLDL levels are statistically lower in the affected members. Serum samples from the transgenic lines were analyzed on a Hitachi 911 instrument using Boehringer Mannheim (for Cholesterol) and Roche (for triglycerides) reagents. The cholesterol was measured via *o*-quinone imine dye (which is formed following enzymatic reactions with cholesterol) photometrically at 505 nm at 37°C. Enzymatic methods for triglyceride measurements are based on determination of the glycerol part of triglyceride after hydrolysis of triglycerides and fatty acids. The end dye product of enzymatic reaction was measured at 505 nm. In 5 week old male Line 2 transgenics, although serum cholesterol was only slightly reduced, serum triglyceride levels were reduced by 26% in the transgenics versus their non-transgenic littermates. In a limited sample of Line 2 animals at 9 weeks of age, triglyceride levels remained 20% lower. Similarly, at 5 weeks of age triglyceride levels in male transgenics from Line 19 were 32% lower. In contrast, at 5 weeks of age both male

and female transgenics of Line 35 did not have lower triglyceride levels. The fact that the 5 week old Line 35 animals did have statistically greater bone volume/total volume suggests that the lipid change may not be directly related to the skeletal phenotype. This would appear to be supported by the fact that the Line 35 animals at 9 weeks of age had only slightly reduced triglyceride levels (11%) but exhibited substantially higher bone density than at 5 weeks of age. Due to the different levels and sites of expression of the transgene in these lines we can not rule out the possibility that serum lipid levels could serve as a surrogate marker for agents favorably affecting a bone phenotype through HBM/Zmax1.

These and other transgenic lines based on HBM or HBM-like genes will serve as valuable models for exploring the nature of bone homeostasis. Bone density in all species accommodates to its customary loading conditions. In the HBM kindred and in the transgenic lines, the sensor/effector systems of the skeleton appear to perceive greater load signals resulting in greater bone density. Experimental models have been established showing that increased bone loading can lead to increased bone density and that unloading or disuse leads to a loss of bone density. Evaluating the histological, biochemical and genetic responses of the skeleton of the transgenic animals in these experimental paradigms will yield much information regarding the sensor/effector system responsible for bone homeostasis. The application of the transgenic animals in other established models of altered bone turnover, including but not limited to steroid deficiency-induced osteopenia and aging-related osteopenia will provide further insight into the role of Zmax1 in bone homeostasis and the nature of the favorable changes induced by the HBM mutation.

21.9.4 *HBM* gene-targeting

The Zmax1 KI/KO gene-targeting vector is electroporated into 129 SvEv, C57BL/6 ES and 129 ES cells. Restriction fragment length analysis of genomic DNA and sequencing of PCR amplified fragments can be used to identify gene targeted clones. The knock-in version of the gene-targeting vector allows for the introduction of the HBM mutation into the endogenous Zmax (LRP5) genomic locus with minimal impact on the mouse genome. It permits the production of the HBM protein in a more natural environment, i.e. not in an over-

expression model such as the transgenic mice or transfected cell lines. The knock-out version of the gene-targeting vector was engineered to contain a transcriptional stop sequence that has the potential to result in loss of one functional LRP5 allele. Breeding heterozygous animals with this mutation would lead to the production of embryos homozygous for the null allele. In a different design of the gene-targeting vector, lox P sites could be positioned in such a way that would facilitate production of a conditional knock-out of the endogenous LRP5 gene. In the presence of Cre recombinase, a critical region of the LRP5 gene would be deleted in between the lox P sites, thus resulting in the potential loss of one functional allele. Animal breeding would then be used to create homozygotes with a null allele. Other recombinase enzyme systems, such as flp recombinase in combination with cognate frt sites, could be used to create the deletion. The recombinase could be administered in a number of ways as described earlier, including plasmid injection into embryos and use of transgenic animals expressing Cre. The promoter used to drive expression of Cre could be chosen in a manner that would result in ubiquitous or tissue-specific deletion of the *LRP5* gene thus resulting in a conditional knockout. In a further embodiment expression of the Cre enzyme itself could be made conditional using inducible systems such as GeneSwitch and Tetracycline paradigms.

21.9.5 Uses of transgenic animals and cells

The transgenic animals and cells of the present invention are useful tools in methods for identifying surrogate markers for the HBM phenotype. The surrogate markers provided by the present invention are also useful tools for the assessment and screening of prospective treatments. Individuals carrying the *HBM* gene have elevated bone mass. The *HBM* gene causes this phenotype by altering the activities, levels, expression patterns, and modification states of other molecules involved in bone development. Using a variety of established techniques, it is possible to identify molecules, preferably proteins or mRNAs, whose activities, levels, expression patterns, and modification states are different between systems containing the *Zmax1* gene and systems containing the *HBM* gene. Such systems can be, for example, cell-free extracts, cells, tissues or living organisms, such as mice or humans. For a

mutant form of Zmax1, a complete deletion of Zmax1, mutations lacking the extracellular or intracellular portion of the protein, or any other mutation in the *Zmax1* gene may be used. It is also possible to use expression of antisense Zmax1 RNA or oligonucleotides to inhibit production of the Zmax1 protein. For a mutant form of HBM, a complete deletion of HBM, mutations lacking the extracellular or intracellular portion of the HBM protein, or any other mutation in the *HBM* gene may be used. It is also possible to use expression of antisense HBM RNA or oligonucleotides to inhibit production of the HBM protein.

Molecules identified by comparison of Zmax1 systems and HBM systems can be used as surrogate markers in pharmaceutical development or in diagnosis of human or animal bone disease. Alternatively, such molecules may be used in treatment of bone disease. *See*, Schena *et al.*, 1995 *Science*, 270: 467-70.

For example, a transgenic mouse carrying the *HBM* gene or HBM-like variant in the mouse homologue locus is constructed. A mouse of the genotype HBM/+ is viable, healthy and has elevated bone mass. To identify surrogate markers for elevated bone mass, HBM/+ (i.e., heterozygous) and isogenic +/+ (i.e., wild-type) mice are sacrificed. Bone tissue mRNA is extracted from each animal, and a "gene chip" corresponding to mRNAs expressed in the +/+ individual is constructed. mRNA from different tissues is isolated from animals of each genotype, reverse-transcribed, fluorescently labeled, and then hybridized to gene fragments affixed to a solid support. The ratio of fluorescent intensity between the two populations is indicative of the relative abundance of the specific mRNAs in the +/+ and HBM/+ animals. Alternatively, mRNA may be isolated from wild-type and transgenic animals. cDNA prepared from these samples is transcribed *in vitro* to obtain labeled mRNA for use on custom made or commercially available gene array chips such as are manufactured by Affymetrix. Sets of genes with altered expression as a function of phenotype may be identified be a variety of routine computational analyses. Genes encoding mRNA over- and under-expressed relative to the wild-type control are candidates for genes coordinately regulated by the *HBM* gene or *HBM*-like gene.

One standard procedure for identification of new proteins that are part of the same signaling cascade as an already-discovered protein is as follows. Cells are treated with

radioactive phosphorous, and the already-discovered protein is manipulated to be more or less active. The phosphorylation state of other proteins in the cell is then monitored by polyacrylamide gel electrophoresis and autoradiography, or similar techniques. Levels of activity of the known protein may be manipulated by many methods, including, for example, comparing wild-type mutant proteins using specific inhibitors such as drugs or antibodies, simply adding or not adding a known extracellular protein, or using antisense inhibition of the expression of the known protein (Tamura *et al.*, 1998 *Science*, 280: 1614-7; Meng, 1998 *EMBO J.*, 17: 4391-403; Cooper *et al.*, 1982 *Cell* 1: 263-73).

In another example, proteins with different levels of phosphorylation are identified in TE85 osteosarcoma cells expressing either a sense or antisense cDNA for Zmax1. TE85 cells normally express high levels of Zmax1 (Dong *et al.*, 1998 *Biochem. & Biophys. Res. Comm.*, 251: 784-90). Cells containing the sense construct express even higher levels of Zmax1, while cells expressing the antisense construct express lower levels. Cells are grown in the presence of ^{32}P, harvested, lysed, and the lysates run on SDS polyacrylamide gels to separate proteins, and the gels subjected to autoradiography (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons (1997)). Bands that differ in intensity between the sense and antisense cell lines represent phosphoproteins whose phosphorylation state or absolute level varies in response to levels of Zmax1. As an alternative to the ^{32}P-labeling, unlabeled proteins may be separated by SDS-PAGE and subjected to immunoblotting, using the commercially available anti-phosphotyrosine antibody as a probe (Thomas *et al.*, 1995 *Nature*, 376: 267-71). As an alternative to the expression of antisense RNA, transfection with chemically modified antisense oligonucleotides can be used (Woolf *et al.*, 1990 *Nucleic Acids Res.*, 18: 1763-9).

Many bone disorders, such as osteoporosis, have a slow onset and a slow response to treatment. It is therefore useful to develop surrogate markers for bone development and mineralization. Such markers can be useful in developing treatments for bone disorders, and for diagnosing patients who may be at risk for later development of bone disorders. Examples of preferred markers are N- and C-terminal telopeptide markers described, for example, in U.S. Patent Nos. 5,455,179, 5,641,837 and 5,652,112, the disclosures of which

are incorporated by reference herein in their entirety. In the area of HIV disease, CD4 counts and viral load are useful surrogate markers for disease progression (Vlahov *et al.*, 1998 *JAMA*, 279(1): 35-40). There is a need for analogous surrogate markers in the area of bone disease.

A surrogate marker can be any characteristic that is easily tested and relatively insensitive to non-specific influences. For example, a surrogate marker can be a molecule such as a protein or mRNA in a tissue or in blood serum. Alternatively, a surrogate marker may be a diagnostic sign such as sensitivity to pain, a reflex response or the like.

In yet another example, surrogate markers for elevated bone mass are identified using a pedigree of humans carrying the *HBM* gene or *HBM*-like gene. Blood samples are withdrawn from three individuals that carry the *HBM* gene or *HBM*-like gene, and from three closely related individuals that do not. Proteins in the serum from these individuals are electrophoresed on a two dimensional gel system, in which one dimension separates proteins by size, and another dimension separates proteins by isoelectric point (Epstein *et al.*, 1996 *Electrophoresis* 17: 1655-70). Spots corresponding to proteins are identified. A few spots are expected to be present in different amounts or in slightly different positions for the HBM individuals compared to their normal relatives. These spots correspond to proteins that are candidate surrogate markers. The identities of the proteins are determined by microsequencing, and antibodies to the proteins can be produced by standard methods for use in diagnostic testing procedures. Diagnostic assays for HBM proteins or other candidate surrogate markers include using antibodies described in this invention and a reporter molecule to detect HBM in human body fluids, membranes, bones, cells, tissues or extracts thereof. The antibodies can be labeled by joining them covalently or noncovalently with a substance that provides a detectable signal. In many scientific and patent literature, a variety of reporter molecules or labels are described including radionuclides, enzymes, fluorescent, chemiluminescent or chromogenic agents (U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241). The transgenic or genetically modified animals can also serve in a method for surrogate marker identification.

Using these antibodies, the levels of candidate surrogate markers are measured in

normal individuals and in patients suffering from a bone disorder, such as osteoporosis, osteoporosis pseudoglioma, Engelmann's disease, Ribbing's disease, hyperphosphatasemia, Van Buchem's disease, melorheostosis, osteopetrosis, pychodysostosis, sclerosteosis, osteopoikilosis, acromegaly, Paget's disease, fibrous dysplasia, tubular stenosis, osteogenesis imperfecta, hypoparathyroidism, pseudohypoparathyroidism, pseudopseudohypoparathyroidism, primary and secondary hyperparathyroidism and associated syndromes, hypercalciuria, medullary carcinoma of the thyroid gland, osteomalacia and other diseases. Techniques for measuring levels of protein in serum in a clinical setting using antibodies are well established. A protein that is consistently present in higher or lower levels in individuals carrying a particular disease or type of disease is a useful surrogate marker.

A surrogate marker can be used in diagnosis of a bone disorder. For example, consider a child that presents to a physician with a high frequency of bone fracture. The underlying cause may be child abuse, inappropriate behavior by the child, or a bone disorder. To rapidly test for a bone disorder, the levels of the surrogate marker protein are measured using the antibody described above.

Levels of modification states of surrogate markers can be measured as indicators of the likely effectiveness of a drug that is being developed. It is especially convenient to use surrogate markers in creating treatments for bone disorders, because alterations in bone development or mineralization may require a long time to be observed. For example, a set of bone mRNAs, termed the "HBM-inducible mRNA set" is found to be over-expressed in HBM/+ mice as compared to +/+ mice, as described above. Expression of this set can be used as a surrogate marker. Specifically, if treatment of +/+ mice with a compound results in over-expression of the HBM-inducible mRNA set, then that compound is considered a promising candidate for further development.

This invention is particularly useful for screening compounds by using the Zmax1 or HBM protein or HBM-like proteins or binding fragments thereof in any of a variety of drug screening techniques.

The Zmax1 or HBM protein or fragment employed in such a test may either be free in solution, affixed to a solid support, or borne on a cell surface. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the protein or fragment, preferably in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, for the formation of complexes between a Zmax1 or HBM protein or fragment and the agent being tested, or examine the degree to which the formation of a complex between a Zmax1 or HBM protein or fragment and a known ligand is interfered with by the agent being tested.

Thus, the present invention provides methods of screening for drugs comprising contacting such an agent with a Zmax1 (LRP5) or HBM protein or fragment thereof and assaying (i) for the presence of a complex between the agent and the Zmax1 or HBM protein or fragment, or (ii) for the presence of a complex between the Zmax1 or HBM protein or fragment and a ligand, by methods well known in the art. In such competitive binding assays the Zmax1 or HBM protein or fragment is typically labeled. Free Zmax1 or HBM protein or fragment is separated from that present in a protein:protein complex, and the amount of free (i.e., uncomplexed) label is a measure of the binding of the agent being tested to Zmax1 or HBM or its interference with Zmax1 or HBM: ligand binding, respectively.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the Zmax1 or HBM proteins and is described in detail in WO 84/03564. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with Zmax1 or HBM proteins and washed. Bound Zmax1 or HBM protein is then detected by methods well known in the art. Purified Zmax1 or HBM can be coated directly onto plates for use in the aforementioned drug screening techniques. However, non-neutralizing antibodies to the protein can be used to capture antibodies to immobilize the Zmax1 or HBM protein on the solid phase.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of specifically binding the Zmax1 or HBM protein compete with a test compound for binding to the Zmax1 or HBM protein or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide that

shares one or more antigenic determinants of the Zmax1 or HBM protein.

A further technique for drug screening involves the use of host eukaryotic cell lines or cells (such as described above) that have a nonfunctional Zmax1 or *HBM* gene. These host cell lines or cells are defective at the Zmax1 or HBM protein level. The host cell lines or cells are grown in the presence of drug compound. The rate of growth of the host cells is measured to determine if the compound is capable of regulating the growth of Zmax1 or HBM defective cells.

The goal of rational drug design is to produce structural analogs of biologically active proteins of interest or of small molecules with which they interact (e.g., agonists, antagonists, inhibitors) in order to fashion drugs which are, for example, more active or stable forms of the protein, or which, e.g., enhance or interfere with the function of a protein *in vivo*. See, e.g., Hodgson, 1991 *Bio/Technology*, 9: 19-21. In one approach, one first determines the three-dimensional structure of a protein of interest (e.g., Zmax1 or HBM protein) or, for example, of the Zmax1- or HBM-receptor or ligand complex, by x-ray crystallography, by computer modeling or most typically, by a combination of approaches. Less often, useful information regarding the structure of a protein may be gained by modeling based on the structure of homologous proteins. An example of rational drug design is the development of HIV protease inhibitors (Erickson *et al.*, 1990 *Science,* 249: 527-33). In addition, peptides (e.g., Zmax1 or HBM protein) are analyzed by an alanine scan (Wells, 1991 *Methods in Enzymol.*, 202: 390-411). In this technique, an amino acid residue is replaced by Ala, and its effect on the peptide's activity is determined. Each of the amino acid residues of the peptide is analyzed in this manner to determine the important regions of the peptide.

It is also possible to isolate a target-specific antibody, selected by a functional assay, and then to solve its crystal structure. In principle, this approach yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced banks of

peptides. Selected peptides would then act as the pharmacore.

Thus, one may design drugs which have, e.g., improved Zmax1 or HBM protein activity or stability or which act as inhibitors, agonists, antagonists, etc. of Zmax1 or HBM protein activity. By virtue of the availability of cloned Zmax1 or HBM sequences, sufficient amounts of the Zmax1 or HBM protein may be made available to perform such analytical studies as X-ray crystallography. In addition, the knowledge of the Zmax1 or HBM protein sequence provided herein will guide those employing computer modeling techniques in place of, or in addition to X-ray crystallography.

Identified drug candidates (known as "leads") may be further studied by use of transgenic animals. The transgenic animals of the present invention are useful for creating an animal model of bone density modulation which may be used to test and refine drug leads. The transgenic animals described above represent a single example of the Zmax1 and HBM or HBM-like transgenic animals contemplated herein. One skilled in the art is aware of variations and the considerations which will be routinely applied in modifying the present invention to a specific purpose. Examples of the development of transgenic animal models are given for example in Strategies in Transgenic Animal Science (1995, Monastersky and Robl Eds., Washington, DC: American Society for Microbiology) and references therein which are all incorporated herein by reference in their entirety.

As an example, at least two groups of transgenic animals can be created as described, so that one group expresses HBM and another group expresses Zmax1. These animals can be treated with the candidate drug for some time spanning from a few days to the remainder of the animal's life-span. The animals are monitored for changes in bone mass and/or surrogate markers for the HBM phenotype. The transgenic animals used in such a study may express human HBM protein and Zmax1 protein or the homologous HBM and Zmax1 proteins defined for each species or variants thereof. Expression may be driven by a ubiquitous promoter or a bone specific promoter as would be known. It will be informative to compare groups of animals utilizing different promoters.

The transgenic animals of the method according to the present inventions may also comprise knock-in (KI) and/or knock-out (KO) animals, such as mice, which express HBM,

Zmax1, or neither under the control of the animal's native promoter. Such animals may be created by homologous recombination in ES cells as described above (and elsewhere in the literature of the art such as, for example, U.S. Patent Nos. 6,187,991 and 6,187,992 and references cited therein which are incorporated herein in their entirety). The experimental groups of transgenic animals treated with candidate drugs may be monitored by non-invasive means, by the monitoring of surrogate markers as described above, and/or by *ex vivo* analysis of bones from sacrificed animals at given time-points.

Likewise the effect of such treatments as dietary control (e.g. varying intake of vitamins, minerals, proteins, lipids, etc.), ovariectomy, direct administration of all or part of purified HBM or Zmax1 proteins, administration of antisense nucleotides, antibodies against Zmax1 or gene therapy in adults may be investigated by systematic administration of the treatment to transgenic animals according to the invention. Such treatments may include, administration of estrogens, tamoxifen, raloxifene, (or other selective estrogen modulators, SERMs), vitamin D analogs, calcitonin, cathepsin K inhibitors, statins (e.g. simvastatin, pravastatin, and lovastatin), bis-phosphonates, parathyroid hormone (PTH), bone morphogenetic proteins (BMP) as described in U.S. Patent Nos. 6,190,880 and 5,866,364, and combinations of the above compounds.

In view of the homology between Zmax1 and LRP6 and to the LDL receptor and the further observations of markers for cardiac health being modulated in HBM subjects, it is an aspect of the present invention to use the novel research methods disclosed herein to screen known cardio-protective treatments for bone modulating effects. Thereby, the present invention provides therapeutic methods which are both cardio-protective and which improve bone quality. The models are useful for testing drugs and researching lipid modulation effects related to Zmax1, LRP6, HBM and HBM like proteins and nucleic acids.

The effect of various mutations of *Zmax1, HBM* and HBM-like genes may be investigated by creation of additional lines of transgenic animals according to the invention, wherein these animals comprise such mutations. By comparison of direct measures of bone development or surrogate markers, an embodiment of the invention provides a useful research tool for screening gene therapy reagents, candidate drug therapies, and elucidating molecular

mechanisms of bone development modulation. One skilled in the art knows how to use the methods of the present invention to achieve these goals.

The present invention provides a method and useful research tools for testing prospective gene therapies. Transgenic knock-out mice are useful for testing prospective gene therapies. A transgenic knock-out animal such as a mouse is created as described above which does not express endogenous Zmax1 or HBM. A prospective gene therapy, such as intravenous injection of a recombinant replication-defective adenovirus encoding the human HBM protein driven by the CMVβActin promoter, is administered. Parameters of bone density and/or surrogate markers are monitored over time following therapy (Ishibashi *et al.*, 1993 *J. Clin. Invest.* 92: 883-93) A TaqMan® primer set such as that described above may be used to measure expression of transgenic HBM. One skilled in the art knows alternative methods such as the Northern blot method. Comparison of treated and untreated animals both within and between groups of germ-line transgenic animals, knock-out (null allele) background, and wild-type endogenous Zmax1 background animals provides complementary controls for assessing the relative effectiveness of various modalities of gene therapy.

Uses for the transgenic animals models contemplated herein also include, but are not limited to: (1) sources for generating bone cell cultures from the calvaria of the transgenic animals to study bone cell (*e.g.*, osteoblast and osteoclast) function and number; (2) models for studying the effects of estrogen loss by ovariectomizing (ovx) the transgenic animals; (3) models for testing mechanical loading on the bones and other stress/strength tests; (4) breeding models with which to breed to other genetically modified or naturally occurring mutant animals that display bone abnormalities; (Chipman *et al.*, 1993 *PNAS*, 90: 1701-05; Phillips *et al.*, 2000 *Bone* 27: 219-26; Kajkenova *et al.*, 1997 *J. Bone Min. Res.* 12: 1772-79; Jilka *et al.*, 1996 *J. Clin. Invest.* 97: 1732-40; Takahashi *et al.*, 1994 *Bone and Mineral* 24: 245-55); (5) bone mis/disuse models to test the effects of weight bearing or gravity; (6) models for identifying and screening reagents which may or are known to modulate bone metabolism (e.g., PTH, estrogen, vitamin D analogs, bisphosphonates, statins, leptin, BMP, apoE); (7) models for investigating prospective treatments to improve fracture repair.

The transgenic animal models can be analyzed using, but not limited to, such methods as bone densitometry by pDEXA, pQCT and microCT; histology, molecular marker analysis, apoptosis, cell proliferation, cell cycle, mineralization, serum biochemistry, transcriptional profiling, and the like.

22. Methods of Use: Avian and Mammalian Animal Husbandry

The Zmax1 (LRP5) DNA and Zmax1 (LRP5) protein and/or the HBM DNA and HBM protein (or LRP6 or an HBM-like nucleic acid or protein as also contemplated herein) can be used for vertebrate and preferably human therapeutic agents and for avian and mammalian veterinary agents, including for livestock breeding. Birds, including, for example, chickens, roosters, hens, turkeys, ostriches, ducks, pheasants and quails, can benefit from the identification of the gene and pathway for high bone mass. In many examples cited in literature (for example, McCoy *et al.*, 1996 *Res. Vet. Sci.*, 60: 185-6), weakened bones due to husbandry conditions cause cage layer fatigue, osteoporosis and high mortality rates. Additional therapeutic agents to treat osteoporosis or other bone disorders in birds can have considerable beneficial effects on avian welfare and the economic conditions of the livestock industry, including, for example, meat and egg production.

23. Methods of use: Diagnostic assays using Zmax1-specific oligonucleotides for detection of genetic alterations affecting bone development

In cases where an alteration or disease of bone development is suspected to involve an alteration of the *Zmax1*, *LRP6*, *HBM* or *HBM*-like gene, specific oligonucleotides may be constructed and used to assess the level of Zmax1 mRNA or HBM mRNA, respectively, in bone tissue or in another tissue that affects bone development.

For example, to test whether a person has the *HBM* gene, which affects bone density, polymerase chain reaction can be used. Two oligonucleotides are synthesized by standard methods or are obtained from a commercial supplier of custom-made oligonucleotides. The length and base composition are determined by standard criteria using the Oligo 4.0 primer Picking program (Wojchich Rychlik, 1992) or any suitable alternative. One of the

oligonucleotides is designed so that it will hybridize only to HBM DNA under the PCR conditions used. The other oligonucleotide is designed to hybridize a segment of Zmax1 genomic DNA such that amplification of DNA using these oligonucleotide primers produces a conveniently identified DNA fragment. For example, the pair of primers CCAAGTTCTGAGAAGTCC (SEQ ID NO:32) and AATACCTGAAACCATACCTG (SEQ ID NO:33) will amplify a 530 base pair DNA fragment from a DNA sample when the following conditions are used: step 1 at 95°C for 120 seconds; step 2 at 95°C for 30 seconds; step 3 at 58°C for 30 seconds; step 4 at 72°C for 120 seconds; where steps 2-4 are repeated 35 times. Tissue samples may be obtained from hair follicles, whole blood, or the buccal cavity.

The fragment generated by the above procedure is sequenced by standard techniques. Individuals heterozygous for the *HBM* gene will show an equal amount of G and T at the second position in the codon for glycine 171. Normal or homozygous wild-type individuals will show only G at this position. Similar routine procedures may be used to develop assays for other polymorphisms and variants according to the invention.

Other amplification techniques besides PCR may be used as alternatives, such as ligation-mediated PCR or techniques involving Q-beta replicase (Cahill *et al.*, *Clin. Chem.*, 37(9):1482-5 (1991)). For example, the oligonucleotides 5'-AGCTGCTCGTAGCTG TCTCTCCCTGGATCACGGGTACATGTACTGGACAGACTGGGT-3'(SEQ ID NO:34) and T5'-GAGACGCCCCGGATTGAGCGGGCAGGGATAGCTTATTCCCTGTGCCGCA TTACGGC-3' (SEQ ID NO: 35) can be hybridized to a denatured human DNA sample, treated with a DNA ligase, and then subjected to PCR amplification using the primer oligonucleotides 5'-AGCTGCTCGTAGCTGTCTCTCCCTGGA-3' (SEQ ID NO:36) and 5'-GCCGTAATGCGGCACAGGGAATAAGCT-3' (SEQ ID NO:37). In the first two oligonucleotides, the outer 27 bases are random sequence corresponding to primer binding sites, and the inner 30 bases correspond to sequences in the *Zmax1* gene. The T at the end of the first oligonucleotide corresponds to the *HBM* gene. The first two oligonucleotides are ligated only when hybridized to human DNA carrying the *HBM* gene, which results in the formation of an amplifiable 114 bp DNA fragment.

Products of amplification can be detected by agarose gel electrophoresis, quantitative hybridization, or equivalent techniques for nucleic acid detection known to one skilled in the art of molecular biology (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratory, Cold Spring, NY (1989)).

Other alterations in the *Zmax1* gene or the *HBM* gene (or *LRP6* or HBM-like nucleic acids, which are also contemplated herein) may be diagnosed by the same type of amplification-detection procedures, by using oligonucleotides designed to identify those alterations. These procedures can be used in animals as well as humans to identify alterations in Zmax1 or HBM that affect bone development.

Expression of Zmax1 or HBM in bone tissue may be accomplished by fusing the cDNA of Zmax1 or HBM, respectively, to a bone-specific promoter in the context of a vector for genetically engineering vertebrate cells. DNA constructs are introduced into cells by packaging the DNA into virus capsids, by the use of cationic liposomes, electroporation, or by calcium phosphate transfection. Transfected cells, preferably osteoblasts, may be studied in culture or may be introduced into bone tissue in animals by direct injection into bone or by intravenous injection of osteoblasts, followed by incorporation into bone tissue (Ko *et al.*, 1996 *Cancer Res.* 56: 4614-9). For example, the osteocalcin promoter, which is specifically active in osteoblasts, may be used to direct transcription of the *Zmax1* gene or the *HBM* gene. Any of several vectors and transfection methods may be used, such as retroviral vectors, adenovirus vectors, or vectors that are maintained after transfection using cationic liposomes, or other methods and vectors described herein.

Alteration of the level of functional Zmax1 protein or HBM protein affects the level of bone mineralization. By manipulating levels of functional Zmax1 protein or HBM protein, it is possible to affect bone development and to increase or decrease levels of bone mineralization. For example, it may be useful to increase bone mineralization in patients with osteoporosis. Alternatively, it may be useful to decrease bone mineralization in patients with osteopetrosis or Paget's disease. Alteration of Zmax1 levels or HBM levels can also be used as a research tool. Specifically, it is possible to identify proteins, mRNA and other molecules whose level or modification status is altered in response to changes in functional

levels of Zmax1 or HBM. The pathology and pathogenesis of bone disorders is known and described, for example, in Rubin and Farber (Eds.), Pathology, 2nd Ed., S.B. Lippincott Co., Philadelphia, PA (1994).

A variety of techniques can be used to alter the levels of functional Zmax1 or HBM. For example, intravenous or intraosseous injection of the extracellular portion of Zmax1 or mutations thereof, or HBM or mutations thereof, will alter the level of Zmax1 activity or HBM activity, respectively, in the body of the treated human, animal or bird. Truncated versions of the Zmax1 protein or HBM protein can also be injected to alter the levels of functional Zmax1 protein or HBM protein, respectively. Certain forms of Zmax1 or HBM enhance the activity of endogenous protein, while other forms are inhibitory.

In a preferred embodiment, the HBM protein is used to treat osteoporosis, fracture, or other bone disorder. In a further preferred embodiment, the extracellular portion of HBM or fragment thereof (e.g., the Dkk binding domain) protein is used. This HBM protein may be optionally modified by the addition of a moiety that causes the protein to adhere to the surface of cells. The protein is prepared in a pharmaceutically acceptable solution and is administered by injection or another method that achieves acceptable pharmacokinetics and distribution.

In a second embodiment of this method, Zmax1, HBM, HBM variant, and/or LRP6 levels are increased or decreased by gene therapy techniques. To increase Zmax1 or HBM levels, osteoblasts or another useful cell type are genetically engineered to express high levels of Zmax1 or HBM as described above. Alternatively, to decrease Zmax1 or HBM levels, antisense constructs that specifically reduce the level of translatable Zmax1 or HBM mRNA can be used. In general, a tissue-nonspecific promoter may be used, such as the CMV promoter or another commercially available promoter found in expression vectors (Wu *et al.*, 1996 *Toxicol. Appl. Pharmacol.* 141: 330-9). In a preferred embodiment, a Zmax1 cDNA or its antisense is transcribed by a bone-specific promoter, such as the osteocalcin or another promoter, to achieve specific expression in bone tissue. In this way, if a Zmax1-expressing DNA construct or HBM-expressing construct is introduced into non-bone tissue, it will not be expressed.

In a third embodiment of this method, antibodies against Zmax1, LRP6, HBM-like or HBM are used to modulate its function. Such antibodies are identified herein.

In a fourth embodiment of this method, drugs that are agonists or antagonists of Zmax1 function or HBM function are used. Such drugs are described herein and optimized according to techniques of medicinal chemistry well known to one skilled in the art of pharmaceutical development.

Zmax1 and HBM interact with several proteins, such as ApoE. Molecules that inhibit the interaction between Zmax1 or HBM and ApoE or another binding partner are expected to alter bone development and mineralization. Such inhibitors may be useful as drugs in the treatment of osteoporosis, osteopetrosis, or other diseases of bone mineralization. Such inhibitors may be low molecular weight compounds, proteins or other types of molecules. *See*, Kim *et al.*, 1998 *J. Biochem.* (Tokyo) 124: 1072-1076.

Inhibitors of the interaction between Zmax1 or HBM and interacting proteins may be isolated by standard drug-screening techniques. For example, Zmax1 protein, (or a fragment thereof) or HBM protein (or a fragment thereof) can be immobilized on a solid support such as the base of microtiter well. A second protein or protein fragment, such as ApoE is derivatized to aid in detection, for example with fluorescein. Iodine, or biotin, then added to the Zmax1 or HBM in the presence of candidate compounds that may specifically inhibit this protein-protein domain of Zmax1 or HBM, respectively, and thus avoid problems associated with its transmembrane segment. Drug screens of this type are well known to one skilled in the art of pharmaceutical development.

Because Zmax1 and HBM are involved in bone development, proteins that bind to Zmax1 and HBM are also expected to be involved in bone development. Such binding proteins can be identified by standard methods, such as co-immunoprecipitation, co-fractionation, or the two-hybrid screen (Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons (1997)). For example, to identify Zmax1-interacting proteins or HBM-interacting proteins using the two-hybrid system, the extracellular domain of Zmax1 or HBM is fused to LexA and expressed for the yeast vector pEG202 (the "bait") and expressed in the yeast strain EGY48. The yeast strain is transformed with a "prey" library in the

appropriate vector, which encodes a galactose-inducible transcription-activation sequence fused to candidate interacting proteins. The techniques for initially selecting and subsequently verifying interacting proteins by this method are well known to one skilled in the art of molecular biology (Ausubel *et al.*, 1997).

In a preferred embodiment, proteins that interact with HBM, but not Zmax1, are identified using a variation of the above procedure (Xu *et al.*, 1997 *Proc. Natl. Acad. Sci. USA,* 94: 12473-8). This variation of the two-hybrid system uses two baits, and Zmax1 and HBM are each fused to LexA and TetR, respectively. Alternatively, proteins that interact with the HBM but not Zmax1 are also isolated. These procedures are well known to one skilled in the art of molecular biology, and are a simple variation of standard two-hybrid procedures.

As an alternative method of isolating substances interacting with Zmax1 or HBM, a biochemical approach is used. The Zmax1 protein or a fragment thereof, such as the extracellular domain, or the HBM protein or a fragment thereof, such as the extracellular domain, is chemically coupled to Sepharose beads. The Zmax1- or HBM-coupled beads are poured into a column. A biological extract, such as a lipid fraction, serum proteins, proteins in the supernatant of a bone biopsy, or cellular contents from gently lysed osteoblast cells, is added to the column. Non-specifically bound compounds are eluted, the column is washed several times with a low-salt buffer, and then tightly binding compounds may be eluted with a high-salt buffer. These are candidate compounds that bind to Zmax1 or HBM, and can be tested for specific binding by standard tests and control experiments. Sepharose beads used for coupling proteins and the methods for performing the coupling are commercially available (Sigma), and the procedures described here are well known to one skilled in the art of protein biochemistry.

As a variation of the above procedure, proteins that are eluted by high salt from the Zmax1- or HBM-sepharose column are then added to an HBM-Zmax1-sepharose column. Proteins that flow through without sticking are proteins that bind to Zmax1 but not to HBM. Alternatively, proteins that bind to the HBM protein and not to the Zmax1 protein can be isolated by reversing the order in which the columns are used.

Isolated compounds may be identified by standard methods such as 2D gel electrophoresis, chromatography, and mass spectroscopy.

24. Method of Use: Transformation-Associated Recombination (TAR) Cloning

Essential for the identification of novel allelic variants of Zmax1 (LRP5) and LRP6 is the ability to examine the sequence of both copies of the gene in an individual. To accomplish this, two "hooks," or regions of significant similarity, are identified within the genomic sequence such that they flank the portion of DNA that is to be cloned. Most preferably, the first of these hooks is derived from sequences 5' to the first exon of interest and the second is derived from sequences 3' to the last exon of interest. These two "hooks" are cloned into a bacterial/yeast shuttle vector such as that described by Larionov *et al.*, 1997 *Proc. Natl. Acad. Sci. USA*, 94: 7384-7. Other similar vector systems may also be used. To recover the entire genomic copy of the *Zmax1* gene, the plasmid containing the two "hooks" is linearized with a restriction endonuclease or is produced by another method such as PCR. This linear DNA fragment is introduced into yeast cells along with human genomic DNA. Typically, the yeast *Saccharomyces cerevisiae* is used as a host cell, although Kourina *et al.*, 1998 *Genome Res.* 8: 666-72 have reported using chicken host cells as well. During and after the process of transformation, the endogenous host cell converts the linear plasmid to a circle by a recombination event whereby the region of the human genomic DNA homologous to the "hooks" is inserted into the plasmid. This plasmid can be recovered and analyzed by methods well known to one skilled in the art. Obviously, the specificity for this reaction requires the host cell machinery to recognize sequences similar to the "hooks" present in the linear fragment. However, 100% sequence identity is not required, as shown by Kouprina *et al.*, 1998 *Genomics* 53: 21-8, where the author describes using degenerate repeated sequences common in the human genome to recover fragments of human DNA from a rodent/human hybrid cell line.

In another example, only one "hook" is required, as described by Larionov *et al.*, 1998 *Proc. Natl. Acad. Sci. USA*, 95: 4469-74. For this type of experiment, termed "radial TAR cloning," the other region of sequence similarity to drive the recombination is derived from a

repeated sequence from the genome. In this way, regions of DNA adjacent to the *Zmax1* gene coding region can be recovered and examined for alterations that may affect function.

25. Methods of Use: Genomic Screening

The use of polymorphic genetic markers linked to the *HBM* gene, or to Zmax1 (LRP5) or to LRP6 is very useful in predicting susceptibility to osteoporosis or other bone diseases. Koller *et al.*, 1998 *Amer. J. Bone Min. Res.* 13: 1903-8 have demonstrated that the use of polymorphic genetic markers is useful for linkage analysis. Similarly, the identification of polymorphic genetic markers within the high bone mass gene will allow the identification of specific allelic variants that are in linkage disequilibrium with other genetic lesions that affect bone development. Using the DNA sequence from the BACs, a dinucleotide CAn repeat was identified and two unique PCR primers that will amplify the genomic DNA containing this repeat were designed, as shown below:

B200E21C16_L: GAGAGGCTATATCCCTGGGC (SEQ ID NO: 38)
B200E21C16_R: ACAGCACGTGTTTAAAGGGG (SEQ ID NO: 39)

and used in the genetic mapping study.

This method has been used successfully by others skilled in the art (e.g., Sheffield *et al.*, 1995 *Genet.*, 4:1837-44; LeBlanc-Straceski *et al.*, 1994 *Genomics*, 19: 341-9; Chen *et al.*, 1995 *Genomics*, 25:1-8). Use of these reagents with populations or individuals will predict their risk for osteoporosis. Similarly, single nucleotide polymorphisms (SNPs), such as those shown in Table 4 above, can be used as well to predict risk for developing bone diseases or resistance to osteoporosis in the case of the *HBM* gene.

26. Methods of Use: Modulators of Tissue Calcification

The calcification of tissues in the human body is well documented. Towler *et al.* (1998 *J. Biol. Chem.* 273: 30427-34) demonstrated that several proteins known to regulate calcification of the developing skull in a model system are expressed in calcified aorta. The expression of Msx2, a gene transcribed in osteoprogenitor cells, in calcified vascular tissue indicates that genes which are important in bone development are involved in calcification of

other tissues.

Treatment with HBM protein, HBM-like proteins and polypeptides, agonists of LRP5 and LRP6 and HBM or antagonists of Dkk-1 are likely to ameliorate calcification (such as the vasculature, dentin and bone of the skull viscera) due to its demonstrated effect on bone mineral density. In experimental systems where tissue calcification is demonstrated, the over-expression or repression of Zmax1(LRP5) activity permits the identification of molecules that are directly regulated by the *Zmax1* gene. These genes are potential targets for therapeutics aimed at modulating tissue calcification. For example, an animal, such as the LDLR -/-, mouse is fed a high fat diet and is observed to demonstrate expression of markers of tissue calcification, including Zmax1. These animals are then treated with antibodies to Zmax1 or HBM protein, antisense oligonucleotides directed against Zmax1 or HBM cDNA, or with compounds known to bind the Zmax1 or HBM protein or its binding partner or ligand. RNA or proteins are extracted from the vascular tissue and the relative expression levels of the genes expressed in the tissue are determined by methods well known in the art. Genes that are regulated in the tissue are potential therapeutic targets for pharmaceutical development as modulators of tissue calcification.

The nucleic acids, proteins, peptides, amino acids, small molecules or other pharmaceutically useful compounds of the present invention that are to be given to an individual may be administered in the form of a composition with a pharmaceutically acceptable carrier, excipient or diluent, which are well known in the art. The individual may be a mammal or a bird, preferably a human, a rat, a mouse or bird. Such compositions may be administered to an individual in a pharmaceutically effective amount. The amount administered will vary depending on the condition being treated and the patient being treated. The compositions may be administered alone or in combination with other treatments.

27. <u>Methods to Identify Agents that Modulate the Expression of a Nucleic Acid Encoding the Dkk and/or LRP5 Proteins and/or Dkk interacting proteins</u>

Another embodiment of the present invention provides methods for identifying agents that modulate the expression of a nucleic acid encoding Dkk, which is part of the Wnt

pathway and that interacts with LRP5, LRP6 and to much lesser extent to HBM and its variants. Such assays may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of Dkk, if it is capable of up- or down-regulating expression of the nucleic acid in a cell (*e.g.*, mRNA).

In one assay format, cell lines that contain reporter gene fusions between the nucleic acid encoding Dkk (or proteins which modulate the activity of Dkk) and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available, including but not limited to the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, 1990 *Anal. Biochem.* 188: 245-54). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of a nucleic acid encoding Dkk or other protein which modulates Dkk activity. Such assays can similarly be used to determine whether LRP5 and even LRP6 activity is modulated by regulating Dkk activity. This can also be performed with the HBM variants.

Additional assay formats may be used to monitor the ability of the agent(s) to modulate the expression of a nucleic acid encoding Dkk, alone or Dkk and LRP5, and/or Dkk interacting proteins such as those identified in Figure 31. For instance, mRNA expression may be monitored directly by hybridization to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (1989); Ausubel *et al.*, Current Protocols in Molecular Biology (Greene Publishing Co., NY, 1995); Maniatis *et al.*, Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1982); and Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology (Frederick M. Ausubel *et al.*, April 1999).

Probes to detect differences in RNA expression levels between cells exposed to the agent and control cells may be prepared from the nucleic acids of the invention. It is

preferable, but not necessary, to design probes which hybridize only with target nucleic acids under conditions of high stringency. Only highly complementary nucleic acid hybrids form under conditions of high stringency. Accordingly, the stringency of the assay conditions determines the amount of complementarity which should exist between two nucleic acid strands in order to form a hybrid. Stringency should be chosen to maximize the difference in stability between the probe:target hybrid and potential probe:non-target hybrids.

Probes may be designed from the nucleic acids of the invention through methods known in the art. For instance, the G+C content of the probe and the probe length can affect probe binding to its target sequence. Methods to optimize probe specificity are commonly available. See for example, Sambrook *et al.* (1989) or Ausubel *et al.* (Current Protocols in Molecular Biology, Greene Publishing Co., NY, 1995).

Hybridization conditions are modified using known methods, such as those described by Sambrook *et al.* (1989) and Ausubel *et al.* (1995), as suitable for each probe. Hybridization of total cellular RNA or RNA enriched for polyA RNA can be accomplished in any available format. For instance, total cellular RNA or RNA enriched for polyA RNA can be affixed to a solid support and the solid support exposed to at least one probe comprising at least one, or part of one of the nucleic acid sequences of the invention under conditions in which the probe will specifically hybridize. Alternatively, nucleic acid fragments comprising at least one, or part of one of the sequences of the invention can be affixed to a solid support, such as a porous glass wafer. The glass or silica wafer can then be exposed to total cellular RNA or polyA RNA from a sample under conditions in which the affixed sequences will specifically hybridize. Such glass wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). By examining for the ability of a given probe to specifically hybridize to an RNA sample from an untreated cell population and from a cell population exposed to the agent, agents which up- or down-regulate the expression of a nucleic acid encoding Dkk, a Dkk interacting protein, and/or LRP5 can be identified.

Microarray technology and transcriptional profiling are examples of methods which can be used to analyze the impact of putative Dkk or Dkk interacting protein modulating compounds. For transcriptional profiling, mRNA from cells exposed *in vivo* to a potential

Dkk modulating agent, such as the Dkk interacting proteins identified in the present invention (*e.g.*, those identified in Fig. 31), agents which modulate Dkk interacting proteins, and mRNA from the same type of cells that were not exposed to the agent could be reverse transcribed and hybridized to a chip containing DNA from numerous genes, to thereby compare the expression of genes in cells treated and not treated with the agent. If, for example a putative Dkk modulating agent down-regulates the expression of Dkk in the cells, then use of the agent may be undesirable in certain patient populations. For additional methods of transcriptional profiling and the use of microarrays, refer to, for example, U.S. Patent No. 6,124,120 issued to Lizardi (2000).

Additional methods for screening the impact of Dkk and Dkk interacting protein modulating compounds or the impact of Dkk or Dkk interacting proteins on modulation of LRP5, LRP6, HBM, HBM variants or the Wnt pathway include the use of TaqMan® PCR, conventional reverse transcriptase PCR (RT-PCR), changes in downstream surrogate markers (*i.e.*, Wnt responsive genes), and anti-Dkk Western blots for protein detection. Other methods would be readily apparent to the artisan of ordinary skill.

28. <u>Methods to Identify Agents that Modulate at Least One Activity of Dkk, a Dkk Interacting Protein, or LRP5/LRP6/HBM/HBM-like</u>

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of Dkk, Dkk interacting proteins, and/or LRP5/LRP6/HBM/HBM-like proteins or preferably which specifically modulate an activity of a Dkk/Dkk interacting protein complex or an LRP5 (or LRP6/HBM/HBM-like)/Dkk complex, or a biologically active fragment of Dkk (*e.g.*, comprising the domain which binds LRP5/LRP6/HBM/HBM-like) or a Dkk interacting protein complex. Such methods or assays may utilize any means of monitoring or detecting the desired activity as would be known in the art (*See, e.g.*, Wu *et al.*, 2000 *Curr. Biol.* 10:1611-4; Fedi *et al.*, 199 *J. Biol. Chem.* 274:19465-72; Grotewold *et al.*, 1999 *Mech. Dev.* 89:151-3; Shibata *et al.*, 2000 *Mech. Dev.* 96: 243-6 ; Wang *et al.*, 2000 *Oncogene* 19: 1843-8; and Glinka *et al.*, 1998 *Nature* 391: 357-62). Potential agents which modulate Dkk include, for example, p53, the

tumor suppressor protein, which can induce Dkk-1. Damage to DNA has also been observed to up-regulate Dkk-1 expression via a stabilization and activation of p53 (Wang *et al.*, 2000 *Oncogene* 19: 1843-48); and, Shou *et al.*, 2002 *Oncogene* 21: 878-89). Additionally, Fedi *et al.* (1999) purportedly showed that Dkk-1 can block the Wnt2-induced oncogenic transformation of NIH-3T3 cells. Furthermore, it has been suggested that Dkk expression may be modulated by BMP signaling in the developing skeleton (Mukhopadhyay *et al.*, 2001 *Dev. Cell.* 1: 423-34; and Grotewold *et al.*, 2002 *EMBO J.* 21: 966-75). Grotewald *et al.* additionally describe altered Dkk expression levels in response to stress signals including UV irradiation and other genotoxic stimuli. They propose that Dkk expression is pro-apoptotic. In the HBMMTIC animals described herein, a reduced osteoblast apoptosis effect was observed. Thus, HBM and HBM like variants may control/alter Dkk's role in programmed cell death. Other agents which potentially modulate Dkk activity include the Dkk interacting proteins identified in Fig. 31.

In one embodiment, the relative amounts of Dkk or a Dkk interacting protein of a cell population that has been exposed to the agent to be tested is compared to an un-exposed control cell population. Antibodies can be used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, as would be known in the art. *See, e.g.,* Ed Harlow and David Lane, Antibodies: A Laboratory Manual (Cold Spring Harbor, NY, 1988) and Ed Harlow and David Lane, Using Antibodies: A Laboratory Manual (Cold Spring Harbor, NY 1998).

For example, N- and C- terminal fragments of Dkk can be expressed in bacteria and used to search for proteins which bind to these fragments. Fusion proteins, such as His-tag or GST fusion to the N- or C-terminal regions of Dkk (or to biologically active domains of Dkk-1) or a whole Dkk protein can be prepared. These fusion proteins can be coupled to, for example, Talon or Glutathione-Sepharose beads and then probed with cell lysates to identify molecules which bind to Dkk. Prior to lysis, the cells may be treated with purified Wnt

proteins, RNA, or drugs which may modulate Wnt signaling or proteins that interact with downstream elements of the Wnt pathway. Lysate proteins binding to the fusion proteins can be resolved by SDS-PAGE, isolated and identified by, for example protein sequencing or mass spectroscopy, as is known in the art. *See, e.g.*, Protein Purification Applications: A Practical Approach (Simon Roe, ed., 2nd ed. Oxford Univ. Press, 2001) and "Guide to Protein Purification" in *Meth. Enzymology* vol. 182 (Academic Press, 1997).

The activity of Dkk, a Dkk interacting protein, or a complex of Dkk with LRP5/LRP6/HBM/HBM-like may be affected by compounds which modulate the interaction between Dkk and a Dkk interacting protein (such as those shown in Fig. 31) and/or Dkk and LRP5/LRP6/HBM/HBM-like. The present invention provides methods and research tools for the discovery and characterization of these compounds. The interaction between Dkk and a Dkk interacting protein and/or Dkk and LRP5/6/HBM/HBM-like may be monitored *in vivo* and *in vitro*. Compounds which modulate the stability of a Dkk - LRP5/LRP6/HBM/HBM-like complex are potential therapeutic compounds. Example *in vitro* methods include: Binding LRP5/6/HBM/HBM-like, Dkk, or a Dkk interacting protein to a sensor chip designed for an instrument such are made by Biacore (Uppsala, Sweden) for the performance of an plasmon resonance spectroscopy observation. In this method, the chip with one of Dkk, a Dkk interacting protein, or LRP5/6 is first exposed to the other under conditions which permit them to form the complex. A test compound is then introduced and the output signal of the instrument provides an indication of any effect exerted by the test compound. By this method, compounds may be rapidly screened. Another, in vitro, method is exemplified by the SAR-by-NMR methods (Shuker *et al.*, *Science*. 274:1531-4 (1996)). Briefly, a Dkk-1 binding domain and/or LRP 5 or 6 LBD are expressed and purified as ^{15}N labeled protein by expression in labeled media. The labeled protein(s) are allowed to form the complex in solution in an NMR sample tube. The heteronuclear correlation spectrum in the presence and absence of a test compound provides data at the level of individual residues with regard to interactions with the test compound and changes at the protein-protein interface of the complex. One of skill in the art knows of many other protocols, e.g. affinity capillary electrophoresis (Okun *et al.*, 2001 *J. Biol. Chem.* 276: 1057-62; Vergnon *et al.*, 1999

Methods, 19: 270-7), fluorescence spectroscopy, electron paramagnetic resonance, etc. which can monitor the modulation of a complex and/or measure binding affinities for complex formation.

In vitro protocols for monitoring the modulation of a Dkk/LRP5/LRP6/HBM/HBM-like complex include the yeast two hybrid protocol. The yeast two hybrid method may be used to monitor the modulation of a complex in vivo by monitoring the expression of genes activated by the formation of a complex of fusion proteins of Dkk and LRP ligand binding domains. Nucleic acids according to the invention which encode the interacting Dkk and LRP LBD domains are incorporated into bait and prey plasmids. The Y2H protocol is performed in the presence of one or more test compounds. The modulation of the complex is observed by a change in expression of the complex activated gene. It will be appreciated by one skilled in the art that test compounds can be added to the assay directly or, in the case of proteins, can be coexpressed in the yeast with the bait and prey compounds. Similarly, fusion proteins of Dkk and Dkk interacting proteins can also be used in a Y2H screen to identify other proteins which modulate the Dkk/Dkk interacting protein complex.

Assay protocols such as these may be used in methods to screen for compounds, drugs, treatments which modulate the Dkk/Dkk interacting protein and/or Dkk/LRP5/6 complex, whether such modulation occurs by competitive binding, or by altering the structure of either LRP 5/6 or Dkk at the binding site, or by stabilizing or destablizing the protein-protein interface. It may be anticipated that peptide aptamers may competitively bind, although induction of an altered binding site structure by steric effects is also possible.

28.1 <u>Antibodies and Antibody Fragments</u>

Polyclonal and monoclonal antibodies and fragments of these antibodies which bind to Dkk or LRP5/LRP6/HBM/HBM-like can be prepared as would be known in the art. For example, suitable host animals can be immunized using appropriate immunization protocols and the peptides, polypeptides or proteins of the invention. Peptides for use in immunization are typically about 8-40 residues long. If necessary or desired, the polypeptide immunogens can be conjugated to suitable carriers. Methods for preparing immunogenic conjugates with

carriers such as bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), or other carrier proteins are well known in the art (*See*, Harlow *et al.*, 1988). In some circumstances, direct conjugation using, for example, carbodiimide reagents, may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co., Rockford, IL, may be desirable to provide accessibility to the polypeptide or hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues, for example, to facilitate linking to a carrier. Administration of the immunogens is conducted generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation.

Anti-peptide antibodies can be generated using synthetic peptides, for example, the peptides derived from the sequence of any Dkk, including Dkk-1, or LRP5/LRP6/HBM/HBM-like. Synthetic peptides can be as small as 2-3 amino acids in length, but are preferably at least 3, 5, 10, or 15 or more amino acid residues long. Such peptides can be determined using programs such as DNAStar. The peptides are coupled to KLH using standard methods and can be immunized into animals such as rabbits. Polyclonal anti-Dkk or anti-LRP5/LRP6/HBM/HBM-like peptide antibodies can then be purified, for example using Actigel beads containing the covalently bound peptide.

While the polyclonal antisera produced in this way may be satisfactory for some applications, for pharmaceutical compositions, use of monoclonal preparations is preferred. Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using the standard method of Kohler and Milstein or modifications which effect immortalization of lymphocytes or spleen cells, as is generally known (See, e.g., Harlow *et al.*, 1988 and 1998). The immortalized cell lines secreting the desired antibodies can be screened by immunoassay in which the antigen is the peptide hapten, polypeptide or protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid.

The desired monoclonal antibodies are then recovered from the culture supernatant or from the ascites supernatant. Fragments of the monoclonal antibodies which contain the

immunologically significant portion can be used as agonists or antagonists of Dkk activity. Use of immunologically reactive fragments, such as the Fab, scFV, Fab', of $F(ab')_2$ fragments are often preferable, especially in a therapeutic context, as these fragments are generally less immunogenic than the whole immunoglobulin.

The antibodies or fragments may also be produced, using current technology, by recombinant means. Regions that bind specifically to the desired regions of Dkk or LRP5/LRP6/HBM/HBM-like can also be produced in the context of chimeras with multiple species origin. Antibody reagents so created are contemplated for use diagnostically or as stimulants or inhibitors of Dkk activity.

In one embodiment, antibodies against Dkk, bind Dkk with high affinity, i.e., ranging from 10^{-5} to 10^{-9} M. Preferably, the anti-Dkk antibody will comprise a chimeric, primate, Primatized®, human or humanized antibody. Also, the invention embraces the use of antibody fragments, *e.g.*, Fab's, Fv's, Fab's, $F(ab)_2$, and aggregates thereof.

Another embodiment contemplates chimeric antibodies which recognize Dkk or LRP5/LRP6/HBM/HBM-like. A chimeric antibody is intended to refer to an antibody with non-human variable regions and human constant regions, most typically rodent variable regions and human constant regions.

A "primatized® antibody" refers to an antibody with primate variable regions, *e.g.*, CDR's, and human constant regions. Preferably, such primate variable regions are derived from an Old World monkey.

A "humanized antibody" refers to an antibody with substantially human framework and constant regions, and non-human complementarity-determining regions (CDRs). "Substantially" refers to the fact that humanized antibodies typically retain at least several donor framework residues (*i.e.*, of non-human parent antibody from which CDRs are derived).

Methods for producing chimeric, primate, primatized®, humanized and human antibodies are well known in the art. See, *e.g.*, U.S. Patent 5,530,101, issued to Queen *et al.*; U.S. Patent 5,225,539, issued to Winter *et al.*; U.S. Patents 4,816,397 and 4,816,567, issued to Boss *et al.* and Cabilly *et al.* respectively, all of which are incorporated by reference in

their entirety.

The selection of human constant regions may be significant to the therapeutic efficacy of the subject anti-Dkk or LRP5/LRP6/HBM/HBM-like antibody. In a preferred embodiment, the subject anti-Dkk or LRP5/LRP6/HBM/HBM-like antibody will comprise human, gamma 1, or gamma 3 constant regions and, more preferably, human gamma 1 constant regions.

Methods for making human antibodies are also known and include, by way of example, production in SCID mice, and *in vitro* immunization.

The subject anti-Dkk or LRP5/LRP6/HBM/HBM-like antibodies can be administered by various routes of administration, typically parenteral. This is intended to include intravenous, intramuscular, subcutaneous, rectal, vaginal, and administration with intravenous infusion being preferred.

The anti-Dkk or LRP5/LRP6/HBM/HBM-like antibody will be formulated for therapeutic usage by standard methods, *e.g.*, by addition of pharmaceutically acceptable buffers, *e.g.*, sterile saline, sterile buffered water, propylene glycol, and combinations thereof.

Effective dosages will depend on the specific antibody, condition of the patient, age, weight, or any other treatments, among other factors. Typically effective dosages will range from about 0.001 to about 30 mg/kg body weight, more preferably from about 0.01 to 25 mg/kg body weight, and most preferably from about 0.1 to about 20 mg/kg body weight.

Such administration may be effected by various protocols, *e.g.*, weekly, bi-weekly, or monthly, depending on the dosage administered and patient response. Also, it may be desirable to combine such administration with other treatments.

Antibodies to Dkk-1 interacting proteins, such as those identified in Fig. 31, are also contemplated according to the present invention, and can be used similarly to the Dkk-1 antibodies mentioned in the above methodology.

The antibodies of the present invention can be utilized in experimental screening, as diagnostic reagents, and in therapeutic compositions.

28.2 Chemical Libraries

Agents that are assayed by these methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of Dkk-1 alone, Dkk-1 interacting proteins alone, or with their associated substrates, binding partners, etc. An example of randomly selected agents is the use of a chemical library or a peptide combinatorial library, or a growth broth of an organism.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

28.3 Peptide Synthesis

The peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production of polypeptides using solid phase peptide synthesis is necessitated if non-nucleic acid-encoded amino acids are to be included.

29. Uses for Agents that Modulate at Least One Activity of Dkk, a Dkk Interacting Protein, a Dkk/Dkk Interacting Protein Complex, or a Dkk/LRP5 or Dkk/LRP6 Complex

The proteins and nucleic acids of the invention, such as the proteins or polypeptides containing an amino acid sequence of LRP5, Dkk, and Dkk interacting proteins are involved in bone mass modulation and lipid modulation of other Wnt pathway mediated activity. Agents that modulate (*i.e.*, up and down-regulate) the expression of Dkk or Dkk interacting proteins, or agents, such as agonists and antagonists respectively, of at least one activity of Dkk or a Dkk interacting protein may be used to modulate biological and pathologic processes associated with the function and activity of Dkk or a Dkk interacting protein.

As used herein, a subject can be preferably any mammal, so long as the mammal is in

need of modulation of a pathological or biological process modulated by a protein of the invention. The term "mammal" means an individual belonging to the class *Mammalia*. The invention is particularly useful in the treatment of human subjects.

As used herein, a biological or pathological process modulated by Dkk or a Dkk interacting protein may include binding of Dkk to a Dkk interacting protein, Dkk to LRP5 or LRP6 or release therefrom, inhibiting or activating Dkk or a Dkk interacting protein mRNA synthesis or inhibiting Dkk or Dkk interacting protein modulated inhibition of LRP5 or LRP6 mediated Wnt signaling. Further bone-related markers may be observed such as alkaline phosphatase activity, osteocalcin production, or mineralization.

Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression or up-regulation of expression of LRP5 or LRP6 and/or Dkk and/or a Dkk interacting protein may be associated with certain diseases or pathological conditions. As used herein, an agent is said to modulate a pathological process when the agent statistically significantly ($p < 0.05$) alters the process from its base level in the subject. For example, the agent may reduce the degree or severity of the process mediated by that protein in the subject to which the agent was administered. For instance, a disease or pathological condition may be prevented, or disease progression modulated by the administration of agents which reduce or modulate in some way the expression or at least one activity of a protein of the invention.

As LRP5/6 and Dkk are involved both directly and indirectly in bone mass modulation, one embodiment of this invention is to use Dkk or Dkk interacting protein expression as a method of diagnosing a bone condition or disease. Certain markers are associated with specific Wnt signaling conditions (*e.g., TCF/LEF* activation). Diagnostic tests for bone conditions may include the steps of testing a sample or an extract thereof for the presence of Dkk or Dkk interacting protein nucleic acids (*i.e.*, DNA or RNA), oligomers or fragments thereof or protein products of TCF/LEF regulated expression. For example, standard *in situ* hybridization or other imaging techniques can be utilized to observe products of Wnt signaling. Other diagnostic techniques, as described herein, would also be useful as would be apparent to the skilled artisan (e.g., a serum marker).

This invention also relates to methods of modulating bone development or bone loss conditions. Inhibition of bone loss may be achieved by inhibiting or modulating changes in the LRP5/6 mediated Wnt signaling pathway. For example, absence of LRP5 activity may be associated with low bone mass. Increased activity LRP5 may be associated with high bone mass. Therefore, modulation of LRP5 activity will in turn modulate bone development. Modulation of the Dkk/LRP5/6 or Dkk/Dkk interacting protein complex via agonists and antagonists is one embodiment of a method to regulate bone development. Such modulation of bone development can result from inhibition of the activity of, for example, a Dkk/LRP(5/6) protein complex, a Dkk/Dkk interacting protein complex, upregulated transcription of the *LRP5* gene or inhibited transcription or translation of Dkk or Dkk interacting protein mRNA.

The agents of the present invention can be provided alone, or in combination with other agents that modulate a particular pathological process. As used herein, two agents are said to be administered in combination when the two agents are administered simultaneously or are administered independently in a fashion such that the agents will act at the same time.

The agents of the present invention can be administered via parenteral, subcutaneous (sc), intravenous (iv), intramuscular (im), intraperitoneal (ip), transdermal or buccal routes. Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

The present invention further provides compositions containing one or more agents which modulate expression or at least one activity of a protein of the invention. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages of the active agent which mediate Dkk or Dkk interacting protein activity comprise from about 0.0001 to about 50 mg/kg body weight. The preferred dosages comprise from about 0.001 to about 50 mg/kg body weight. The most preferred dosages comprise from about 0.1 to about 1 mg/kg body weight. In an average human of 70 kg, the range would be from about 7 μg to about 3.5 g, with a preferred range of about 0.5 mg to about 5 mg.

In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, (*e.g.*, ethyl oleate or triglycerides). Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol and/or dextran. Optionally, the suspension may also contain stabilizers. Liposomes and other non-viral vectors can also be used to encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral, or topical (top) administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic administration of the active ingredient.

Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

Potentially, any compound which binds Dkk or a Dkk interacting protein or modulates the Dkk/LRP5 or Dkk/LRP6 or Dkk/Dkk interacting protein complex may be a therapeutic compound. In one embodiment of the invention, a peptide or nucleic acid aptamer according to the invention is used in a therapeutic composition. Such compositions may comprise an aptamer, or a LRP5 or LRP6 fragment unmodified or modified. In another embodiment, the therapeutic compound comprises a Dkk-1 interacting protein, or biologically active fragment thereof.

Nucleic acid aptamers have been used in compositions for example by chemical bonding to a carrier molecule such as polyethylene glycol (PEG) which may facilitate uptake

or stabilize the aptamer. A di-alkylgylcerol moiety attached to an RNA will embed the aptamer in liposomes, thus stabilizing the compound. Incorporating chemical substitutions (i.e. changing the 2'OH group of ribose to a 2'NH in RNA confers ribonuclease resistance) and capping, etc. can prevent breakdown. Several such techniques are discussed for RNA aptamers in Brody and Gold *(Rev. Mol. Biol.* 74:3-13, 2000).

Peptide aptamers may by used in therapeutic applications by the introduction of an expression vector directing aptamer expression into the affected tissue such as for example by retroviral delivery, by encapsulating the DNA in a delivery complex or simple by naked DNA injection. Or, the aptamer itself or a synthetic analog may be used directly as a drug. Encapsulation in polymers and lipids may assist in delivery. The use of peptide aptamers as therapeutic and diagnostic agents is reviewed by Hoppe-Syler and Butz *(J. Mol. Med.* 78:426-430 (2000)).

In another aspect of the invention. The structure of a constrained peptide aptamer of the invention may be determined such as by NMR or X-ray crystallography. (Cavanagh *et al.*, Protein NMR Spectroscopy: Principles and Practice, Academic Press, 1996; Drenth, Principles of Protein X-Ray Crystallography, Springer Verlag, 1999) Preferably the structure is determined in complex with the target protein. A small molecule analog is then designed according to the positions of functional elements of the 3D structure of the aptamer. (Guidebook on Molecular Modeling in Drug Design, Cohen, Ed., Academic Press, 1996; Molecular Modeling and Drug Design (Topics in Molecular and Structural Biology), Vinter and Gardner Eds., CRC Press, 1994) Thus the present invention provides a method for the design of effective and specific drugs which modulate the activity of Dkk, Dkk interacting proteins, Dkk/Dkk interacting protein complex and the Dkk/LRP complex. Small molecule mimetics of the peptide aptamers of the present invention are encompassed within the scope of the invention.

In practicing the methods of this invention, the compounds of this invention may be used alone or in combination, or in combination with other therapeutic or diagnostic agents. In certain preferred embodiments, the compounds of this invention may be co-administered along with other compounds typically prescribed for these conditions according to generally

accepted medical practice. For example, the compounds of this invention can be administered in combination with other therapeutic agents for the treatment of bone loss. Bone loss mediating agents include bone resorption inhibitors such as bisphosphonates (*e.g.*, alendronic acid, clodronic acid, etidronic acid, pamidronic acid, risedronic acid and tiludronic acid), vitamin D and vitamin D analogs, cathepsin K inhibitors, hormonal agents (*e.g.*, calcitonin and estrogen), and selective estrogen receptor modulators or SERMs (e.g., raloxifene). And bone forming agents such as parathyroid hormone (PTH) and bone morphogenetic proteins (BMP).

Additionally contemplated are combinations of agents which regulate Dkk-1 and agents which regulate lipid levels such as HMG-CoA reductase inhibitors (*i.e.*, statins such as Mevacor®, Lipitor® and other inhibitors such as Baycol®, Lescol®, Pravachol® and Zocor®), bile acid sequestrants (e.g., Colestid® and Welchol®), fibric acid derivatives (Atromid-S®, Lopid®, Tricor®), and nicotinic acid.

The compounds of this invention can be utilized *in vivo*, ordinarily in vertebrates and preferably in mammals, such as humans, sheep, horses, cattle, pigs, dogs, cats, rats and mice, or *in vitro*.

30. Peptide and Nucleotide Aptamers and Peptide Aptamer Mimetics

Another embodiment contemplates the use of peptide and nucleotide aptamer technology to screen for agents which interact with Dkk, which block Dkk from interacting with LRP5, LRP6, HBM, or HBM-like molecules, or which block any other Dkk ligand interaction, or which interact with Dkk interacting proteins, such as those shown in Figure 5. Peptide aptamers are molecules in which a variable peptide domain is displayed from a scaffold protein. Thioredoxin A (trxA) is commonly used for a scaffold. The peptide insert destroys the catalytic site of trxA. It is recognized that numerous proteins may also be used as scaffolding proteins to constrain and/or present a peptide aptamer. Other scaffold proteins that could display a constrained peptide aptamer could include staphylococcal nuclease, the protease inhibitor eglin C, the *Streptomyces tendea* alpha-amylase inhibitor Tendamistat, Sp1, green fluorescent protein (GFP) (reviewed in Hoppe-Seyler *et al.*, 2001 *J. Steroid*

Biochem Mol. Biol. 78: 105-11), and the S1 nucleas from *Staphyloccus* or M13 for phage display.. Any molecule to which the aptamer could be anchored and presented in its bioactive conformation would be suitable.

Aptamers can then specifically bind to a given target protein *in vitro* and *in vivo* and have the potential to selectively block the function of their target protein. Peptide aptamers are selected from randomized expression libraries on the basis of their *in vivo* binding capacity to the desired target protein. Briefly, a target protein (e.g., Dkk, a Dkk interacting protein, or LRP5/6) is linked to a heterologous DNA binding domain (BD) and expressed as bait in a yeast test strain. Concomitantly, a library coding for different peptides (e.g., 16-mers) of randomized sequence inserted in a scaffold protein sequence, which are linked to a heterologous transcriptional activation domain (AD) is expressed as prey. If a peptide binds to a target protein, a functional transcription factor is reconstituted, in which the BD and AD are bridged together by interacting proteins. This transcription factor is then able to activate the promoter of a marker gene which can be monitored by colorimetric enzymatic assays or by growth selection. Additional variation, methods of preparing and screening methodologies are described in, for example, Hoppe-Seyler *et al.*, 2000 *J. Mol. Med.* 78: 426-430.

Nucleotide aptamers are described for example in Brody *et al.,* 2000 *Trends Mol. Biotechnol.* 74: 5-13. Additional methods of making and using nucleotide aptamers include SELEX, *i.e.*, Systematic Evolution of Ligands by Exponential Enrichment. SELEX is a process of isolating oligonucleotide ligands of a chosen target molecule (see Tuerk and Gold, *Science* 249:505-510 (1990); U.S. Pat. Nos. 5,475,096, 5,595,877, and 5,660,985). SELEX, as described in Tuerk and Gold, involves admixing the target molecule with a pool of oligonucleotides (*e.g.*, RNA) of diverse sequences; retaining complexes formed between the target and oligonucleotides; recovering the oligonucleotides bound to the target; reverse-transcribing the RNA into DNA; amplifying the DNA with polymerase chain reactions (PCR); transcribing the amplified DNA into RNA; and repeating the cycle with ever increasing binding stringency. Three enzymatic reactions are required for each cycle. It usually takes 12-15 cycles to isolate aptamers of high affinity and specificity to the target.

An aptamer is an oligonucleotide that is capable of binding to an intended target substance but not other molecules under the same conditions.

In another reference, Bock *et al.*, 1990 *Nature* 355: 564-6, describe a different process from the SELEX method of Tuerk and Gold in that only one enzymatic reaction is required for each cycle (*i.e.*, PCR) because the nucleic acid library in Bock's method is comprised of DNA instead of RNA. The identification and isolation of aptamers of high specificity and affinity with the method of Bock *et al.* still requires repeated cycles in a chromatographic column.

Other nucleotide aptamer methods include those described by Conrad *et al.,* 1996 *Meth. Enzymol.* 267: 336-367. Conrad *et al.* describe a variety of methods for isolating aptamers, all of which employ repeated cycles to enrich target-bound ligands and require a large amount of purified target molecules. More recently described methods of making and using nucleotide aptamers include, but are not limited to those described in U.S. Patent Nos. 6,180,348; 6,051,388; 5,840,867; 5,780,610, 5,756,291 and 5,582,981.

Potentially, any compound which binds Dkk or a Dkk interacting protein or modulates the Dkk/Dkk interacting protein or Dkk/LRP5, Dkk/LRP6, Dkk/HBM, or Dkk/HBM-like complex may be a therapeutic compound. In one embodiment of the invention, a peptide or nucleic acid aptamer according to the invention is used in a therapeutic composition. Such compositions may comprise an aptamer, or a LRP5 or LRP6 fragment unmodified or modified.

Nucleic acid aptamers have been used in compositions for example by chemical bonding to a carrier molecule such as polyethylene glycol (PEG) which may facilitate uptake or stabilize the aptamer. A di-alkylglycerol moiety attached to an RNA will embed the aptamer in liposomes, thus stabilizing the compound. Incorporating chemical substitutions (*i.e.*, changing the 2'-OH group of ribose to a 2'-NH in RNA confers ribonuclease resistance) and capping, etc. can prevent breakdown. Several such techniques are discussed for RNA aptamers in Brody *et al.*, 2000 *Rev. Mol. Biol.* 74: 3-13.

Peptide aptamers may by used in therapeutic applications by the introduction of an expression vector directing aptamer expression into the affected tissue such as for example by

retroviral delivery, by encapsulating the DNA in a delivery complex or simple by naked DNA injection. Or, the aptamer itself or a synthetic analog may be used directly as a drug. Encapsulation in polymers and lipids may assist in delivery. The use of peptide aptamers as therapeutic and diagnostic agents is reviewed by Hoppe-Syler *et al.,* 2000 *J. Mol. Med.* 78: 426-430.

In another aspect of the invention, the structure of a constrained peptide aptamer of the invention may be determined such as by NMR or X-ray crystallography. (Cavanagh et al., Protein NMR Spectroscopy : Principles and Practice, Academic Press, 1996; Drenth, Principles of Protein X-Ray Crystallography, Springer Verlag, 1999) Preferably the structure is determined in complex with the target protein. A small molecule analog is then designed according to the positions of functional elements of the 3D structure of the aptamer. (Guidebook on Molecular Modeling in Drug Design, Cohen, Ed., Academic Press, 1996; Molecular Modeling and Drug Design (Topics in Molecular and Structural Biology), Vinter and Gardner Eds., CRC Press, 1994) Thus, a method is provided for the design of effective and specific drugs which modulate the activity of Dkk, Dkk interacting proteins, Dkk/Dkk interacting protein complex, and the Dkk/LRP complex. Small molecule mimics of the peptide aptamers of the present invention are also encompassed within the scope of the invention.

EXAMPLES

The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

Example 1

The propositus was referred by her physicians to the Creighton Osteoporosis Center for evaluation of what appeared to be unusually dense bones. She was 18 years old and came to medical attention two years previous because of back pain, which was precipitated by an

auto accident in which the car in which she was riding as a passenger was struck from behind. Her only injury was soft tissue injury to her lower back that was manifested by pain and muscle tenderness. There was no evidence of fracture or subluxation on radiographs. The pain lasted for two years, although she was able to attend school full time. By the time she was seen in the Center, the pain was nearly resolved and she was back to her usual activities as a high school student. Physical exam revealed a normal healthy young woman standing 66 inches and weighing 128 pounds. Radiographs of the entire skeleton revealed dense looking bones with thick cortices. All bones of the skeleton were involved. Most importantly, the shapes of all the bones were entirely normal. The spinal BMC was 94.48 grams in L1-4, and the spinal BMD was 1.667 gm/cm^2 in L1-4. BMD was 5.62 standard deviations (SD) above peak skeletal mass for women. These were measured by DXA using a Hologic 2000~. Her mother was then scanned and a lumbar spinal BMC of 58.05 grams and BMD of 1.500 gm/cm^2 were found. Her mother's values place her 4.12 SD above peak mass and 4.98 SD above her peers. Her mother was 51 years old, stood 65 inches and weighed 140 pounds. Her mother was in excellent health with no history of musculoskeletal or other symptoms. Her father's lumbar BMC was 75.33 grams and his BMD was 1.118 gm/cm^2. These values place him 0.25 SD above peak bone mass for males. He was in good health, stood 72 inches tall, and weighed 187 pounds.

These clinical data suggested that the propositus inherited a trait from her mother, which resulted in very high bone mass, but an otherwise normal skeleton, and attention was focused on the maternal kindred. In U.S. Patent No. 5,691,153, twenty- two of these members had measurement of bone mass by DXA. In one case, the maternal grandfather of the propositus, was deceased, however, medical records, antemortem skeletal radiographs and a gall bladder specimen embedded in paraffin for DNA genotyping were obtained. His radiographs showed obvious extreme density of all of the bones available for examination including the femur and the spine, and he was included among the affected members. In this invention, the pedigree has been expanded to include 37 informative individuals. These additions are a significant improvement over the original kinship (Johnson *et al.*, *Am. J. Hum. Genet.*, 60:1326-1332 (1997)) because, among the fourteen individuals added since the

original study, two individuals harbor key crossovers. X-linkage is ruled out by the presence of male-to-male transmission from individual 12 to 14 and 15.

Example 2

The present invention describes DNA sequences derived from two BAC clones from the *HBM* gene region, as evident in Table 7 below, which is an assembly of these clones. Clone b200e21-h (ATCC No. 980812; SEQ ID NOS: 10-11) was deposited at the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209 U.S.A., on December 30, 1997. Clone b527d12-h (ATCC No. 980720; SEQ ID NOS: 5-9) was deposited at the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209 U.S.A., on October 2, 1998. These sequences are unique reagents that can be used by one skilled in the art to identify DNA probes for the *Zmax1* gene, PCR primers to amplify the gene, nucleotide polymorphisms in the *Zmax1* gene, or regulatory elements of the *Zmax1* gene.

Example 3

Yeast-2 Hybrid screen for peptide aptamer sequences to Dkk-1

Peptide aptamer library construction. A peptide aptamer library, Tpep, was constructed, which provides a means to identify chimeric proteins that bind to a protein target (or bait) of interest using classic yeast two hybrid (Y2H) assays. The Tpep library is a combinatorial aptamer library composed of constrained random peptides, expressed within the context of the disulfide loop of *E. coli* thioredoxin (trxA), and as C-termini fusion to the *S. cerevisiae* Gal4 activation domain. The Tpep library was generated using a restriction enzyme modified recombinant Y2H prey vector, pPC86 (Gibco), which contains the trxA scaffold protein.

Generation of aptamer-encoding sequences. Aptamer-encoding sequences were produced as follows. DNA encoding random stretches of approximately sixteen amino acids surrounded by appropriate restriction sites were generated by semi-random oligonucleotide

synthesis. The synthetic oligonucleotides were PCR-amplified, restriction digested, and cloned into the permissive sites within the trxA scaffold protein. The cloning strategy was to insert the random oligonucleotide sequence is in-frame with the scaffold protein coding sequence, resulting in expression of a scaffold protein-aptamer chimera. The scaffold protein is itself in-frame with the activation domain of Gal4, within the pPC86 vector that is appropriate for the aptamer to be expressed and functional in a regular Y2H assay. Additional methods of preparing aptamers would be apparent to the skilled artisan.

Generation of a permissive recombinant pPC86 vector containing the trxA coding sequence. First the *Rsr*II restriction site located within the Gal4 activation domain of pPC86 (Gibco) was eliminated by site-directed mutagenesis (Quickchange™ kit, Stratagene). The amino acid sequence of the Gal4 activation domain was unchanged by this modification. The strength of different control interactions was verified to be unchanged by the modification.

Second, the *E. coli* trxA coding sequence was cloned into the *Sal*I and *Not*I sites of the *Rsr*II-modified pPC86. *Eco*RI and *Spe*I sites were then introduced within the trxA *Rsr*II site. The oligonucleotides encoding the peptide aptamers were cloned into the *Eco*RI and *Spe*I sites of the resulting vector.

TABLE 13

Contig	ATCC No.	SEQ ID NO.	Length (base pairs)
b527d12-h_contig302G	980720	5	3096
b527d12-h_contig306G	980720	6	26928
b527d12-h_contig307G	980720	7	29430
b527d12-h_contig308G	980720	8	33769
b527d12-h_contig309G	980720	9	72049
b200e21-h_contig1	980812	10	8705
b200e21-h_contig4	980812	11	66933

Example 4

Generation of antibodies

In each of the following antibody-generating examples, the synthesis of these linear peptides is followed by injection into two New Zealand Rabbits. Subsequent boosts and

bleeds are taken according to a standard ten-week protocol. The end-user receives back 5 mgs of peptide, aliquots of pre-bleeds, roughly 80 ml of crude sera from each of the two rabbits and, and ELISA titration data is obtained.

Generation of LRP5 Polymorphism-specific antibodies. Antibodies were generated to the following peptides to obtain antibodies which distinguish the HBM polymorphism versus wild-type LRP5/Zmax: MYWTDWVETPRIE (SEQ ID NO:) (mutant peptide) and MYWTDWGETPRIE (SEQ ID NO:) (wild-type peptide for negative selection). Immunofluorescence data confirmed that the antibody, after affinity purification, is specific for HBM and does not recognize LRP5 (Fig. 32).

Generation of LRP5 Monospecific antibodies. LRP5 monospecific polyclonal antibodies were generated to the following amino acid sequences of LRP5: Peptide 1 (a.a. 265-277) - KRTGGKRKEILSA (SEQ ID NO:), Peptide 2 (a.a. 1178-1194) - ERVEKTTGDKRTRIQGR (SEQ ID NO:), and Peptide 3 (a.a. 1352-1375) - KQQCDSFPDCIDGSDE (SEQ ID NO:). Immunofluorescence confirmed that the antibody generated detects LRP5.

Generation of Dkk-1 monospecific polyclonal antibodies. Dkk-1 monospecific polyclonal antibodies were generated to the following amino acid sequences of Dkk-1:
Peptide 1 - GNKYQTIDNYQPYPC (SEQ ID NO:),
Peptide 2- LDGYSRRTTLSSKMYHTKGQEG (SEQ ID NO:),
Peptide 3 - RIQKDHHQASNSSRLHTCQRH (SEQ ID NO:),
Peptide 4 - RGEIEETITESFGND (SEQ ID NO:), and
Peptide 5 - EIFQRCGEGLSCRIQKD (SEQ ID NO:) of human Dkk-1. Western Blots demonstrated that the antibodies generated against peptides 2 and 4 are specific toward Dkk-1.

Example 5

Effects of exogenous Dkk-1 on Wnt-mediated signaling in the Xenopus embryo assay

Xenopus embryos are an informative and well-established *in vivo* assay system to evaluate the modulation of Wnt signaling (McMahon *et al.*, 1989 *Cell* 58: 1075-84; Smith *et*

al., 1991 reviewed in Wodarz and Nusse, 1998).

Modification of the Wnt signaling pathway can be visualized by examining the embryos for a dorsalization phenotype (duplicated body axis) after RNA injection into the ventral blastomere at the 4- or 8-cell stage. On the molecular level, phenotypes can be analyzed by looking for expression of various marker genes in stage 10.5 embryos. Such markers would include general endoderm, mesoderm, and ectoderm markers as well as a variety of tissue-specific transcripts.

Analysis can be done by RT-PCR/TaqMan® and can be done on whole embryo tissue or in a more restricted fashion (microdissection). Because this system is very flexible and rapid, by injecting combinations of transcripts, such as HBM and different Wnts or Wnt antagonists, the mechanism of HBM in the Wnt pathwaycan thereby be dissected. Furthermore, investigations are conducted to determine whether Zmax/LRP5 and HBM differentially modulate Wnt signaling either alone, or in combination with other components. Previous studies have demonstrated that LRP6 alone or LRP5 + Wnt5a were able to induce axis duplication (dorsalization) in this system (Tamai *et al.*, 2000 *Nature* 407: 530-35).

Constructs for Xenopus Expression (Vector pCS2$^+$). Constructs were prepared using the vector pCS2$^+$. DNA inserts were subcloned in the sense orientation with respect to the vector SP6 promoter. The pCS2$^+$ vector contains an SV40 virus polyadenylation signal and T3 promoter sequence (for generation of antisense mRNA) downstream of the insert.

Full length Zmax/LRP5 and HBM ORF cDNA: Insert cDNA was isolated from the full length cDNA retrovirus constructs (with optimized Kozak sequences) by *Bgl*II-*Eco*RI digestion and subcloned into the *Bam*HI-*Eco*RI sites of the pCS2$^+$ vector. cDNAs encoding a HBM-like molecule could be subcloned into pCS2$^+$ vectors and processed similarly by one of ordinary skill.

Full length XWnt8: This cDNA was PCR amplified from a Xenopus embryo cDNA library using oligos 114484 (SEQ ID NO:) (5'-CAGTGAATTCACCATGCAAAACACC ACTTTGTTC-3') and 114487 (SEQ ID NO:) (5'-CAGTTGCGGCCGCTCATCTCCGGTG GCCTCTG-3'). The oligos were designed to amplify the ORF with a consensus Kozak sequence at the 5' end as determined from GenBank #X57234. PCR was carried out using

the following conditions: 96°C, 45 sec.; 63°C, 45 sec.; 72°C, 2 min. for 30 cycles. The resulting PCR product was purified, subcloned into pCRII-TOPO (Invitrogen Corp.), sequence verified, and digested with *Bam*HI/*Xho*I. This insert was subcloned into the vector at the *Bam*HI-*Xho*I sites.

Full length Wnt5a: A murine Wnt5a cDNA clone was purchased from Upstate Biotechnology (Lake Placid, NY) and subcloned into the *Eco*RI site of the vector. Sequencing confirmed insert orientation.

Full length human Dkk-1: A human cDNA with GenBank accession number AF127563 was available in the public database. Using this sequence, PCR primers were designed to amplify the open reading frame with a consensus Kozak sequence immediately upstream of the initiating ATG. Oligos 117162 (SEQ ID NO:) (5'-CAATAGTCGACGAATTCACCATGGCTCTGGGCGCAGCGG-3') and 117163 (SEQ ID NO:) (5'-GTATTGCGGCCGCTCTAGATTAGTGTCTCTGACAAGTGTGAA-3') were used to screen a human uterus cDNA library by PCR. The resulting PCR product was purified, subcloned into pCRII-TOPO (Invitrogen Corp.), sequence verified, and digested with *EcoR*I/*Xho*I. This insert was subcloned into the pCS2^{+} vector at the *Eco*RI-*Xho*I sites.

Full length human Dkk-2: A full length cDNA encoding human Dkk-2 was isolated to investigate the specificity of the Zmax/LRP5/HBM interaction with the Dkk family of molecules. Dkk-1 was identified in yeast as a potential binding partner of Zmax/LRP5/HBM. Dkk-1 has also been shown in the literature to be an antagonist of the Wnt signaling pathway, while Dkk-2 is not (Krupnik *et al.*, 1999). The Dkk-2 full length cDNA serves as a tool to discriminate the specificity and biological significance of Zmax/LRP5/HBM interactions with the Dkk family (*e.g.*, Dkk-1, Dkk-2, Dkk-3, Dkk-4, Soggy, their homologs and variant, etc.). A human cDNA sequence for Dkk-2 (GenBank Accession No. NM_014421) was available in the public database. Using this sequence, PCR primers were designed to amplify the open reading frame with a consensus Kozak sequence immediately upstream of the initiating ATG. Oligos 51409 (SEQ ID NO:) (5'-CTAACGGATCCACCATGGCCGCGTTGATGCGG-3') and 51411 (SEQ ID NO:) (5'-GATTCGAATTCTCAAATTTTCTGACACACATGG-3') were used to screen human

embryo and brain cDNA libraries by PCR. The resulting PCR product was purified, subcloned into pCRII-TOPO, sequence verified, and digested with *Bam*HI/*Eco*RI. This insert was subcloned into the pCS2$^+$ vector at the *Bam*HI-*Eco*RI sites.

Full length LRP6 was isolated from the pED6dpc4 vector by *Xho*I-*Xba*I digestion. The full length cDNA was reassembled into the *Xho*I-*Xba*I sites of pCS2$^+$. Insert orientation was confirmed by DNA sequencing.

mRNA Synthesis and Microinjection Protocol. mRNA for microinjection into *Xenopus* embryos is generated by *in vitro* transcription using the cDNA constructs in the pCS2$^+$ vector described above as template. RNA is synthesized using the Ambion mMessage mMachine high yield capped RNA transcription kit (Cat. #1340) following the manufacturer's specifications for the Sp6 polymerase reactions. RNA products were brought up to a final volume of 50 µl in sterile, glass-distilled water and purified over Quick Spin Columns for Radiolabeled RNA Purification G50-Sephadex (Roche, Cat. #1274015) following the manufacturer's specifications. The resulting eluate was finally extracted with phenol:chloroform:isoamyl alcohol and isopropanol precipitated using standard protocols (Sambrook *et al.*, 1989). Final RNA volumes were approximately 50 µl. RNA concentration was determined by absorbance values at 260 nm and 280 nm. RNA integrity was visualized by ethidium bromide staining of denaturing (formaldehyde) agarose gel electrophoresis (Sambrook *et al.*, 1989). Various amounts of RNA (2 pg to 1 ng) are injected into the ventral blastomere of the 4- or 8-cell *Xenopus* embryo. These protocols are described in Moon *et al.*, 1989 *Technique-J. of Methods in Cell & Mol. Biol.* 1: 76-89; and Peng, 1991 *Meth. Cell. Biol.* 36: 657-62.

Screening for Duplicated Body Axis. *In vitro* transcribed RNA is purified and injected into a ventral blasomere of the 4- or 8-cell *Xenopus* embryo (approx. 2 hours post-fertilization). At stage 10.5 (approx. 11 hours post-fertilization), the injected embryos are cultured for a total of 72 hours and then screened for the presence of a duplicated body axis (dorsalization) (Fig. 33). Using XWnt8-injected (2-10 pg) as a positive control (Christian *et al.*, 1991) and water-injected or non-injected embryos as negative controls, we replicated the published observation that Zmax(LRP5) + Wnt5a (500 and 20 pg, respectively) could induce

axis duplication. Wnt5a (20 pg) alone could not induce axis duplication (as previously reported by Moon *et al.*, 1993). We have also injected GFP RNA (100-770 pg) as a negative control to show that the amount of RNA injected is not perturbing embryo development (not shown). Strikingly, HBM + Wnt5a (500 and 20 pg, respectively) yielded an approximately 3.5 fold more robust response of the phenotype (p=0.043 by Fisher's exact test) compared to Zmax(LRP5) + Wnt5a, suggesting that the HBM mutation is activating the Wnt pathway (Figs. 34 and 35). The HBM/Wnt5a embryos also appear to be more "anteriorized" than the Zmax(LRP5)/Wnt5a embryos, again suggestive of a gain-of-function mutation.

The role of Dkk-1 as a modulator of Zmax/LRP5- and HBM-mediated Wnt signaling was investigated. Literature reports have previously characterized *Xenopus* and murine Dkk-1 as antagonists of the canonical Wnt pathway in the *Xenopus* system (Glinka *et al.*, 1998 *Nature* 391: 357-62). Using the human Dkk-1 construct, a dose-response assay was performed to confirm that our construct was functional and to identify the optimal amount of RNA for microinjection. Using 250 pg/embryo of hDkk-1 RNA, over 90% ($p<0.001$) of the embryos were observed to display enlarged anterior structures (big heads) as anticipated from the published reports (Fig. 36).

The mechanism of hDkk-1 modulation of Wnt signaling in the presence of Zmax/LRP5 or HBM was also investigated. Without any hDkk-1 present, it was confirmed that HBM + Wnt5a was a more potent activator of Wnt signaling than Zmax/LRP5 + Wnt5a ($p<0.05$). Interestingly, in the presence of hDkk-1 (250 pg), Zmax/LRP5-mediated Wnt signaling was repressed ($p<0.05$) but hDkk-1 was unable to repress HBM-mediated Wnt signaling ($p<0.01$) (Fig. 37). The specificity of this observation can be further addressed by investigating other members of the Dkk family, other Wnt genes, LRP6, additional Zmax/LRP5 mutants, and the peptide aptamers.

Example 6

Effects of exogenous Dkk and LRP5 on Wnt signaling in the TCF-luciferase Assay

Wnt activity can be antagonized by many proteins including secreted Frizzled related proteins (SFRPs), Cerberus, Wnt Inhibitory Factor-1 and Dkk-1 (Krupnik *et al.*, 1999). The

Dkk family of proteins consists of Dkk-1-4 and Soggy, a Dkk-3-like protein. Dkk-1 and Dkk-4 have been shown to antagonize Wnt mediated *Xenopus* embryo development, whereas Dkk-2, Dkk-3, and Soggy do not. Unlike many of these proteins that antagonize Wnt activity by directly interacting with Wnt proteins, Dkk-1 acts by binding to two recently identified Wnt coreceptors, LRP5 and LRP6 (Mao *et al.*, 2001; Bafico *et al.*, 2001). The details of this interaction have been examined by the present inventors and Mao et al. using deletion constructs of LRP6, which demonstrated that EGF repeats 3 and 4 are important for Dkk-1 interaction. Accordingly, the activity of two Dkk proteins, Dkk-1 and Dkk-2, were investigated with various Wnt members, LRP5, LRP6, and the mutant form of LRP5, designated HBM. The present invention explores whether there is any functional difference between LRP5 and HBM with regard to Dkk action on Wnt mediated signaling. Various reagents were developed, including Dkk-1 peptides, constrained LRP5 peptide aptamers, constrained Dkk-1 peptide aptamers and polyclonal antibodies to Dkk-1 (in Example 4 above) to identify factors that mimic HBM mediated Wnt signaling.

Methods. Various LRP5 constrained peptides were developed. Specifically, four peptides that interact with the LBD of LRP5 (Fig. 38,constructs OST259-262 in Fig. 39) and three peptides that interact with the cytoplasmic domain of LRP5 (constructs OST266-OST268 in Fig. 39). In addition two Dkk-1 peptides were developed: constructs OST264 and OST265 in Fig. 39, corresponding to Dkk-1 amino acids 139-266 and 96-245, containing the smallest region of Dkk-1 that interacts with LRP5 (Fig. 40). The cDNA clones encoding the LRP5 LBD interacting peptides and the Dkk-1 peptides were subcloned into pcDNA3.1 with the addition of a Kozak and signal sequence to target the peptide for secretion. The constructs encoding the three peptides interacting with the cytoplasmic domain of LRP5 were also subcloned into pcDNA3.1. However, these latter constructs do not contain a signal sequence.

HOB-03-CE6 osteoblastic cells developed by Wyeth Ayerst (Philadelphia, PA) were seeded into 24-well plates at 150,000 cells per well in 1 ml of the growth media (D-MEM/F12 phenol red-free) containing 10% (v/v) heat-inactivated FBS, 1X penicillin streptomycin, and 1X Glutamax-1, and incubated overnight at 34°C. The following day, the

cells were transfected using Lipofectamine 2000® (as described by the manufacturer, Invitrogen) in OptiMEM (Invitrogen) with 0.35 μg /well of LRP5, HBM, or control plasmid DNA (empty vector pcDNA3.1) and either Wnt1 or Wnt3a plasmid DNA. Similar experiments were performed with LRP6 plasmid DNA (0.35μg/well) or a control pEDdpc4 empty vector. Furthermore, each of these groups were then divided into three groups, those receiving 0.35 μg/well Dkk-1, Dkk-2, or pcDNA3.1 control DNA. All wells were transfected with 0.025 μg/well of CMV beta-galactosidase plasmid DNA and 0.35 μg/well 16X TCF(AS)-luciferase reporter DNA (developed by Ramesh Bhat, Wyeth-Ayerst (Philadelphia, PA)). After 4 hours of incubation, the cells were rinsed and 1 ml of fresh growth media was added to each well. The cells were cultured overnight at 34°C, followed by a wash and a change of media. Cells were cultured for an additional 18-24 hours at 37°C. Cells were then lysed with 50 μl/well of 1X lysis buffer. The extracts were assayed for beta-galactosidase activity (Galacto Reaction Buffer Diluent & Light Emission Accelerator, Tropix) using 5 μl extract + 50 μl beta-galactosidase diluent and luciferase activity (Luciferase Assay Reagent, Promega) using 20 μl extract.

U2OS human osteosarcoma cells were also utilized. U2OS cells (ATCC) were seeded into 96-well plates at 30,000 cells per well in 200 µl of the growth media (McCoy's 5A) containing 10% (v/v) heat-inactivated FBS, 1X penicillin streptomycin, and 1X Glutamax-1, and incubated overnight at 37°C. The following day, the media was replaced with OptiMEM (Invitrogen) and cells were transfected using Lipofectamine 2000® (as described by the manufacturer, Invitrogen) with 0.005 µg/well of LRP5, HBM, LRP6 or contol plasmid DNA (empty vector pcDNA3.1) and either Wnt1 (0.0025 µg/well) or Wnt3a (0.0025 µg/well) plasmid DNA. In addition, the 16x-(AS) TCF-TK-firefly-luciferase and control TK-renilla luciferase (Promega Corp.) were co-transfected at 0.3 µg/well and 0.06 µg/well respectively in all experiments. Furthermore, each of these groups was then divided into different groups, those receiving 0.05 µg/well Dkk-1, Dkk-2, Dkk3, Dkk1-Alkaline Phosphatase (AP), mutant Dkk-1 (C220A), Soggy or pcDNA3.1 control DNA. In other experiments, cells were co-transfected with 0.005 µg/well of LRP5, 0.0025 µg/well of Wnt1 or Wnt3a (using 0.0025 µg/well of a control pcDNA3.1) with LRP5-interacting aptamers

(0.05 μg/well). Cells were cultured for an additional 18-20 hours at 37°C. Culture medium was removed. Cells were cultured for an additional 18-20 hours at 37°C. Culture medium was removed. Cells were then lysed with 100 μl/well of 1X Passive Lysis Buffer (PLB) of Dual Luciferase Reagent kit (DLR-kit-Promega Corp.) 20 μl of the lysates were combined with LARII reagent of DLR-kit and assayed for TCF-firefly luciferase signal in Top Count (Packard) instrument. After measuring the Firefly readings, 100 μl of the "Stop and Glo" reagent of DLR kit that contains a quencher and a substrate for renilla luciferase was added into each well. Immediately the renilla luciferase reading was measured using the Top Count (Packard) Instrument. The ratios of the TCF-firefly luciferase to control renilla readings were calculated for each well and the mean ratio of triplicate or more wells was expressed in all data.

Results. The results of these experiments demonstrate that Dkk-1, in the presence of Wnt1 and LRP5, significantly antagonized TCF-luciferase activity (Fig. 41). In marked contrast, Dkk-1 had no effect on HBM/Wnt1 mediated TCF-luciferase activity (Fig. 41). In similar experiments, Dkk-1 was also able to antagonize LRP5/Wnt3a but not HBM/Wnt3a mediated TCF-luciferase activity (Fig. 42). These results indicate that the HBM mutation renders Dkk-1 inactive as an antagonist of Wnt1 and Wnt3a signaling in HOB03CE6 osteoblastic cells. In other experiments with Wnt1, Dkk-1 had no effect on LRP5 or HBM mediated TCF-luciferase activity (Fig. 41). In contrast, with either LRP5 or HBM in the presence of Wnt3a, Dkk-2 was able to antagonize the TCF-luciferase activity (Fig. 42). These latter results indicate that the HBM mutation has no effect on Dkk-2 action in the presence of Wnt3a. Experiments were also performed using the closely related LRP6 cDNA in HOB-03-CE6 cells. In these experiments, LRP6/Wnt1 and LRP6/Wnt3a mediated TCF-luciferase were regulated in the same manner as LRP5. Specifically, Dkk-1 antagonized LRP6/Wnt1 mediated TCF-luciferase activity, whereas Dkk-2 had no effect (Fig. 41). However, similar to the action of Dkk-2 with LRP5/Wnt3a, Dkk-2 was able to antagonize LRP6/Wnt3a mediated TCF-luciferase activity (Fig. 42).

The results in the U2OS cells show a robust effect of the OST262 LRP5 peptide aptamer activation of Wnt signaling in the presence of Wnt3a (Fig. 43). These functional

results are confirmed by the results shown below in Example 7 using LRP5 peptide aptamers in the Xenopus assay. Such results affirmatively demonstrate that the effects of small molecules on LRP5/LRP6/HBM signaling can be detected using the TCF-luciferase assay.

These data demonstrate that there is a functional difference between LRP5 and HBM regarding the ability of Dkk-1 to antagonize Wnt1 and Wnt3a signaling. These data and previous data showing that Dkk-1 directly interacts with LRP5 suggests that the inability of Dkk-1 to antagonize HBM/Wnt signaling may in part contribute to the HBM phenotype. These experiments further demonstrate the ability to test various molecules (e.g., small molecules, aptamers, peptides, antibodies, LRP5 interacting proteins or Dkk-1 interacting proteins, and the like) for a LRP5 ligand that mimics HBM mediated Wnt signaling or factors that block Dkk-1 interaction with LRP5.

This was the assay that was used to show the responsiveness of two HBM-like variants. See Figs. 29 and 30. The data also demonstrates that these variants are less susceptible to modulation by Dkk.

Example 7

Cell-Based Functional High-Throughput Assay

To develop a high throughput assay, the TCF-luciferase assay described in Example 6 was modified utilizing low level expression of endogenous LRP5/6 in U2OS and HEK293 cells. However, HOB-03-CE6 cells and any other cells which show a differential response to Dkk depending on whether LRP5, LRP6 or HBM are expressed. Using U2OS (human osteosarcoma) and HEK293 (ATCC) cells, the TCF-luciferase and tk-Renilla reporter element constructs were co-transfected along with Wnt3a/1 and Dkk. Wnt3a alone, by using endogenous LRP5/6, was able to stimulate TCF reporter gene activation. When Dkk, is co-transfected with Wnt3a/Wnt 1 and reporters (TCF-luci and tk-Renilla), Dkk represses reporter element activity. In addition, the TCF-luci signal is activated by Wnt3a/Wnt1 can be repressed by the addition of Dkk-enriched conditioned media to the cells containing Wnt3a/Wnt1 and reporters. The assay is further validated by the lack of TCF-reporter inhibition by a point mutant construct (C220A) of Dkk1.

The Dkk-mediated repression of the reporter is dependent upon the concentration of transfected Dkk cDNA or on the amount of Dkk-conditioned media added. In addition, the Dkk-mediated reporter suppression can be altered by the co-transfection of LRP5, LRP6, and HBM cDNAs in the U2OS or HEK293 cells. In general, U2OS cells show greater sensitivity to Dkk-mediated reporter suppression than that in HEK-293 cells. In U2OS cells, the transfection of LRP5/LRP6/HBM/HBM-like cDNA leads to moderate activation of TCF-luci in the absence of Wnt3a/Wnt1 transfection. This activation presumably utilizes the endogenous Wnts present in U2OS cells. Under this condition, Dkk1 can repress TCF-luci and shows a differential signal between LRP5 and HBM. By co-transfecting Wnt3a/Wnt1, there is a generalized increase in the TCF-luci signal in the assay. Further, one can detect Dkk-mediated differential repression of the reporter due to LRP5 and HBM cDNA expression as well as between LRP5 and LRP6 cDNA. The repression is maximal with LRP6, moderate with LRP5, and least with HBM cDNA expression. In addition, the assay can detect the functional impact of the LRP5 interacting peptide aptamers (Fig. 38), Dkk1 interacting aptamers and binding domains of Dkk-1 (Fig. 40; OST264 and OST265 of Figs. 39 and 44).

Using this system with a suppressed Wnt-TCF signal due to the presence of both Dkk and Wnt3a, one can screen for compounds that could alter Dkk modulation of Wnt signaling, by looking for compounds that activate or the TCF-luciferase reporter, and thereby relieve the Dkk-mediated repression of the Wnt pathway. Such compounds identified may potentially serve as HBM-mimetics and be useful, for example, as osteogenic therapeutics. Data generated from this high throughput screen are demonstrated in Figs. 45-47. Fig. 45 shows that Dkk1 represses Wnt3a-mediated signaling in U2OS bone cells. Fig. 46 demonstrates the functional differences between LRP5, LRP6, and HBM. Dkk-1 represses LRP6 and LRP5 but has little or no effect on HBM-generated Wnt1 signaling in U2OS cells. Fig. 47 demonstrates the differential effects of various Dkk family members and modified Dkks, including Dkk-1, a mutated Dkk-1 (C220A), Dkk-1-AP (modified with alkaline phosphatase), Dkk-3, and Soggy.

Example 8

DKK/LRP5/6/HBM/HBM-like ELISA Assay

A further method to investigate Dkk binding to LRP or HBM and HBM like polypeptides is via ELISA assay. Two possible permutations of this assay are exemplified. LRP5 is immobilized to a solid surface, such as a tissue culture plate well. One skilled in the art will recognize that other supports such as a nylon or nitrocellulose membrane, a silicon chip, a glass slide, beads, etc. can be utilized. In this example, the form of LRP5 used is actually a fusion protein where the extracellular domain of LRP5 is fused to the Fc portion of human IgG. The LRP5-Fc fusion protein is produced in CHO cell extracts from stable cell lines. The LRP5-Fc fusion protein is immobilized on the solid surface via anti-human Fc antibody or by Protein-A or Protein G-coated plates, for example. The plate is then washed to remove any non-bound protein. Conditioned media containing secreted Dkk protein or secreted Dkk-epitope tagged protein (or purified Dkk or purified Dkk-epitope tagged protein) is incubated in the wells and binding of Dkk to LRP is investigated using antibodies to either Dkk or to an epitope tag. Dkk-V5 epitope tagged protein would be detected using an alkaline phosphatase tagged anti-V5 antibody.

Alternatively, the Dkk protein could be directly fused to a detection marker, such as alkaline phosphatase. Here the detection of the Dkk-LRP interaction can be directly investigated without subsequent antibody-based experiments. The bound Dkk is detected in an alkaline phosphatase assay. If the Dkk-alkaline phosphatase fusion protein is bound to the immobilized LRP5, alkaline phosphatase activity would be detected in a colorimetric readout. As a result, one can assay the ability of small molecule compounds to alter the binding of Dkk to LRP using this system. Compounds, when added with Dkk (or epitope-tagged Dkk) to each well of the plate, can be scored for their ability to modulate the interaction between Dkk and LRP based on the signal intensity of bound Dkk present in the well after a suitable incubation time and washing. The assay can be calibrated by doing cold competition experiments with unlabeled Dkk or with a second type of epitope-tagged Dkk. Any small molecule that is able to modulate the Dkk-LRP interaction may be a suitable therapeutic candidate, more preferably an osteogenic therapeutic candidate.

Example 9

Functional Evaluation of Peptide Aptamers in Xenopus

The constrained peptide aptamers constructs OST258-263 (where 258 contains the signal sequence by itself and 263 contains an irrelevant constrained peptide) (Figs. 39 and 44) were used to generate RNA substantially as described in Example 6, except the vector was linearized by restriction endonuclease digestion and RNA was generated using T7 RNA polymerase.

Aptamer RNA was injected at 250 pg per blastomere using the protocol of Example 6. Wnt signaling was activated, as visualized by embryo dorsalization (duplicated body axis) with aptamers 261 and, more strongly, 262. The results of this assay are shown in Figs. 48 and 49. These results suggest that aptamers 261 and 262 are able to activate Wnt signaling possibly by binding to the LBD of LRP, thereby preventing the modulation of LRP-mediated signaling by Dkk.

The aptamers of the present invention can serve as HBM-mimetics. In the Xenopus system they are able to induce Wnt signaling all by themselves. They may also serve as tools for rational drug design by enhancing the understanding of how peptides are able to interact with LRP and modulate Wnt signaling at the specific amino acid level. Thus, one would be able to design small molecules to mimic their effects as therapeutics. In addition, the aptamers identified as positives in this assay may be used as therapeutic molecules themselves.

Example 10

Homogenous Assay

An excellent method to investigate perturbations in protein-protein interactions is via Fluorescence Resonance Energy Transfer (FRET). FRET is a quantum mechanical process where a fluorescent molecule, the donor, transfers energy to an acceptor chromophore molecule which is in close proximity. This system has been successfully used in the literature to characterize the intermolecular interactions between LRP5 and Axin (Mao *et al.*, *Molec. Cell Biol.* 7: 801-9). There are many different fluorescent tags available for such

studies and there are several ways to fluorescently tag the proteins of interest. For example, CFP (cyan fluorescent protein) and YFP (yellow fluorescent protein) can be used as donor and acceptor, respecively. Fusion proteins, with a donor and an acceptor, can be engineered, expressed, and purified.

For instance, purified LRP protein, or portions or domains thereof, fused to CFP and purified Dkk protein, or portions or domains thereof that interact with Dkk or LRP respectively, fused to YFP can be generated and purified using standard approaches. If LRP-CFP and Dkk-YFP are in close proximity, the transfer of energy from CFP to YFP will result in a reduction of CFP emission and an increase in YFP emission. Energy is supplied with an excitation wavelength of 450 nm and the energy transfer is recorded at emission wavelengths of 480 nm and 570 nm. The ratio of YFP emission to CFP emission provides a guage for changes in the interaction between LRP and Dkk. This system is amenable for screening small molecule compounds that may alter the Dkk-LRP protein-protein interaction. Compounds that disrupt the interaction would be identified by a decrease in the ratio of YFP emission to CFP emission. Such compounds that modulate the LRP-Dkk interaction would then be considered candidate HBM mimetic molecules. Further characterization of the compounds can be done using the TCF-luciferase or *Xenopus* embryo assays to elucidate the effects of the compounds on Wnt signaling.

While the above example describes a cell-fee, solution-phase assay using purified components, a similar cell-based assay could also be performed. For example, LRP-CFP fusion protein can be expressed in cells. The Dkk-YFP fusion protein then could be added to the cells either as purified protein or as conditioned media. The interaction of LRP and Dkk is then monitored as described above.

Example 11

Identification of Variants of LRP5/Zmax1/HBM

Because the YWTD repeats constitute the major part of domain which interacts with Dkk-1, a search was begun from the repeats to look for protein folds that contain such repeats. Springer, 1998 *J. Mol. Biol.* 283: 837-62 proposed that these YWTD repeats, which

had been previously described as "spacers" and considered to have no defined structure, are in fact the propeller-blade subdomains of highly structured six-bladed β-propellers. Springer (1998) therefore proposed two theoretically modeled protein structures with such YWTD repeats.

The Model. A set of LRP5 propeller domain sequences from mouse and human were assembled and aligned using CLUSTALW, together with the sequences corresponding to two of the modeled YWTD-propeller structures of Springer (1998) [1lpx, based on the LRP1 β-propeller domain no. 7 from chicken (SwissProt LRP1_CH7), and 1ndx, based on human nidogen (Swiss-Prot NIDO_HU1)]. The alignment was manually edited based on the rationale and knowledge of protein structures. Fig. 50 depicts a schematic model of LRP5. The secondary structures consist exclusively of β-strands and turns. The secondary structure assignments were verified by the predictive program, DSC (Discrimination of Protein Secondary Structure Class available at http://bioweb.pasteur.fr/seqanal/interfaces/dsc.html). Preliminary checks of the exon-intron boundaries were performed manually. A tertiary-structure homology model for human LRP5 using the 1lpx model as a template was built with InsightII (Accelrys Inc., San Diego, CA) and examined using the graphics display programs from Insight II and Rasmol (freely available at http://www.umass.edu/microbio/rasmol/index2.html).

Results. Based on the homology alignments and modeling, the domain diagram of LRP5 in Fig. 50 was obtained. Fig. 51 shows the complete alignment and secondary structure assignments for the propeller domains of mouse LRP5 and LRP6, human LRP5 and human LRP6, and the sequences corresponding to the two theoretical models constructed by Springer (1998).

To a good first approximation, the sequence alignments support the proposal that there are four 6-bladed β-propeller domains in human LRP5. This model nicely accommodates the sequence (as should be expected since it derives from a carefully constructed model of a chicken LRP propeller domain). The overall shape of this domain resembles a disk with inward-sloping sides and a hole down the middle. The polypeptide chain enters and leaves from the same (comparatively flat) "bottom" surface. As indicated in

the alignment (Fig. 51) and in several of the structure illustrations, the G171V mutation falls into a loop on the outer or "top" face of the domain. This immediately suggests that – contrary to what one might expect, given the role of highly conserved glycine residues in determining protein folds – the mutation should not have any significant effect on the domain's tertiary structural stability. It is rather more likely that the mutation interferes with binding of some ligand, possibly a macromolecule (Smith *et al.*, 1999 *Trends Biochem. Sci.* 24: 181-5) or alters a protein-protein interaction.

Closer scrutiny of the protein in the vicinity of G171 shows that this residue sits at the bottom of a pocket on the outer edge of the top surface of the domain. Moreover, one side of this pocket consists of a cluster of very hydrophobic side chains, while the other side has more polar groups, most notably glutamate 172. In the mutant form of the protein, with V171 in place of the glycine, the pocket largely disappears as the isopropyl group of valine replaces the hydrogen side chain of glycine. It is easy to understand how such a substitution could seriously disrupt ligand binding if the ligand normally protrudes into the pocket. By the same rationale, any other mutations that block such pockets in any of the four propellers could also result in impaired ligand binding.

The reasonableness of the proposed model is based on Springer's results as well as additional data. For example, data derived from the typical features of such protein domains (including the well-studied YWTD repeats), e.g., that are robust and rigid tertiary structures. Loop conformations may vary somewhat, especially for the longer loops, but the basic features of the protein scaffold are almost certainly well predicted. Of course we would be on somewhat more secure ground if there were a crystal structure for one of these domains. That naturally implies that some of the more interesting features, such as the identity of residues exposed on the outer, putative ligand-binding surface, will also be well-predicted. Note that in Fig. 51 these residues are marked in red on the sequences corresponding to Springer's (1998) models. Even though different models could possibly be built that are not dependent on Springer's assumptions and lead to a different topology of the propeller, this would not alter the conclusion that the G171V mutation lies in a surface loop.

At the very least, the model affords an opportunity to think about this protein in

molecular terms and that should facilitàte both experimental design and evaluation of results, *i.e.*, candidate epitopes might be selected more rationally. One interesting aspect, evoked forcefully by the diagram in Fig. 50, is the question of how the different modular propeller domains interact. The EGF-like domains are well-studied (dozens of crystal and NMR structures exist, see for example Bork *et al.*, *1996 Quart. Rev. Biophys.* 29: 119-67). The EGF-like domains consist mainly of a couple of β-hairpins, cross-linked by disulfide bonds, and in some cases they have tightly bound calcium ions, which must further stabilize their structure. Interestingly, in contrast to the YWTD propellers, the EGF-like domains have the polypeptide chain entering at one end and exiting at the other. Thus, mechanically, these domains could act as spacers, even swivels (since rotation can occur around the tails that extend from either end). Given the size of the propellers, there are almost certainly inter-domain interactions between them as they assemble in some higher-order structure, connected by the EGF-like domains. Because of the topology of the propellers, their "top" faces would have to face outward since the EGF-like domains will tie them together by their protruding N- and C-terminal extensions.

A more sophisticated analysis of the β-propeller structure was modeled using X-ray crystallographic data from the LDL receptor. The primary amino acid sequences of the various beta propeller domains of LRP5 (and other domains) were used to develop homology models of their 3-dimensional structures according to the following method:

(A) Search for suitable structural templates and check sequence identity with target. The ExNRL-3D database (derived from the Protein Data Bank (http://pdb.ccdc.cam.ac.uk/pdb/) was searched using BLASTP2 (Altschul *et al.*, 1990 *J. Mol. Biol.* 215: 403-10; Huang *et al.*, 1991 *Adv. Appl. Math.* 12: 337-67; and Peitsch, 1995 *PDB Quart. Newsletter* 72: 4) to find all similarities of the target sequence with sequences of known structure. This program selects all templates with sequence identities above 25% and projected model size greater than 20 residues. This step also detects domains that can be modelled based on unrelated templates. Use of this step resulted in the selection of Protein Data Bank (PDB) structure, 1IJQ ("Crystal Structure Of The LDL Receptor YWTD-EGF Domain Pair") (Jeon *et al.*,

2001 *Nat. Struct. Biol.* 8: 499).

(B) Create ProModII (Altschul *et al.*, 1990; Huang *et al.*, 1991; and Peitsch, 1995) jobs and generate models with ProModII.

(C) Superimpose related 3D structures. This method is based upon the diagonals of sequence similarity (the Dynamic sequence alignment algorithm (SIM)(Altschul *et al.*, 1990; Huang *et al.*, 1991; and Peitsch, 1995). Specifically, the following steps are performed:

(i) Primary match: Regions with sequence similarity are selected automatically (manual selection is also possible) and the corresponding residues matched in three-space. (ii) The primary match is further refined using expanding context spheres.

(D) Generate a multiple alignment comprising the sequences to be modeled.

(E) Generate a framework for the new sequence.

(F) Based on the topological arrangement of corresponding atoms: (a) atoms which occupy a similar portion of space and are expected to have a structural counterpart in the new structure are used to compute the framework coordinates (averaged positions); (b) Side chains with fully incorrect geometries are removed.

(G) Rebuild the lacking loops based on the geometry of the loop stems: (a) the stems of the loops to rebuild are used to scan a database of structural fragments derived from the Brookhaven Data Bank. Either the best fitting fragment or a framework derived from the five best fragments, is used as the new loop, or (b) the conformational space is searched using a CSP approach (seven allowed Φ-Ψ angle combinations, space allocation for the loop, space allocation for each α-carbon in the loop). Both methods will place only α-carbons when loops are in steric conflict with the surrounding context.

(H) Rebuilt incomplete backbones based on the position of the a-carbons, the backbone was rebuilt using a set of seven allowed Φ-Ψ angle combinations and a database of backbone fragments (a sliding window of five residues was run through the protein sequence. The best matching backbone fragment for each overlapping pentapeptide was then stored. A framework for the main chain atoms is derived from

these peptides, using only the coordinates of the three central residues of each pentapeptide.

(I) The model's structural quality is verified and packing is checked as follows:

(i) Verification of structural quality is based on the method described by R. Luthy *et al.*, 1992 *Nature* 356: 83-85. This method analyzes the 3D context of each residue and allows the identification of mis-folded regions.

(ii) Packing is checked based on a probe accessible surface (Connoly surface) computation and a cubic grid passed through the structure. Inside and outside surfaces are detected and the center and size of each cavity is computed. The algorithm then compares the size and distribution of these cavities between the model and the structure in order to detect possibly mis-folded regions.

(J) Refine structure by energy minimization and molecular dynamics based on force field computations following Gromos96 (*Methods for the evaluation of long-range electrostatic forces in computer simulations of molecular systems*, IN COMPUTER SIMULATION OF BIOMOLECULAR SYSTEMS, THEORETICAL AND EXPERIMENTAL APPLICATIONS, Vol. 2, 182-212 (W.F. van Gunsteren *et al.*, eds., Escom Science Publishers, Leiden, The Netherlands, 1993); van Gunsteren *et al.*, 1990 *Angew. Chem. Int. Ed. Engl.* 29: 992-1023; van Gunsteren *et al.*, 1992 *Eur. J. Biochem.* 204: 947-961; Torda and W.F. van Gunsteren. *Molecular Modeling Using Nuclear Magnetic Resonance Data*, IN REVIEWS IN COMPUTATIONAL CHEMISTRY, Vol. III, 143-172 (K. B. Lipkowitz *et al.*, eds., VCH Publishers, Inc. New York, 1992); van Gunsteren, *Molecular dynamics and stochastic dynamics simulation: A primer.* in COMPUTER SIMULATION OF BIOMOLECULAR SYSTEMS, THEORETICAL AND EXPERIMENTAL APPLICATIONS 3-36; van Gunsteren *et al.*, *Computation of free energy in practice: choice of approximations and accuracy limiting factors*. IN COMPUTER SIMULATION OF BIOMOLECULAR SYSTEMS, THEORETICAL AND EXPERIMENTAL APPLICATIONS 315-348; Smith *et al.*, *Methods for the evaluation of long-range electrostatic forces in computer simulations of molecular systems*, IN COMPUTER

SIMULATION OF BIOMOLECULAR SYSTEMS, THEORETICAL AND EXPERIMENTAL APPLICATIONS 182-212; van Gunsteren *et al.*, *Accounting for Molecular Mobility in Structure Determination Based on Nuclear Magnetic Resonance Spectroscopic and X-Ray Diffraction Data,* in Methods IN ENZYMOLOGY: NUCLEAR MAGNETIC RESONANCE, Vol. 239 619-654 (T.L. James *et al.*, eds., Academic Press, New York, 1994); van Gunsteren *et al.*, 1994 *Quart. Rev. Biophysics* 27: 435-481; van Gunsteren *et al.*, 1995 *Biomolecular Modelling: Overview of Types of Methods to Search and Sample Conformational Space,* IN PROCEEDINGS OF THE 1ST EUROPEAN CONFERENCE ON COMPUTATIONAL CHEMISTRY, AMERICAN INSTITUTE OF PHYSICS CONF. PROC. 330: 253-268; and van Gunsteren *et al.*, 1995 *Computer Phys. Communications* 91: 305-319).

(K) The structure is then manually refined based on sequence alignment and structural elements using Deep View, the SWISS-PDB Viewer (Guex *et al.*, 1997 *Electrophoresis* 18: 2714-23).

Uses of structural model. Having a three-dimensional model of the protein domain allows one to appreciate the context of the HBM mutation, or other HBM-like mutations, in three dimensional space. This facilitates the prediction of possible mechanisms of action in a manner impossible in any other way because one cannot predict from primary sequence alone the proximity of one distant (in sequence space) amino acid to another. This also allows one to make functional predictions that can then be tested using molecular/cellular biology techniques to further refine the model and validate the target. For example, the structural model of the G171V mutation predicted an alteration in side chain-side chain interactions, so we were able to use this information to successfully predict similar mutations in other amino acids that would have analogous structural effects. Overlaying other functional data on this model would also able highlight other potentially important regions of the protein domain. Additionally, such models show the accessible residues, which would be useful for developing small compounds, antibodies and the like which recognize and bind to this region.

Results. Based on the space filling hypothesis set forth in Section 3 above, two residues from blade 6 of propeller 1 were identified as being in structurally equivalent locations to residue 171 in blade 4. Accordingly, substitutions with valine were engineered: F241V and A242V.

Residues that were predicted to be accessible to the interior surface of the propeller were identified in both blades 3 and 5 of Zmax1 (LRP5). Original predictions from the Springer model identified G199 on blade 5 and E128 on blade 3 as the equivalent position to residue 171 of blade 4 (HBM). Using the more sophisticated model described above, G199 and E128 are not predicted to be in the equivalent position to residue 171 of blade 4. Based on the new, more sophisticated model, the following residues were chosen for valine substitutions:

Blade No.	Mutations
5	L200V, T201V and I202V
3	S127V

Another residue T125 was selected for a conservative substitution with T125S as well as a less conservative substitution of T125G.

The role of the YWTD repetitive motifs in the β-propeller was examined by carrying out an alanine replacement scan over this region in Blade 4. These repeats are predicted to create the β-sheet blades of the propeller. Based on this model data, the following additional mutations were prepared in propeller 1: Y164A, M165A, Y166A, W167A, T168A, and D169A. These substitutions would be predicted to be detrimental to the β-propeller structure.

The spacing filling or occupied space model was further examined by mutating a residue predicted by the above methods to reside on the exterior surface of propellar 1, blade 4. This mutation, K215V (K→V at position 215), was selected because it was believed to not produce an HBM-like effect.

Based on this information, the following model of the HBM G171V mutation was obtained. Specifically, substitutions of valine at specific locations within propeller 1 could result in the creation of hydrophobic patches on the surface of the propeller. For example,

the V at residue 171 of the HBM mutant comes in close proximity to L150 on the adjacent strand, potentially creating a hydrophobic patch that was not present with the wild type G171. An example of this prediction, and others are presented in a separate file (Fig. 52).

Based on this model, a mutation of L150G which would remove the hydrophobic side chain at this site may not produce an HBM effect. In addition, a double mutant of G171V (HBM) and L150G may not produce an HBM effect due to the elimination of the hydrophobic side chain interactions. The model can also be used to test this prediction on a different propeller 1 blade. The substitution A214V was shown to result in an HBM effect. I194 is the residue that is in the equivalent position to A214 on blade 5 as L150 is to G171 on blade 4. While the mutation of I194G alone may not be predicted to result an HBM effect, the double mutant of I194G and A214V may no longer permit a hydrophobic patch to form and as a result not generate the HBM effect observed with A214V. Additional analyses of the residues in proximity to A214 that may contribute to the formation of hydrophobic patches identified P240 and F241. Mutations of either P240G or F241G together with A214V may no longer permit the formation of hydrophobic patches and may eliminate the HBM effect observed with A214V alone.

Lastly, the new model was used to investigate specific aspects of the other three propellers. The relevance of residues R494, R570 and V667 in the three other propellars was investigated. These three residues were chosen since they have been reported to be the site of osteoporosis pseudoglioma disease causing missense mutations: R494Q, R570W and V667M (Gong *et al.*, 2001 *Cell* 107: 513-523). Based on the structural location of these residues on the outer surface of the propeller, the model would not predict that these substitutions are either gain- or loss-of-function substitutions (Fig. 53A-C). For example, the mutations related to osteoporosis-pseudoglioma syndrome (OPPG) result in patients having very low bone mass and who are prone to developing fractures and deformation. This genetic condition is known now to result from mutations in LRP5 (Gong *et al.*, 2001 *Cell* 107: 513-23). Based on this information, this mutation would be categorized as a loss in function mutation.

As a result, we have engineered these receptor variant to functionally test. These new

receptor variants were generated exactly as described above with the following oligonucleotides:

L150GF	GAAGGTGCTCTTCTGGCAGGACGGTGACCAGCCGAGGGCC
L150GR	GGCCCTCGGCTGGTCACCGTCCTGCCAGAAGAGCACCTTC
I194GF	GATCATTGTGGACTCGGACGGTTACTGGCCCAATGGACTG
I194GR	CAGTCCATTGGGCCAGTAACCGTCCGAGTCCACAATGATC
L200VF	CATTTACTGGCCCAATGGAGTGACCATCGACCTGGAGGAGCAGAAGC
L200VR	GCTTCTGCTCCTCCAGGTCGATGGTCACTCCATTGGGCCAGTAAATG
T201VF	CATTTACTGGCCCAATGGACTGGTCATCGACCTGGAGGAGCAGAAGC
T201VR	GCTTCTGCTCCTCCAGGTCGATGACCAGTCCATTGGGCCAGTAAATG
I202VF	CATTTACTGGCCCAATGGACTGACCGTCGACCTGGAGGAGCAGAAGC
I202VR	GCTTCTGCTCCTCCAGGTCGACGGTCAGTCCATTGGGCCAGTAAATG
T125SF	GGCAAGAAGCTGTACTGGTCGGACTCAGAGACCAACCGCATC
T125SR	GATGCGGTTGGTCTCTGAGTCCGACCAGTACAGCTTCTTGCC
T125GF	GGCAAGAAGCTGTACTGGGGGGACTCAGAGACCAACCGCATC
T125GR	GATGCGGTTGGTCTCTGAGTCCCCCCAGTACAGCTTCTTGCC
S127VF	GAAGCTGTACTGGACGGACGTAGAGACCAACCGCATCGAGGTG
S127VR	CACCTCGATGCGGTTGGTCTCTACGTCCGTCCAGTACAGCTTC
F241VF	CCTGACGCACCCCGTCGCCCTGACGCTCTCCGGGGACACTC
F241VR	GAGTGTCCCCGGAGAGCGTCAGGGCGACGGGGTGCGTCAGG
A242VF	CCTGACGCACCCCTTCGTCCTGACGCTCTCCGGGGACACTC
A242VR	GAGTGTCCCCGGAGAGCGTCAGGACGAAGGGGTGCGTCAGG
K215VF	CTACTGGGCTGACGCCGTGCTCAGCTTCATCCACCGTGCC
K215VR	GGCACGGTGGATGAAGCTGAGCACGGCGTCAGCCCAGTAG
Y164AF	CTTGGACCCCGCTCACGGGGCCATGTACTGGACAGACTGG
Y164AR	CCAGTCTGTCCAGTACATGGCCCCGTGAGCGGGGTCCAAG
M165AF	GGACCCCGCTCACGGGTACGCGTACTGGACAGACTGGGGTG
M165AR	CACCCCAGTCTGTCCAGTACGCGTACCCGTGAGCGGGGTCC
Y166AF	CCCGCTCACGGGTACATGGCCTGGACAGACTGGGGTGAGAC
Y166AR	GTCTCACCCCAGTCTGTCCAGGCCATGTACCCGTGAGCGGG
W167AF	CGCTCACGGGTACATGTACGCGACAGACTGGGGTGAGACGC
W167AR	GCGTCTCACCCCAGTCTGTCGCGTACATGTACCCGTGAGCG

T168AF	GCTCACGGGTACATGTACTGGGCAGACTGGGGTGAGACGCC
T168AR	GGCGTCTCACCCCAGTCTGCCCAGTACATGTACCCGTGAGC
D169AF	CACGGGTACATGTACTGGACAGCCTGGGGTGAGACGCCCCG
D169AR	CGGGGCGTCTCACCCCAGGCTGTCCAGTACATGTACCCGTG
R494QF	CAACTTGGATGGGCAGGAGCAGCGTGTGCTGGTCAATGCCTC
R490QR	GAGGCATTGACCAGCACACGCTGCTCCTGCCCATCCAAGTTG
R570WF	GCAGCGCCGCAGCATCGAGTGGGTGCACAAGGTCAAGGCCAG
R570WR	CTGGCCTTGACCTTGTGCACCCACTCGATGCTGCGGCGCTGC
V667MF	CGAGACCAATAACAACGACATGGCCATCCCGCTCACGGGCG
V667MR	CGCCCGTGAGCGGGATGGCCATGTCGTTGTTATTGGTCTCG

Point mutations in other molecules with beta-propellers have been described in the literature. For example, alpha4-integrin (Guerrero-Esteo *et al.*, 1998 *FEBS Letter* 429: 123-8) has had two mutations introduced, which resulted in altered protein function (*i.e.*, G130R and G190S). Both of these glycines are in structurally equivalent locations to G171 of LRP5, just located on different blades of the beta-propeller at the upper surface. Using the model discussed above, we mapped these residues of the alpha4-integrin and confirmed their placement. The result of these substitutions in the alpha4 integrin was loss of ligand binding and reduced affinity to its heterodimer binding partner: integrin-beta1, such that the alpha4-beta1 ($\alpha4\beta1$) heterodimer cannot be formed. Examples of modulation of other residues in integrin-alpha4 with functional consequences are referenced within Guerrero-Esteo *et al.* (1998). Thus, these data support the notion that disruption of beta-propeller structure can result in significant and dramatic effects on receptor function.

All references cited are herein incorporated by reference in their entirety for all purposes. The following applications are also incorporated by reference in their entirety herein: U.S. Application Nos. 09/543,771 and 09/544,398 filed on April 5, 2000, which are a continuation-in-part of Application No. 09/229,319, filed January 13, 1999, which claims benefit of U.S. Provisional Application No. 60/071,449, filed January 13, 1998, and U.S. Provisional Application No. 60/105,511, filed October 23, 1998. Additionally This application claims priority of Application Nos. 60/290,071 filed May 11, 2001; 60/291,311

filed May 17, 2001; 60/353,058 filed February 1, 2002, and 60/361,293 filed March 4, 2002 the texts of which are herein incorporated by reference in their entirety for all purposes.

CLAIMS

What is claimed is:

1. A nucleic acid comprising a mutation in LRP5 or LRP6 which results in a HBM-like phenotype when expressed in a cell, wherein said HBM-like phenotype results in bone mass modulation and/or lipid level modulation.

2. A LRP5 nucleic acid comprising at least one mutation of Tables 2 or 3 or which results in a mutation of one of the following G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V when expressed in a cell, and wherein expression of the nucleic acid in a subject results in bone mass modulation and/or lipid level modulation.

3. A LRP6 nucleic acid comprising at least one of Tables 2 or 3 or which results in a mutation of one of the following G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V when expressed in a cell, and wherein said mutation occurs in LRP6 in a position equivalent to LRP5 such that expression of the nucleic acid in a subject results in bone mass modulation and/or lipid level modulation.

4. A LRP5 nucleic acid encoding at least one amino acid mutation in propeller 1.

5. The LRP5 nucleic acid of claim 4, wherein said nucleic acid encodes for at least one mutation selected from the group consisting of: G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, and S127V.

6. A LRP6 nucleic acid encoding at least one amino acid mutation in propeller 1.

7. The LRP6 nucleic acid of claim 6, wherein said nucleic acid encodes for at least one mutation in an equivalent position of LRP6 selected from the group of LRP5 mutations consisting of: G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, and S127V.

8. The nucleic acid of claims 1-7, wherein the mutation is G171V, A214V,

A65V, M282V, G171K, G171F, G171I or G171Q in LRP5 or in an equivalent domain in LRP6.

9. A polypeptide encoded by a nucleic acid of claims 1 to 8, wherein said polypeptide when expressed in a cell modulates Wnt signaling, Dkk activity, LRP5 activity and/or LRP6 activity.

10. The polypeptide of claim 9, wherein said polypeptide modulates bone mass and/or lipid levels when expressed in a subject.

11. A vector comprising a nucleic acid of claims 1 to 8.

12. A cell comprising the vector of claim 11.

13. The cell of claim 12, wherein said cell is a cancer cell, a liver cell or a bone cell.

14. A polypeptide or biologically active fragment thereof derived from LRP5 comprising at least one amino acid change of Table 2, G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V.

15. The polypeptide or biologically active fragment of claim 14, wherein said protein or biologically active fragment comprises at least one amino acid change of G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V.

16. A polypeptide or biologically active fragment thereof derived from LRP6 comprising at least one amino acid change of Table 2, G171V, A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V when the amino acid change is expressed in an equivalent position in LRP6.

17. The polypeptide or biologically active fragment of claim 16, wherein said protein or biologically active fragment comprises at least one amino acid change of G171V,

A214V, A65V, M282V, G171K, G171F, G171I, G171Q, L200V, T201V, I202V, or S127V.

18. A polypeptide or biologically active fragment which when expressed in a subject has a HBM-like phenotype comprising at least one amino acid mutation in propeller 1 with the proviso that if the mutation is GV171 that a second mutation which maintains the HBM-like phenotype is also present.

19. The polypeptide or biologically active fragment of claim 18, wherein said polypeptide is derived from LRP5, LRP6 or HBM.

20. The polypeptide or biologically active fragment of claims 14-19, wherein the amino acid change is G171V, A214V, A65V, M282V, G171K, G171F, G171I or G171Q of LRP5 or an equivalent position in LRP6.

21. An antibody or immunogenic fragment thereof which binds to a polypeptide or antigenic fragment thereof of claims 14 to 20.

22. The antibody or immunogenic fragment thereof of claim 21, wherein the antibody is a monoclonal antibody, a chimeric antibody, a bispecific antibody, a humanized antibody, a primatized® antibody, a human antibody, or a labeled antibody.

23. An antibody which binds to a polypeptide comprising ^{208}KLYWADAKLSFIHRAN^{223}, ^{277}ALYSPMDIQVLSQER^{291}, ^{61}GLEDAAAVDFQFSKGA^{73}, ^{234}EGSLTHPFALTLSG^{247}, ^{249}TLYWTDWQTRSIHACN^{264}, ^{144}VLFWQDLDQPRAI^{156}, ^{194}IYWPNGLTIDLEEQKLY^{210}, ^{34}LLLFANRRDVRLVD^{47}, ^{75}GAVYWTDVSEEAIKQ^{89}, ^{121}KLYWTDSETNRIEVA^{135} of LRP5 or an equivalent domain on LRP6 or variants thereof.

24. An antibody which binds to a polypeptide comprising ^{969}LILPLHGLRNVKAIDYDPLDKFIYW^{993}, ^{989}KFIYWVDGRQNIKRAKDDGTQPFVL^{1013}, ^{1009}QPFVLTSLSQGQNPDRQPHDLSIDI^{1033}, ^{1029}LSIDIYSRTLFWTCEATNTINVHRL^{1053}, ^{1049}NVHRLSGEAMGVVLRGDRDKPRAIV^{1073}, ^{1253}CGEPPTCSPDQFAC^{1266},

^{1278}WRCDGFPECDDQSDEEGC^{1295}, ^{1316}RCDGEADCQDRSDEADC^{1332}, ^{1370}CEITKPPSDDSPAH^{1383} of LRP5 or an equivalent domain on LRP6 or variants thereof, wherein said antibody modulates binding of LRP5, HBM, LRP6 or variants thereof to Dkk.

25. A method of diagnosing a HBM-like phenotype in a subject comprising

(A) obtaining a biological sample from the subject;

(B) exposing the sample to an antibody or an immunogenic fragment of claims 21-24; and

(C) detecting whether the antibody bound a protein from the biological sample from the subject to determine whether the subject has a HBM-like phenotype.

26. A composition for modulating bone mass and/or lipid levels in a subject comprising a therapeutically effective amount of an antibody of claims 21-24 and a pharmaceutically acceptable carrier.

27. An antibody or an immunogenic fragment thereof of claims 21-24, wherein the antibody or immunogenic fragment thereof can (1) discriminate between LRP5 and an HBM-like protein, (2) discriminate between LRP6 and an HBM-like protein, or (3) discriminate between HBM and an HBM-like protein.

28. A transgenic animal having somatic and/or germ cells comprising a nucleic acid which comprises a promoter region that directs protein expression in animal and/or human cells operably linked to a nucleic acid of claims 1 to 8, and wherein said transgenic animal has at least three bone parameters modulated by the expression of said nucleic acid.

29. The transgenic animal of claim 28, wherein the promoter region is selected from the group consisting of CMV, RSV, SV40, and EF-1a, CMVβbActin, histone, type I collagen, TGFβ1, SX2, cfos/cjun, Cbfa1, Fra/Jun, Dlx5, osteocalcin, osteopontin, bone sialoprotein, and collagenase promoter regions.

30. A transgenic animal having somatic and/or germ cells comprising a nucleic

acid which comprises a sequence which encodes a polypeptide of claims 9 or 10, and wherein the nucleic acid further comprises an operably linked promoter region that directs protein expression in animal and/or human cells, and wherein the transgenic animal has at least three bone parameters modulated by the expression of said nucleic acid.

31. An animal embryo comprising a nucleic acid comprising a promoter region that directs protein expression in animal and/or human cells operably linked to a nucleic acid of claims 1 to 8.

32. An animal or human cell transfected with a nucleic acid which comprises a promoter region that directs protein expression in animal and/or human cells operably linked to a nucleic acid of claims 1 to 8.

33. The transgenic animal of claim 28, wherein a human HBM-like protein is expressed and passes the human *HBM*-like gene to its offspring.

34. A transgenic animal produced from the transgenic animal of claim 33 or its offspring.

35. An animal model for the study of bone density modulation and/or lipid level modulation comprising a first group of animals composed of the transgenic animal of claim 28 and a second group of control animals.

36. The animal model of claim 35, wherein the group of transgenic animals have cells which comprise a nucleic acid encoding human an HBM-like protein or biologically active polypeptide fragment thereof.

37. An animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animals of claim 30 and a second group of control animals.

38. A method of identifying agents which modulate the activity of an HBM-like

nucleic acid comprising:

(a) transfecting a cell with a vector of claim 11;

(b) exposing the transfected cell of step (a) to a compound; and

(c) determining whether the compound modulates the activity of the HBM-like nucleic acid.

39. A method of identifying agents which modulate the activity of an HBM-like protein comprising:

(a) transfecting a cell with a vector of claim 11;

(b) exposing the transfected cell of step (a) to a compound; and

(c) determining whether the compound modulates the activity of the HBM-like protein.

40. The method of claim 39, wherein the compound is a hormone, a growth factor, a peptide, RNA, shRNA, siRNA, DNA, a mineral, a vitamin, a natural product, or a synthetic organic compound.

41. A method for identifying compounds which modulate the interaction of Dkk with the Wnt signaling pathway comprising:

(a) transfecting cells with constructs containing a nucleic acid of claims 1 to claim 8;

(b) assessing changes in expression of a reporter element linked to a Wnt-responsive promoter; and

(c) identifying as a Dkk/Wnt interaction modulating compound any compound which alters reporter gene expression compared with cells transfected with a Dkk construct alone.

42. The method according to Claim 41, wherein the cells are cancer cells, liver cells or bone cells.

43. The method according to Claim 42, wherein the cells are U2-OS, HOB-03-CE6, or HEK293 cells.

44. The method according to Claim 41, wherein the reporter element used is TCF-luciferase, tk-Renilla, or a combination thereof.

45. A method of diagnosing a subject as expressing a nucleic acid comprising a nucleotide change of Tables 2 or 3, the method comprising the steps of:

(A) obtaining a biological sample from the subject; and

(B) assaying for the presence of the nucleotide change which results in HBM phenotype.

46. A method for identifying agents which modulate LRP5, LRP6, or HBM comprising the steps of:

(A) providing cells according to claim 32;

(B) exposing the cells to a test compound; and

(C) measuring the expression of LRP5, LRP6 or HBM respectively.

47. The method for identifying agents of claim 42, further comprising a step of determining whether the agent further modulates bone mass and/or lipid levels.

48. An agent identified by the method of claims 46 or 47.

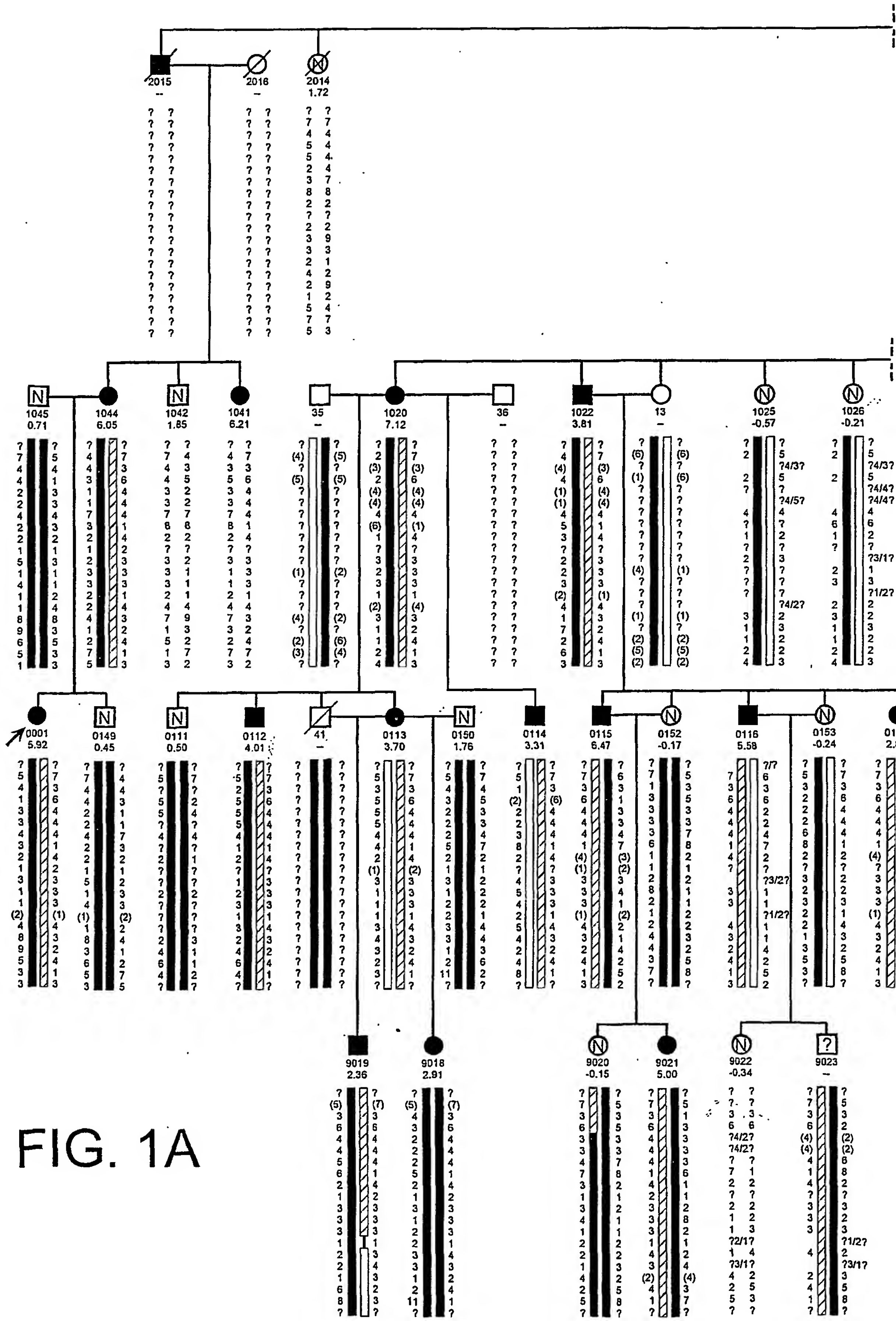


FIG. 1A

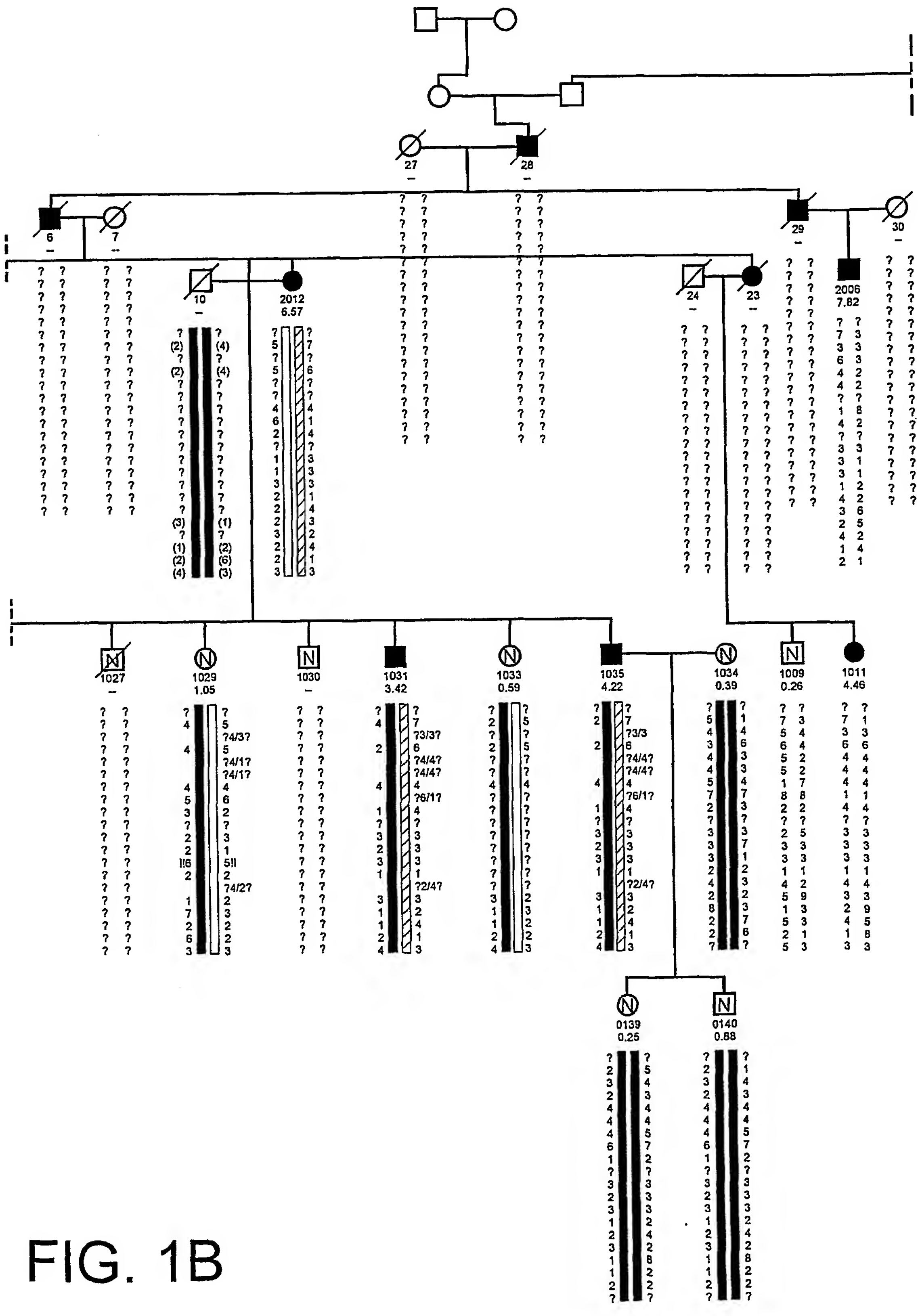


FIG. 1B

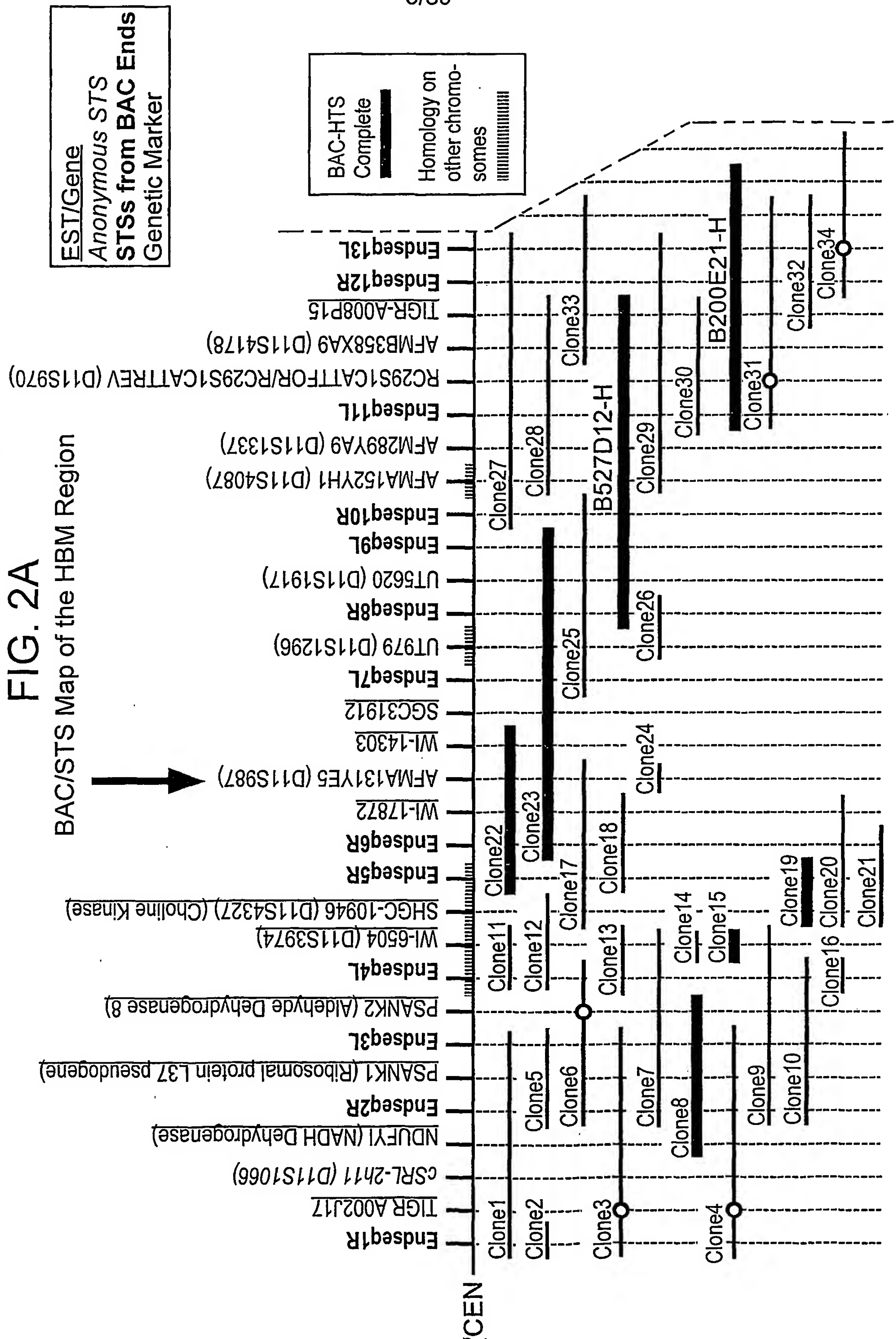
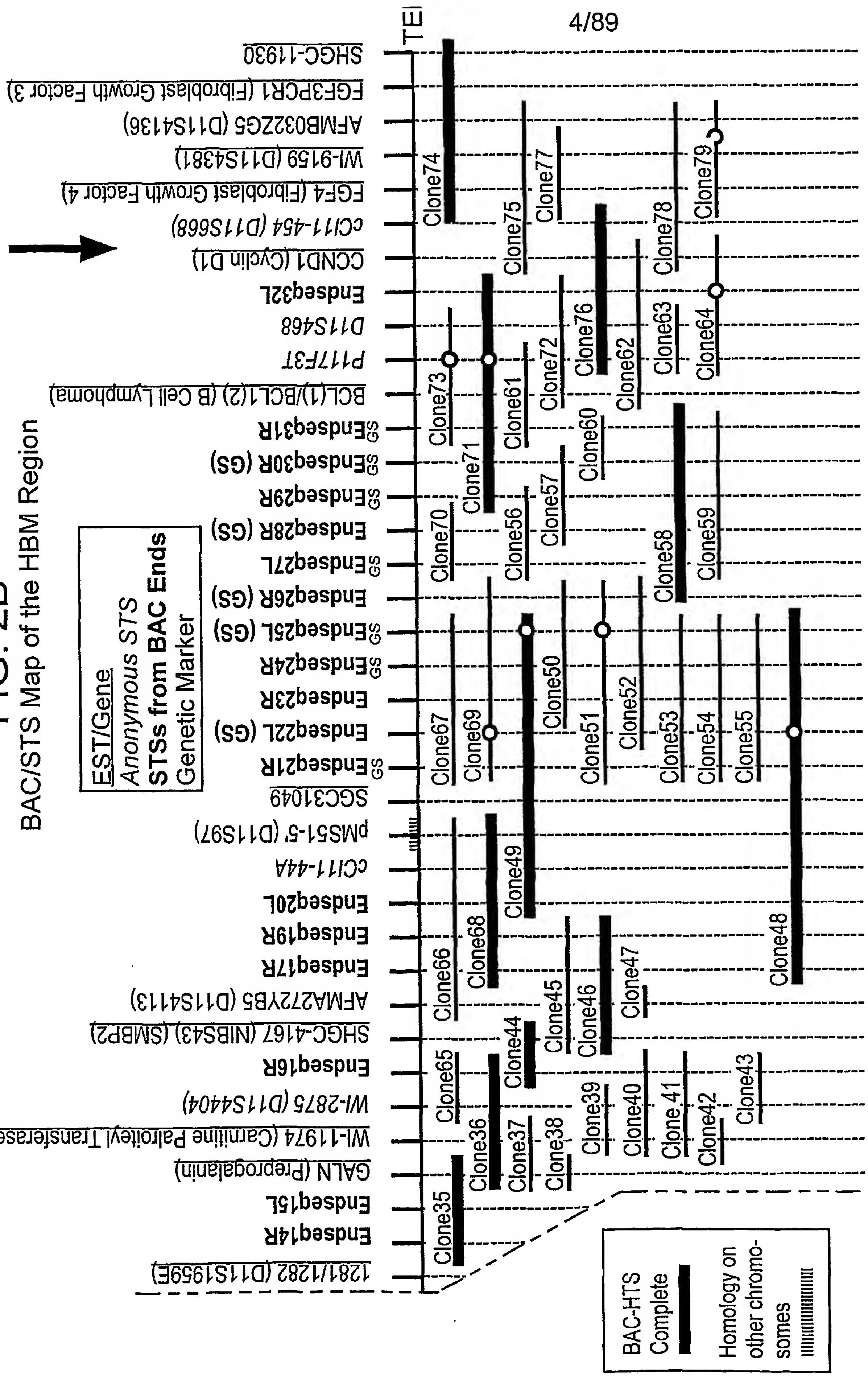


FIG. 2A

BAC/STS Map of the HBM Region

FIG. 2B

BAC/STS Map of the HBM Region



Exon 1
ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCG GGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCGCCGCCCGGGCCG CCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC TGCCCGGCCCCCGCCGCGGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549
gccccacag**CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGC TGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGC GGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGC CGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCT GAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGG TCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACT GGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGC ACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCC ATCGCCTTGGACCCCGCTCACGG**gtaaaccctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945
ccccgtcacag**GTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTG AGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCG GACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG GACGGCTCGTTCCG**gtaggtacccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850
tccctgactgcag**GCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCC CTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGC TCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGAT CCTGAGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGA GCGGCAGCCTTTCT**gtgagtgccgg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088
tttctcag**TCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTG TGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACG GGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAG**gtgaggcggtgg gacg

FIG. 3A

... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100
ctccacag**GAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTAC
GGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGG
TGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGG
GCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCG
TACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAA
CGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTG
GACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCA
CCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCC
ATCGCACTGCACCCCGTGATGGG**gtaagacgggc

..... 3211 nt .....

Exon 7 Coordinates: 527d12_Contig309G 11311-11482
ttcttctccag**CCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGA
GTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTC
CCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGC
TCTACTGGGGAGACGCCAAGACAGACAAGATCGAG**gtgaggctcctgtgg

...... 13445 nt .....

Exon 8 Coordinates: 527d12_Contig309G 24927-25143
ccgtcctgcag**GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGA
GGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCAT
CTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGG
TCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGG
GGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCG**gtgagtccggggggtc

....2826 nt ......

Exon 9 Coordinates: 527d12_Contig309G 27969-28256
gttcgcttccag**GAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCA
CCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGG
CCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTT
CTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGAC
CAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTC
AGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGT
CAGCCTGAAG**gtagcgtgggc

......3102.....

FIG. 3B

Exon 10 Coordinates: 527d12_Contig309G 31358-31582
cctgctgccagACCATCAGCCGCGCCTTCATGAACGGAGCTCGGTGGAGCA
CGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTG
GATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGA
AGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGG
ACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGgtaagtgtt
tgcctgtc

......1297 nt......

Exon 11 Coordinates: 527d12_Contig309G 32879-33064
gtgccttccagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCG
TGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAG
GTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTC
TACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTG
Ggtgagggccgggct

.......2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454
gtgttcatgcagGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG
TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAAT
CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCAC
CCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCA
CTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCA
GTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCT
GCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCgtaag
tgcctcatggt

.......2006 nt......

Exon 13 Coordinates: 527d12_Contig309G 37460-37659
gcctcctctaCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG
TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCT
GCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAA
GTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGA
CGACGGGACCCAGgcaggtgccctgtgg

......6965 nt......

FIG. 3C

Exon 14 Coordinates: 527d12_Contig309G 44624-44832
ctttgtcttacag**CCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGAC AGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGG GGAAGCCATGGGGGTGGTGCTGCGTGGGACCGCGACAAGCCCAGGG CCATCGTCGTCAACGCGGAGCGAGG**gtaggaggccaac

……1404 nt…..

Exon 15 Coordinates: 527d12_Contig309G 46236-46427
ccaccctcccgcag**GTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAA GATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCA CCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGG GCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGT GACCTGTCAG**gtacgcgccccgg

…..686 nt…..

Exon 16 Coordinates: 527d12_Contig309G 47113-47322
ggctgcttgcag**GGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCA GCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCG CCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGC GGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAG TGGAGGAAGTCAGCCTGGAGGAGTTCT**gtacgtgggggc

…..3884 nt……

Exon 17 Coordinates: 527d12_Contig309G 51206-51331
ttgtctttgcag**CAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACA TCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCC ACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAG**gtaggtgtgacctaggtgc

….3905 nt…….

Exon 18 Coordinates: 527d12_Contig309G 55236-55472
gttctcctctgtccctcccccag**AGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGT GCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGG CTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGT GCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGC GCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAG GTGGACTGTGACG**gtgaggccctcc

…….3052 nt…..

FIG. 3D

Exon 19 Coordinates: 527d12_Contig309G 58524-58634
tctccttgcag**CCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGT GTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACG GCTCCGACGAGCTCATGTGTG**gtgagccagctt

........1448 nt......

Exon 20 Coordinates: 527d12_Contig309G 60082-60319
gtttgtctctggcag**AAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACA GCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCAT GGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGC GGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGC ACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCT TCACAG**gtaaggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552
cttccctgccag**GCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTG ATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCAC AGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCC GCCG**gtgaggggcggg

......6513 nt......

Exon 22 Coordinates: 527d12_Contig309G 68065-68162
ttggctctcctcag**ATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCC TGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGA GACCGTACAG**gtaggacatcccctgcag

.......2273 nt.....

FIG. 3E

Exon 23 Coordinates: 527d12_Contig309G 70435-70901
tcaaacattccggccactgcgagaccgtacag**GCCCTACATCATTCGAGGAATGGCGCCCC
CGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCC
AGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCA
GACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCG
GAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCAT
CTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCC**TGACCTCGGC
CGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAA
AGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAA
AAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTT
TGTACAGTGGAGAAATATTTATAAACTTAATTTTGTAAAACA

FIG. 3F

Model for a LDL Receptor-Related protein, Zmax1

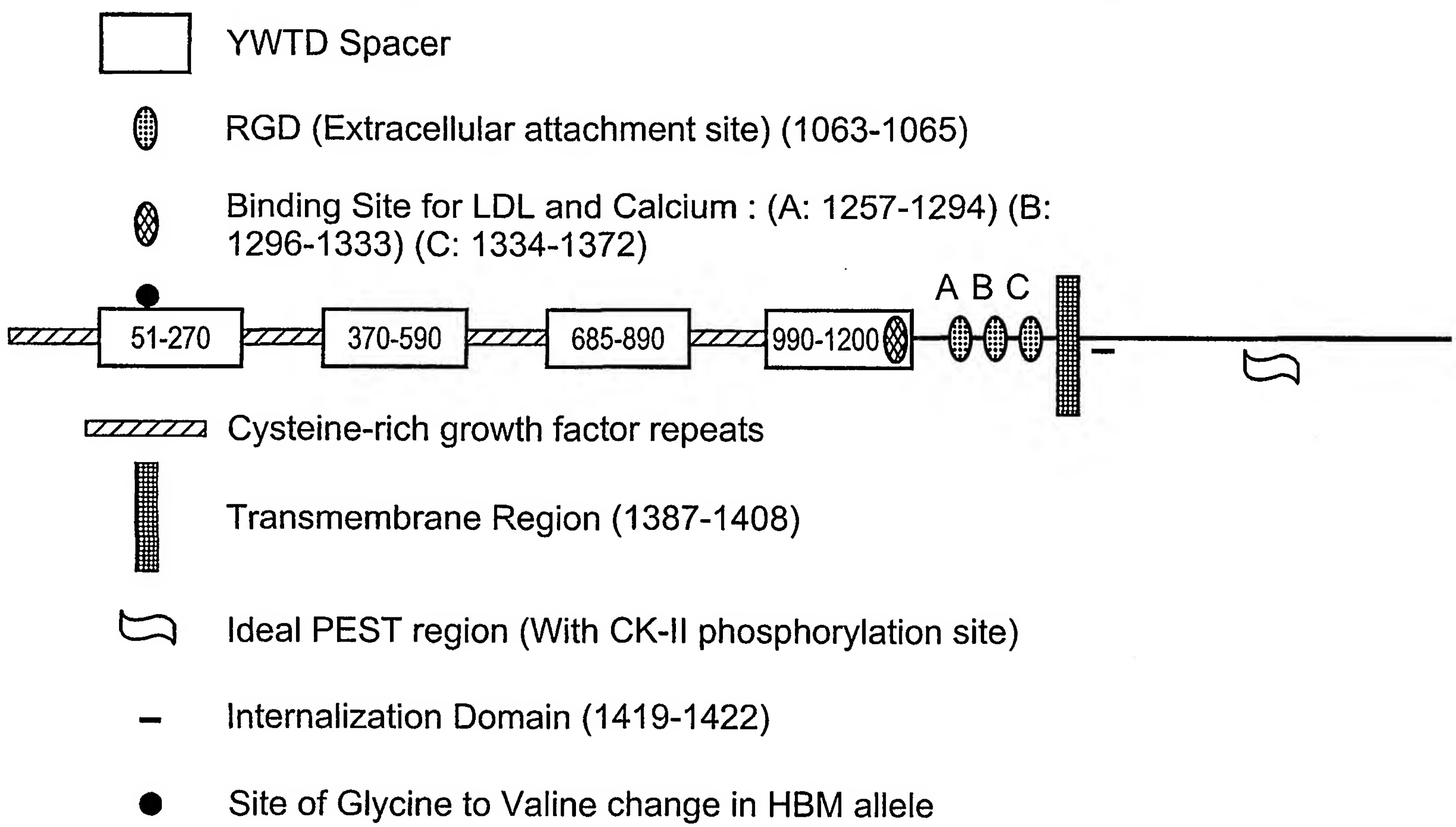


FIG. 4

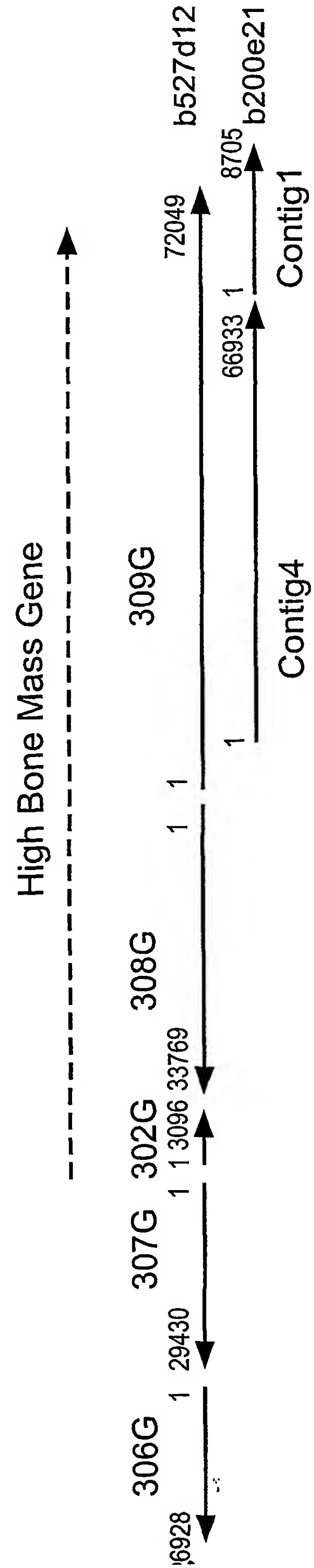

High Bone Mass Gene
306G
307G
302G
308G
309G
6928
1
29430
1
1
3096
33769
1
1
72049
b527d12
1
Contig4
66933
1
Contig1
8705
b200e21

FIG. 5

FIG. 6A

```
  1  ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGCCCGTCCGGCC   60
 61  GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT  120
  1                     M  E  A  A  P  P  G  P  P  W  P  L  L  L  L  L  L   17

121  GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT  180
 18   L  L  L  A  L  C  G  C  P  A  P  A  A  A  S  P  L  L  L  F   37

181  TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT  240
 38   A  N  R  R  D  V  R  L  V  D  A  G  G  V  K  L  E  S  T  I   57

241  CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT  300
 58   V  V  S  G  L  E  D  A  A  A  V  D  F  Q  F  S  K  G  A  V   77

301  GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC  360
 78   Y  W  T  D  V  S  E  E  A  I  K  Q  T  Y  L  N  Q  T  G  A   97

361  CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG  420
 98   A  V  Q  N  V  V  I  S  G  L  V  S  P  D  G  L  A  C  D  W  117

421  GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT  480
118   V  G  K  K  L  Y  W  T  D  S  E  T  N  R  I  E  V  A  N  L  137

481  CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC  540
138   N  G  T  S  R  K  V  L  F  W  Q  D  L  D  Q  P  R  A  I  A  157

541  CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA  600
158   L  D  P  A  H  G  Y  M  Y  W  T  D  W  G  E  T  P  R  I  E  177
```

FIG. 6B

```
601  GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC  660
178   R  A  G  M  D  G  S  T  R  K  I  I  V  D  S  D  I  Y  W  P   197

661  CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG  720
198   N  G  L  T  I  D  L  E  E  Q  K  L  Y  W  A  D  A  K  L  S   217

721  CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT  780
218   F  I  H  R  A  N  L  D  G  S  F  R  Q  K  V  V  E  G  S  L   237

781  GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC  840
238   T  H  P  F  A  L  T  L  S  G  D  T  L  Y  W  T  D  W  Q  T   257

841  CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC  900
258   R  S  I  H  A  C  N  K  R  T  G  G  K  R  K  E  I  L  S  A   277

901  CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC  960
278   L  Y  S  P  M  D  I  Q  V  L  S  Q  E  R  Q  P  F  F  H  T   297

961  TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC  1020
298   R  C  E  E  D  N  G  G  C  S  H  L  C  L  L  S  P  S  E  P   317

1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA  1080
318   F  Y  T  C  A  C  P  T  G  V  Q  L  Q  D  N  G  R  T  C  K   337

1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT  1140
338   A  G  A  E  E  V  L  L  L  A  R  R  T  D  L  R  R  I  S  L   357
```

FIG. 6C

```
1141  GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC  1200
358    D  T  P  D  F  T  D  I  V  L  Q  V  D  D  I  R  H  A  I  A   377

1201  CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT  1260
378    I  D  Y  D  P  L  E  G  Y  V  Y  W  T  D  D  E  V  R  A  I   397

1261  CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA  1320
398    R  R  A  Y  L  D  G  S  G  A  Q  T  L  V  N  T  E  I  N  D   417

1321  CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC  1380
418    P  D  G  I  A  V  D  W  V  A  R  N  L  Y  W  T  D  T  G  T   437

1381  GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA  1440
438    D  R  I  E  V  T  R  L  N  G  T  S  R  K  I  L  V  S  E  D   457

1441  CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA  1500
458    L  D  E  P  R  A  I  A  L  H  P  V  M  G  L  M  Y  W  T  D   477

1501  CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT  1560
478    W  G  E  N  P  K  I  E  C  A  N  L  D  G  Q  E  R  R  V  L   497

1561  GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT  1620
498    V  N  A  S  L  G  W  P  N  G  L  A  L  D  L  Q  E  G  K  L   517

1621  CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG  1680
518    Y  W  G  D  A  K  T  D  K  I  E  V  I  N  V  D  G  T  K  R   537
```

FIG. 6D

```
1681  GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT  1740
 538   R  T  L  L  E  D  K  L  P  H  I  F  G  F  T  L  L  G  D  F   557

1741  CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG  1800
 558   I  Y  W  T  D  W  Q  R  R  S  I  E  R  V  H  K  V  K  A  S   577

1801  CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC  1860
 578   R  D  V  I  I  D  Q  L  P  D  L  M  G  L  K  A  V  N  V  A   597

1861  CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT  1920
 598   K  V  V  G  T  N  P  C  A  D  R  N  G  G  C  S  H  L  C  F   617

1921  CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT  1980
 618   F  T  P  H  A  T  R  C  G  C  P  I  G  L  E  L  L  S  D  M   637

1981  GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG  2040
 638   K  T  C  I  V  P  E  A  F  L  V  F  T  S  R  A  A  I  H  R   657

2041  GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC  2100
 658   I  S  L  E  T  N  N  N  D  V  A  I  P  L  T  G  V  K  E  A   677

2101  CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA  2160
 678   S  A  L  D  F  D  V  S  N  N  H  I  Y  W  T  D  V  S  L  K   697

2161  GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT  2220
 698   T  I  S  R  A  F  M  N  G  S  S  V  E  H  V  V  E  F  G  L   717
```

FIG. 6E

```
2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
 718  D  Y  P  E  G  M  A  V  D  W  M  G  K  N  L  Y  W  A  D  T  737

2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
 738  G  T  N  R  I  E  V  A  R  L  D  G  Q  F  R  Q  V  L  V  W  757

2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
 758  R  D  L  D  N  P  R  S  L  A  L  D  P  T  K  G  Y  I  Y  W  777

2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
 778  T  E  W  G  G  K  P  R  I  V  R  A  F  M  D  G  T  N  C  M  797

2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
 798  T  L  V  D  K  V  G  R  A  N  D  L  T  I  D  Y  A  D  Q  R  817

2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
 818  L  Y  W  T  D  L  D  T  N  M  I  E  S  S  N  M  L  G  Q  E  837

2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
 838  R  V  V  I  A  D  D  L  P  H  P  F  G  L  T  Q  Y  S  D  Y  857

2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
 858  I  Y  W  T  D  W  N  L  H  S  I  E  R  A  D  K  T  S  G  R  877

2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
 878  N  R  T  L  I  Q  G  H  L  D  F  V  M  D  I  L  V  F  H  S  897
```

FIG. 6F

```
2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
 898  S  R  Q  D  G  L  N  D  C  M  H  N  N  G  Q  C  G  Q  L  C  917

2821 CCTTGCCATCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
 918  L  A  I  P  G  G  H  R  C  G  C  A  S  H  Y  T  L  D  P  S  937

2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
 938  S  R  N  C  S  P  P  T  T  F  L  L  F  S  Q  K  S  A  I  S  957

2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
 958  R  M  I  P  D  D  Q  H  S  P  D  L  I  L  P  L  H  G  L  R  977

3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
 978  N  V  K  A  I  D  Y  D  P  L  D  K  F  I  Y  W  V  D  G  R  997

3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
 998  Q  N  I  K  R  A  K  D  D  G  T  Q  P  F  V  L  T  S  L  S  1017

3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
1018  Q  G  Q  N  P  D  R  Q  P  H  D  L  S  I  D  I  Y  S  R  T  1037

3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
1038  L  F  W  T  C  E  A  T  N  T  I  N  V  H  R  L  S  G  E  A  1057

3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
1058  M  G  V  V  L  R  G  D  R  D  K  P  R  A  I  V  V  N  A  E  1077
```

FIG. 6G

```
3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
1078  R  G  Y  L  Y  F  T  N  M  Q  D  R  A  A  K  I  E  R  A  A  1097

3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
1098  L  D  G  T  E  R  E  V  L  F  T  T  G  L  I  R  P  V  A  L  1117

3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
1118  V  V  D  N  T  L  G  K  L  F  W  V  D  A  D  L  K  R  I  E  1137

3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
1138  S  C  D  L  S  G  A  N  R  L  T  L  E  D  A  N  I  V  Q  P  1157

3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
1158  L  G  L  T  I  L  G  K  H  L  Y  W  I  D  R  Q  Q  Q  M  I  1177

3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
1178  E  R  V  E  K  T  T  G  D  K  R  T  R  I  Q  G  R  V  A  H  1197

3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
1198  L  T  G  I  H  A  V  E  E  V  S  L  E  E  F  S  A  H  P  C  1217

3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
1218  A  R  D  N  G  G  C  S  H  I  C  I  A  K  G  D  G  T  P  R  1237

3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
1238  C  S  C  P  V  H  L  V  L  L  Q  N  L  L  T  C  G  E  P  P  1257
```

FIG. 6H

```
3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
1258  T  C  S  P  D  Q  F  A  C  A  T  G  E  I  D  C  I  P  G  A  1277

3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
1278  W  R  C  D  G  F  P  E  C  D  D  Q  S  D  E  E  G  C  P  V  1297

3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
1298  C  S  A  A  Q  F  P  C  A  R  G  Q  C  V  D  L  R  L  R  C  1317

4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
1318  D  G  E  A  D  C  Q  D  R  S  D  E  V  D  C  D  A  I  C  L  1337

4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
1338  P  N  Q  F  R  C  A  S  G  Q  C  V  L  I  K  Q  Q  C  D  S  1357

4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
1358  F  P  D  C  I  D  G  S  D  E  L  M  C  E  I  T  K  P  P  S  1377

4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
1378  D  D  S  P  A  H  S  S  A  I  G  P  V  I  G  I  I  L  S  L  1397

4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
1398  F  V  M  G  G  V  Y  F  V  C  Q  R  V  V  C  Q  R  Y  A  G  1417

4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
1418  A  N  G  P  F  P  H  E  Y  V  S  G  T  P  H  V  P  L  N  F  1437
```

FIG. 6I

```
4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
1438  I  A  P  G  G  S  Q  H  G  P  F  T  G  I  A  C  G  K  S  M  1457

4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
1458  M  S  S  V  S  L  M  G  G  R  G  G  V  P  L  Y  D  R  N  H  1477

4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
1478  V  T  G  A  S  S  S  S  S  S  S  T  K  A  T  L  Y  P  P  I  1497

4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
1498  L  N  P  P  P  S  P  A  T  D  P  S  L  Y  N  M  D  M  F  Y  1517

4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
1518  S  S  N  I  P  A  T  A  R  P  Y  R  P  Y  I  I  R  G  M  A  1537

4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
1538  P  P  T  T  P  C  S  T  D  V  C  D  S  D  Y  S  A  S  R  W  1557

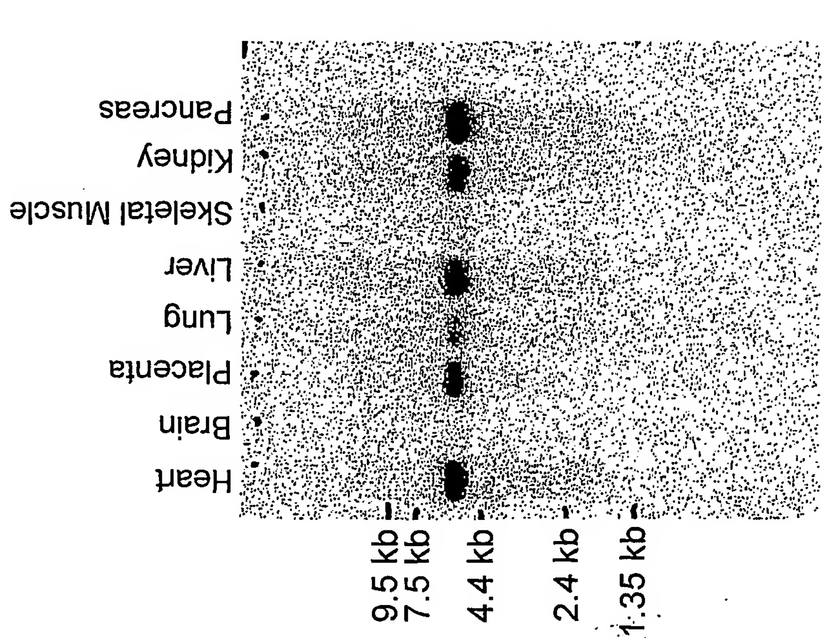
4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
1558  K  A  S  K  Y  Y  L  D  L  N  S  D  S  D  P  Y  P  P  P  P  1577

4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
1578  T  P  H  S  Q  Y  L  S  A  E  D  S  C  P  P  S  P  A  T  E  1597

4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
1598  R  S  Y  F  H  L  F  P  P  P  P  S  P  C  T  D  S  S        1615
```

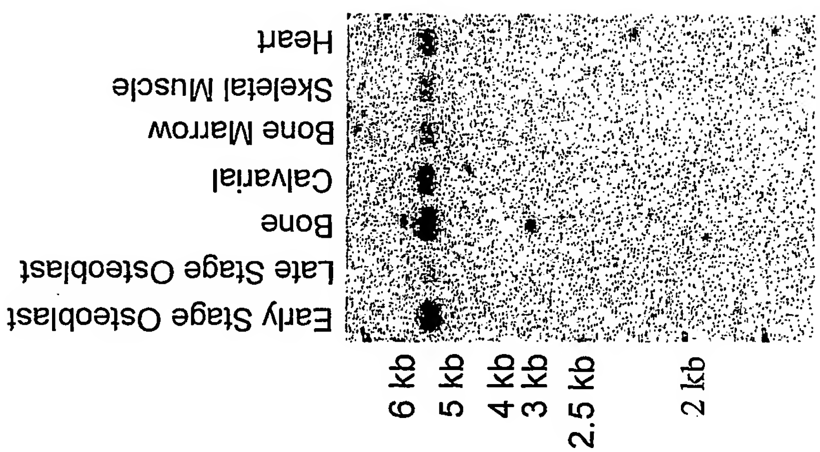
FIG. 6J

```
4921   TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA   4980
4981   AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA   5040
5041   TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT   5100
5101   AAACTTAATTTTGTAAAACA   5120
```



Northern Blot Analysis - Zmax 1

FIG. 7A



Northern Blot Analysis - Zmax 1

FIG. 7B

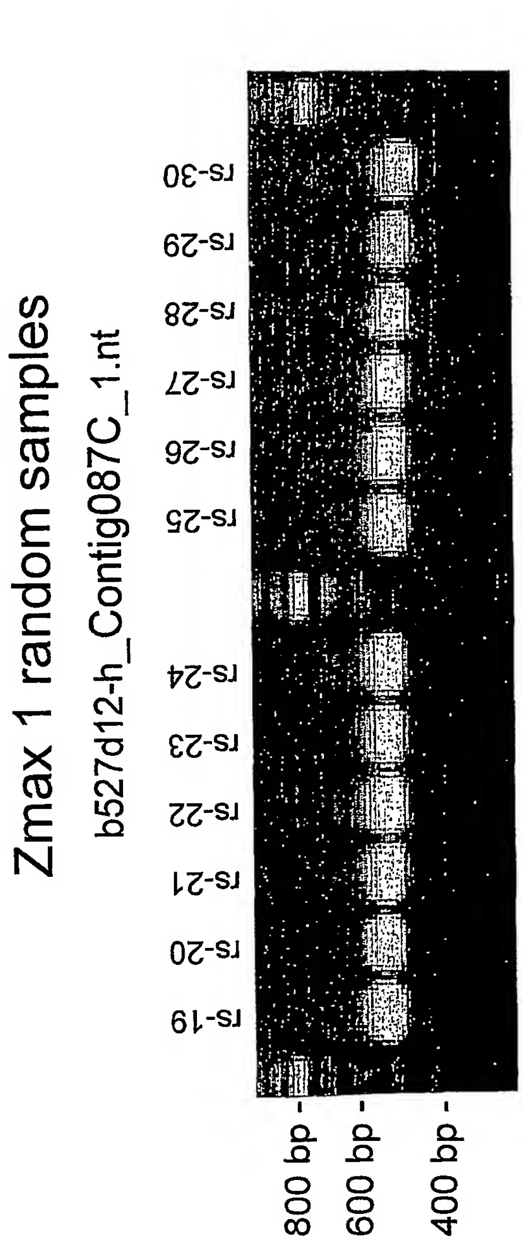

Zmax 1 random samples
b527d12-h_Contig087C_1.nt
rs-19
rs-20
rs-21
rs-22
rs-23
rs-24
rs-25
rs-26
rs-27
rs-28
rs-29
rs-30
800 bp
600 bp
400 bp

FIG. 8

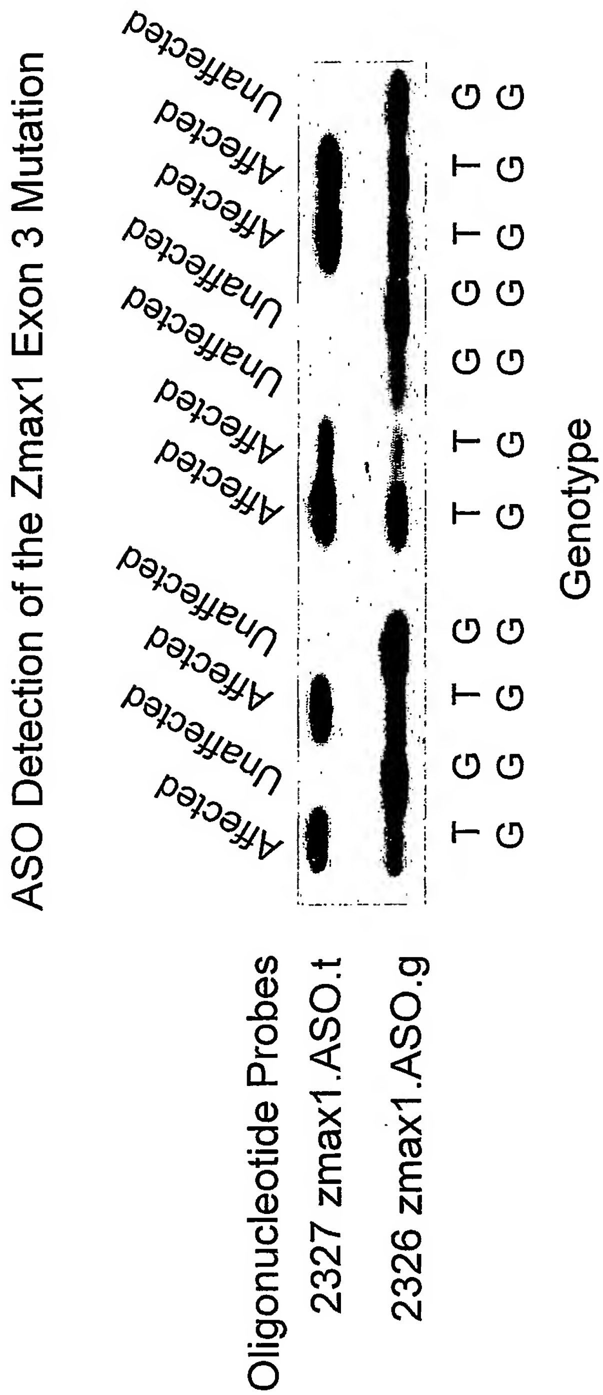

ASO Detection of the Zmax1 Exon 3 Mutation
Affected
Unaffected
Affected
Unaffected
Affected
Affected
Unaffected
Unaffected
Affected
Affected
Unaffected
Oligonucleotide Probes
2327 zmax1.ASO.t
2326 zmax1.ASO.g
T G T G T T G G T T G
G G G G G G G G G G G
Genotype

FIG. 9

Mouse Zmax1 In situ hybridization
100X Magnification

Antisense probe

FIG. 10A

Mouse Zmax1 In situ hybridization
100X Magnification

Sense probe

FIG. 10B

Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

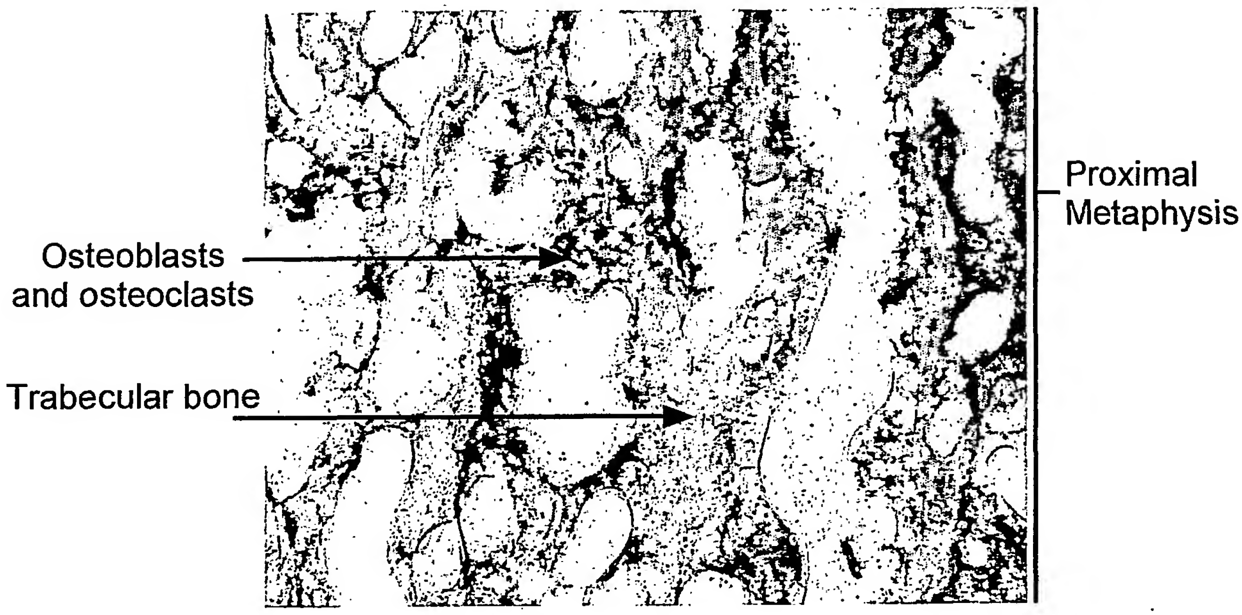


FIG. 11A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

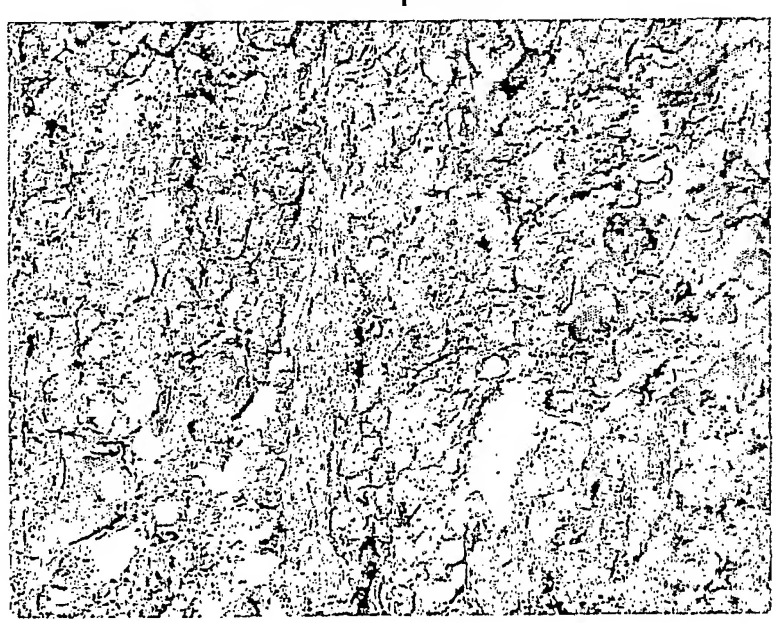


FIG. 11B

Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

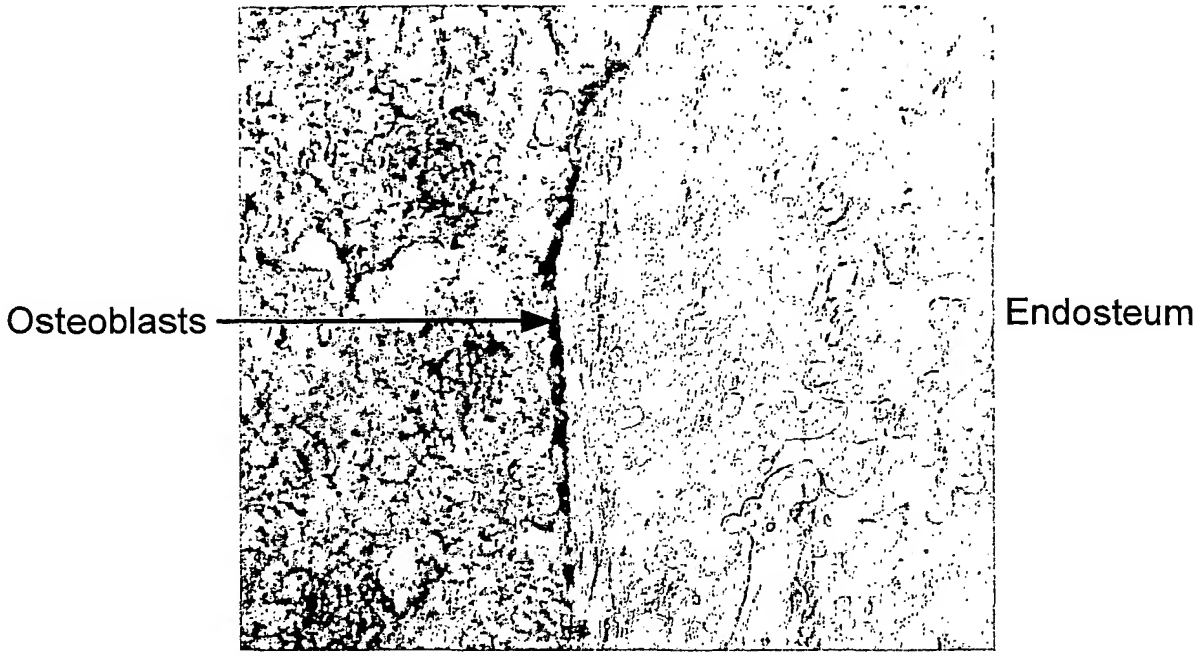


FIG. 12A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

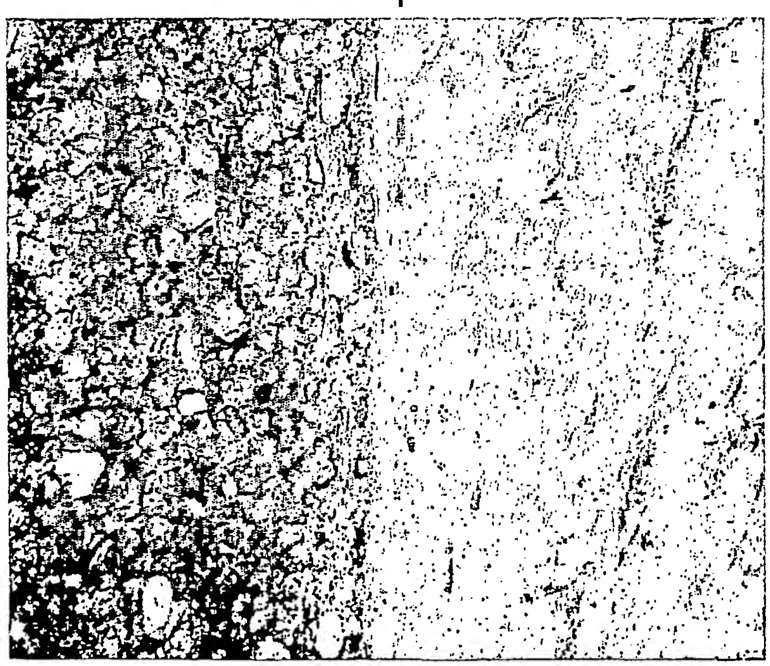
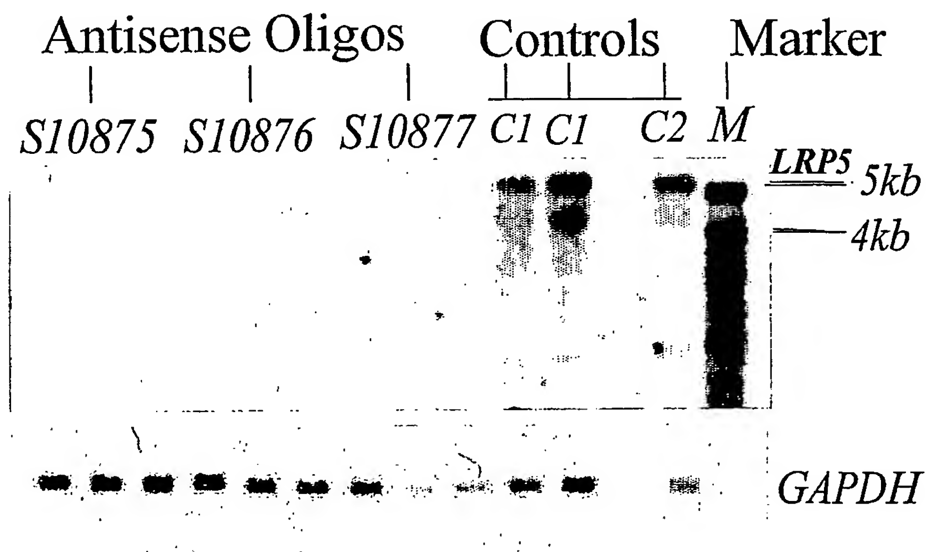


FIG. 12B

Antisense Inhibition of Zmax1 Expression



MC-3T3 cells

FIG. 13

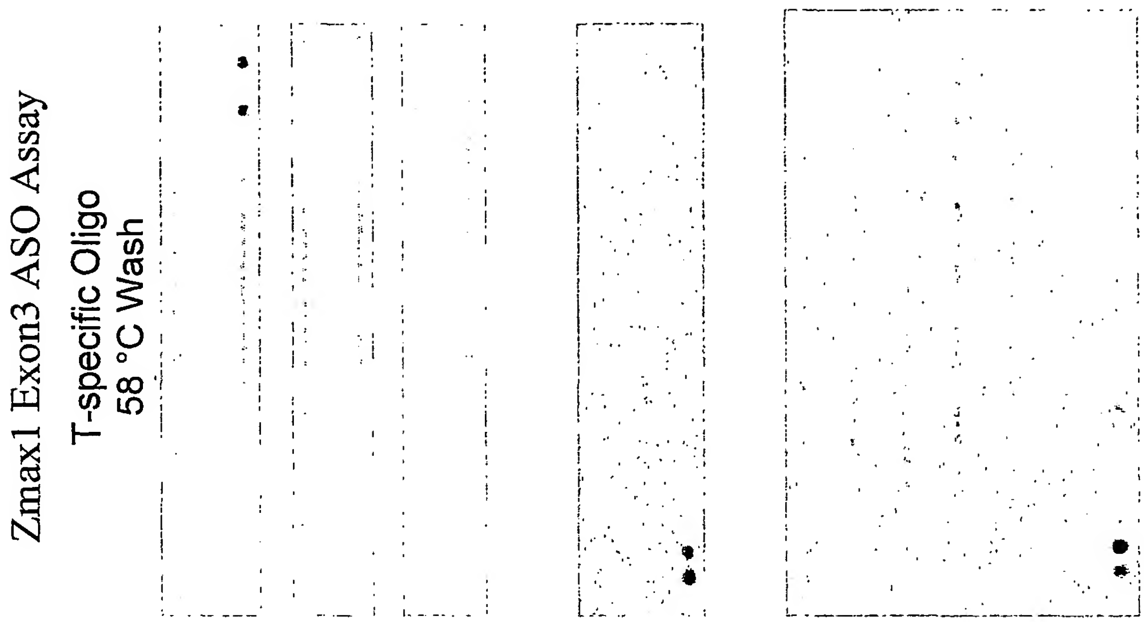


FIG. 14B

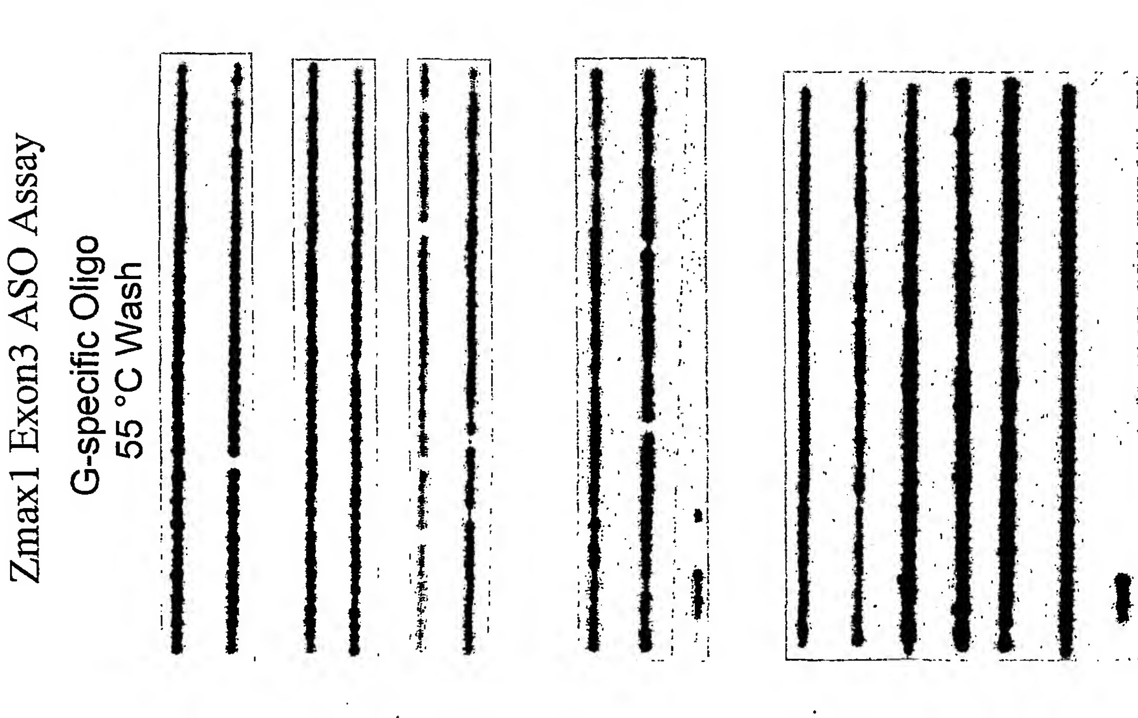


FIG. 14A

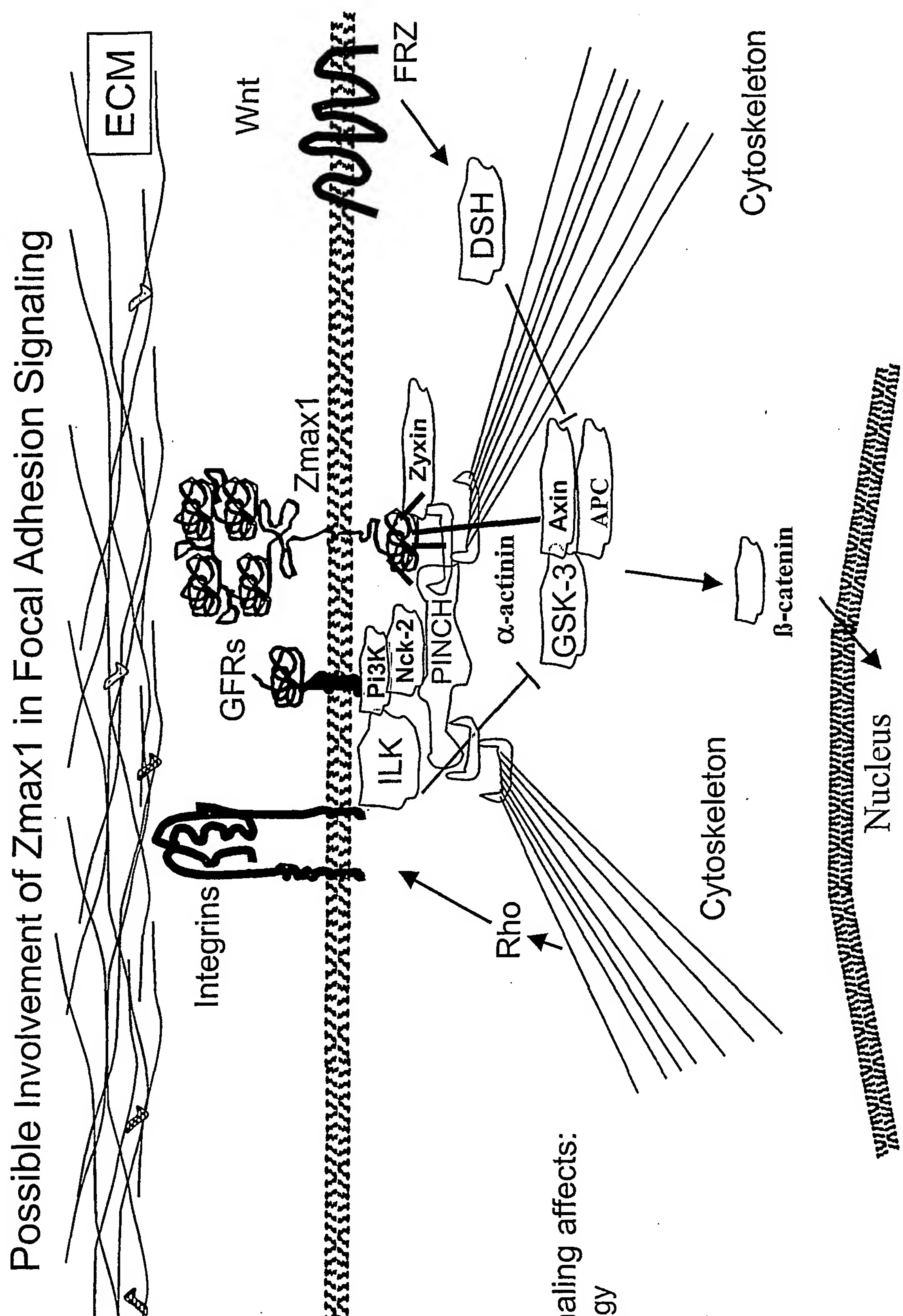

Possible Involvement of Zmax1 in Focal Adhesion Signaling
ECM
Wnt
FRZ
DSH
Cytoskeleton
Zmax1
Zyxin
Axin
APC
GSK-3
α-actinin
β-catenin
GFRs
PI3K
Nck-2
PINCH
ILK
Integrins
Rho
Cytoskeleton
Nucleus
Integrin signaling affects:
Cell morphology
Cell adhesion
Cell migration
Proliferation
Differentiation
Apoptosis

FIG. 15

ZMAX Gene Targeting Knock-in / Knock-out vectors

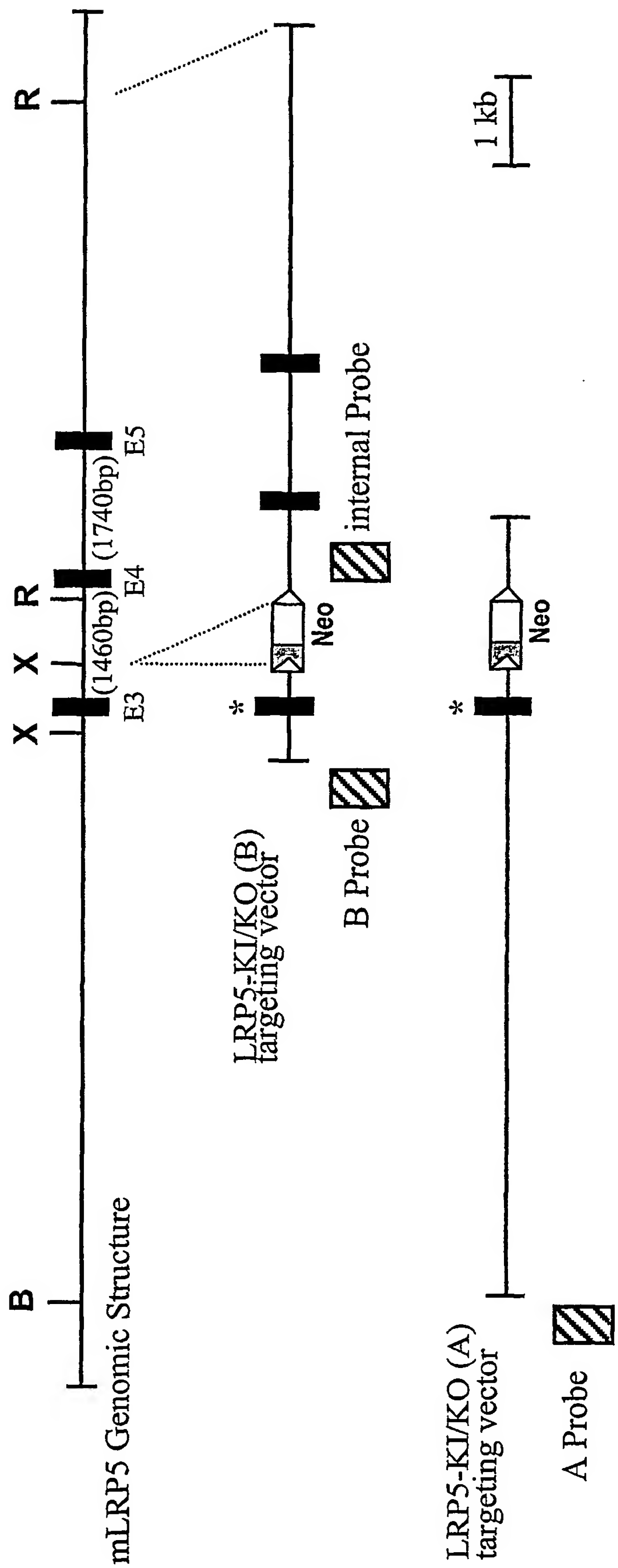


FIG. 16

HBM: Constructs for transgenic mice

Confirmation of expression

*Transient transfection into HOB-02-02 cells**

CMV βActin		Type I collagen	
HBM	Zmax1	HBM	Zmax1
X 1,000	X 1,000	X 10	X 10

**Fold increase compared to Zmax1*
in cells transfected with empty vector

FIG. 17

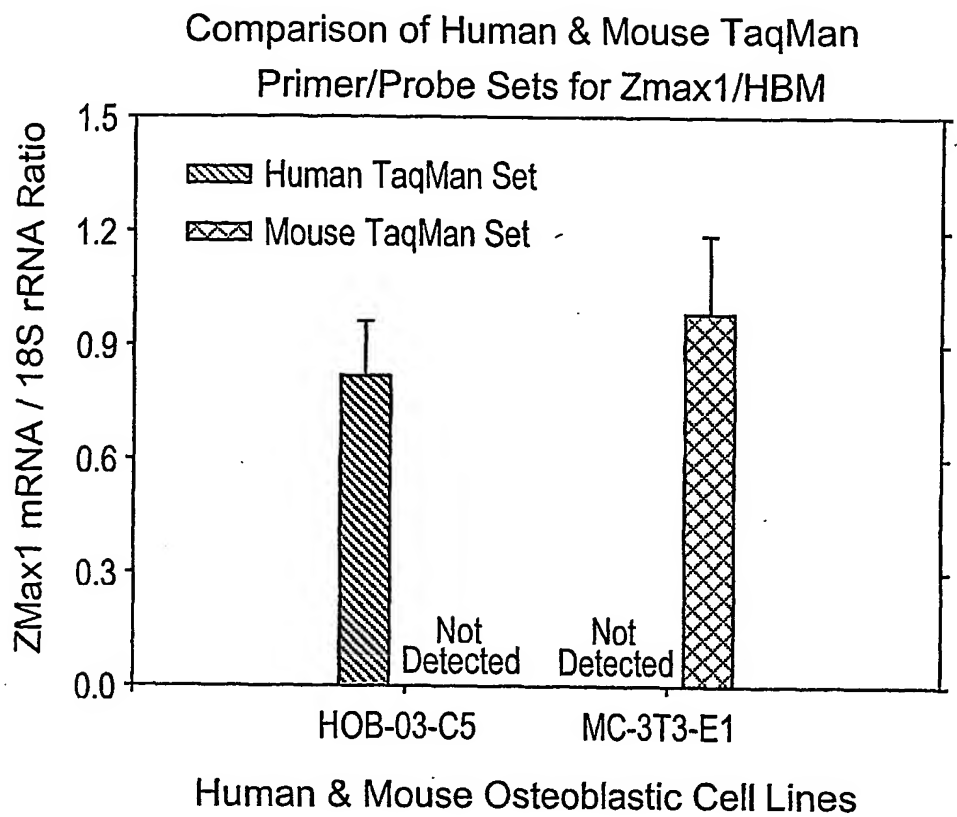

Comparison of Human & Mouse TaqMan
Primer/Probe Sets for Zmax1/HBM
ZMax1 mRNA / 18S rRNA Ratio
1.5
1.2
0.9
0.6
0.3
0.0
Human TaqMan Set
Mouse TaqMan Set
Not Detected
Not Detected
HOB-03-C5
MC-3T3-E1
Human & Mouse Osteoblastic Cell Lines

FIG. 18

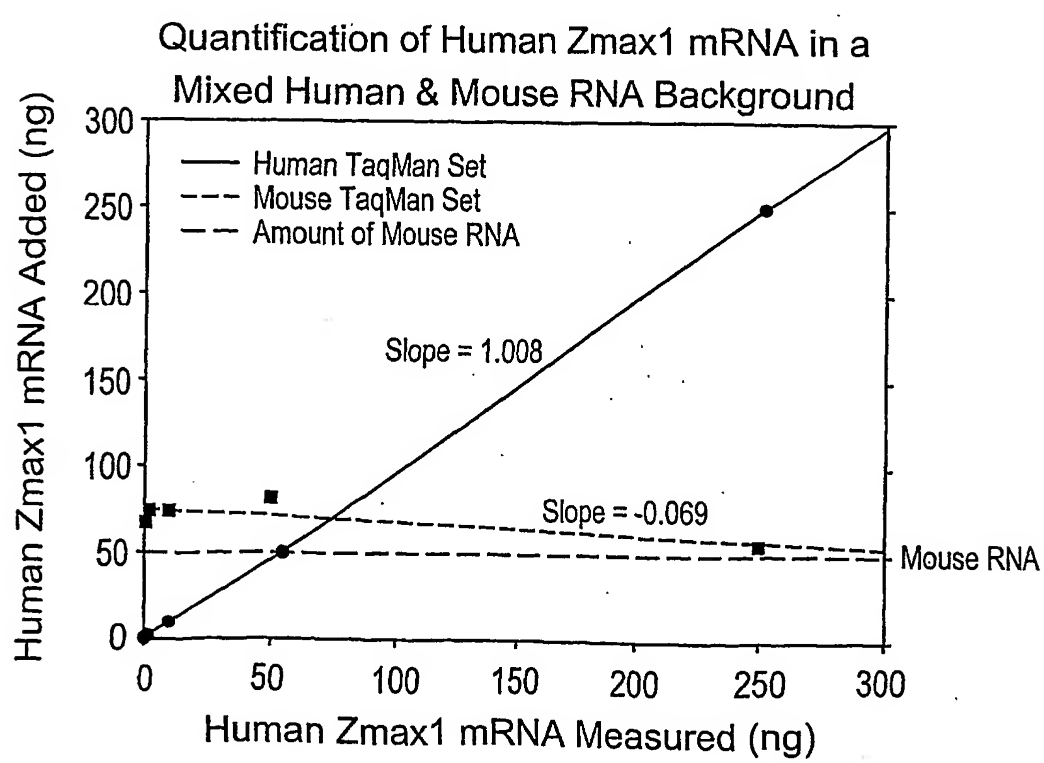

Quantification of Human Zmax1 mRNA in a
Mixed Human & Mouse RNA Background
Human Zmax1 mRNA Added (ng)
300
250
200
150
100
50
0
Human TaqMan Set
Mouse TaqMan Set
Amount of Mouse RNA
Slope = 1.008
Slope = -0.069
Mouse RNA
0
50
100
150
200
250
300
Human Zmax1 mRNA Measured (ng)

FIG. 19

HBM: Transgenic mice

*mRNA expression by Taqman analysis**

	Tissue						
Line	Tibia	Femur	Heart	Gonad	Brain	Kidney	Liver
HBMMCBA							
2	7-10		20-90	2-30	6-11	5-9	<1
13	1-2		6-7	3-4	5-6	<1	<1
18	10-11						
HBMMTIC							
19	7-8	19-20	1				1
35	1	1	0				0

* relative to Zmax1 in HOB-03-C5

FIG. 20

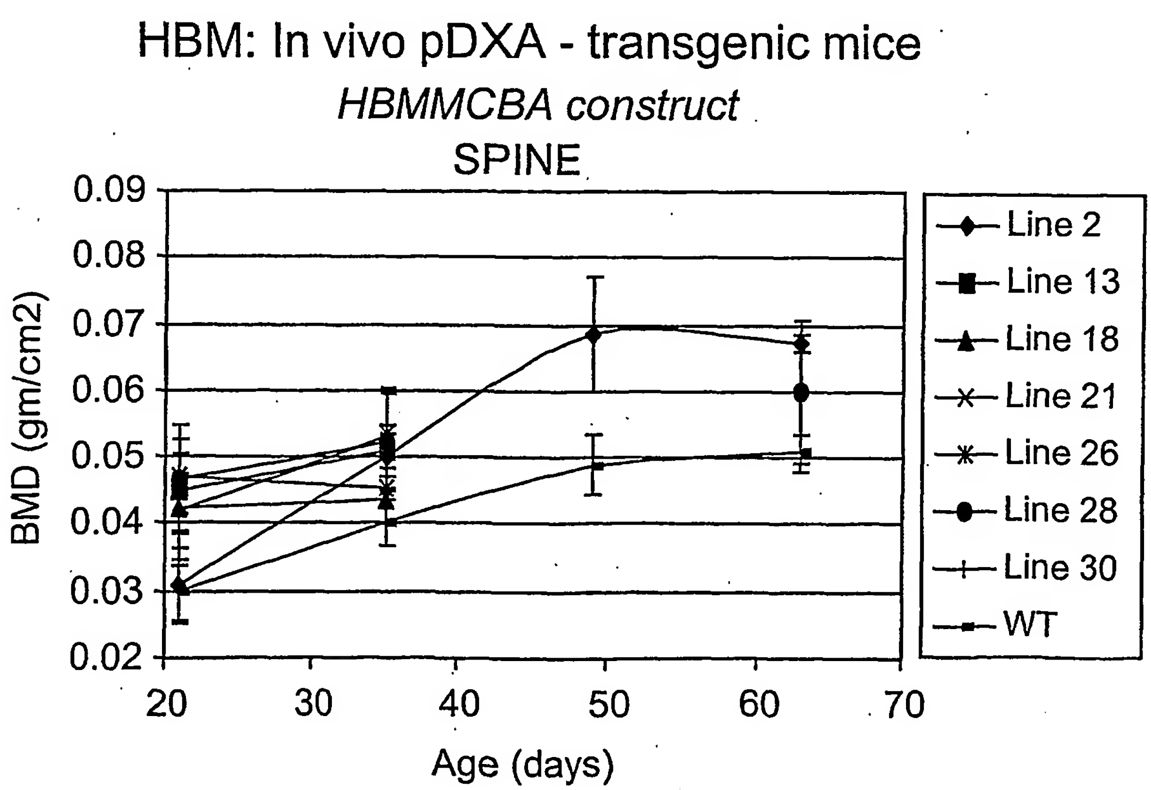


FIG. 21A

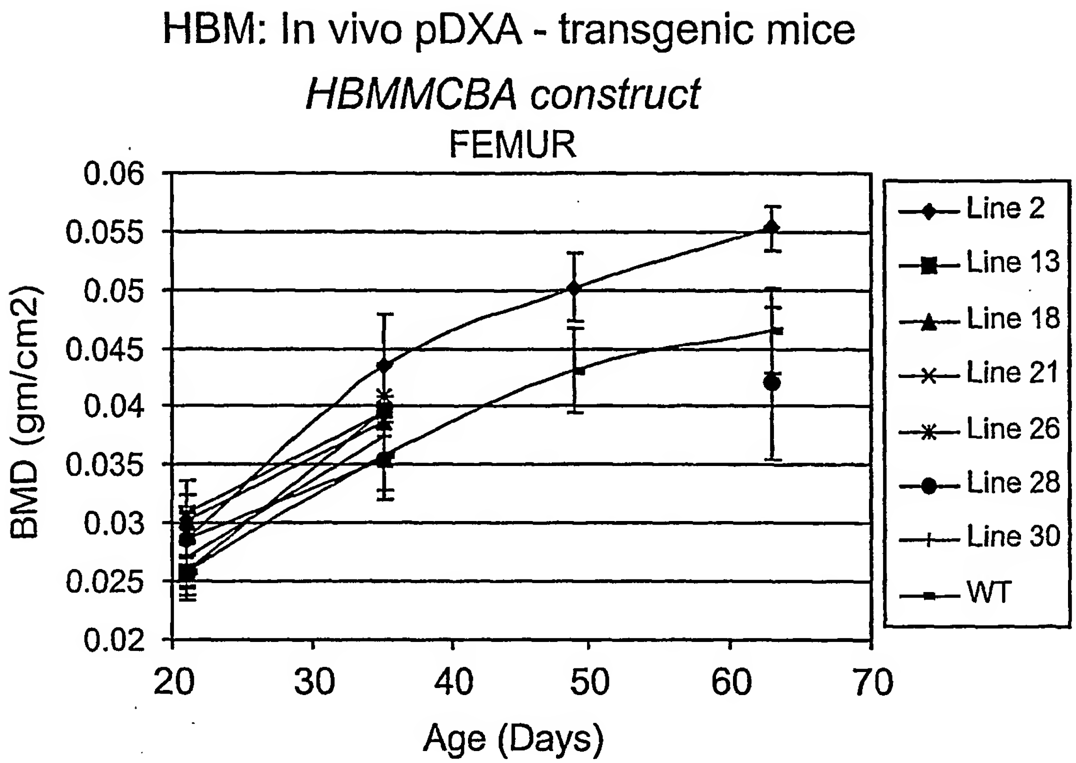


FIG. 21B

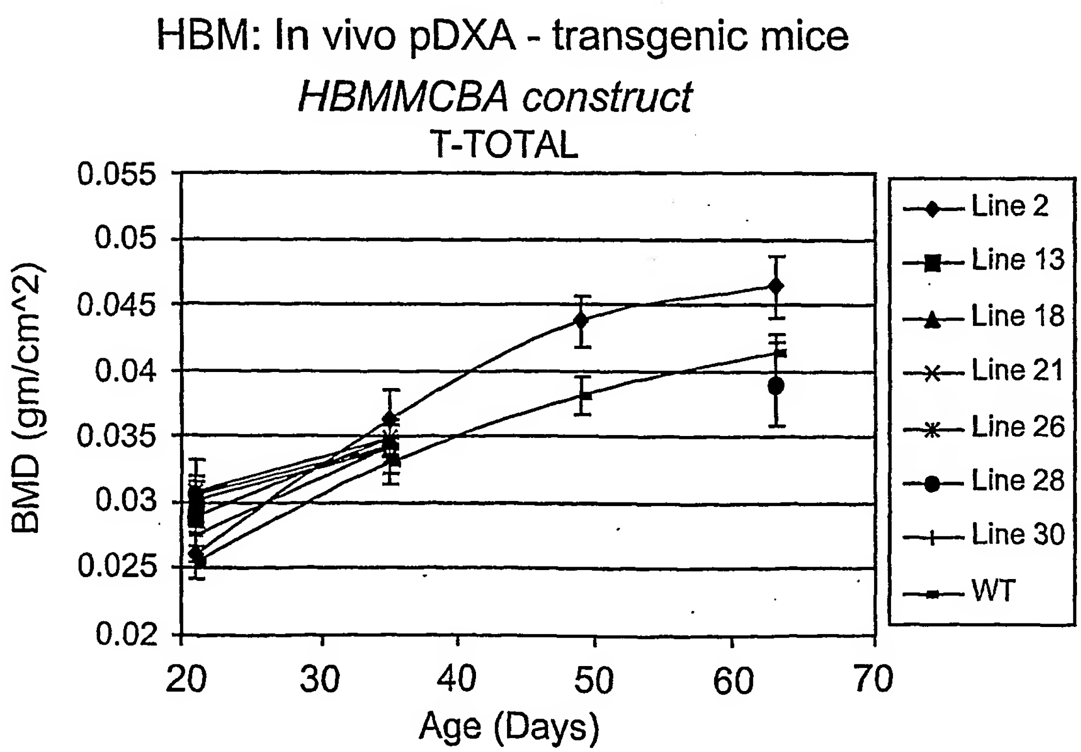


FIG. 21C

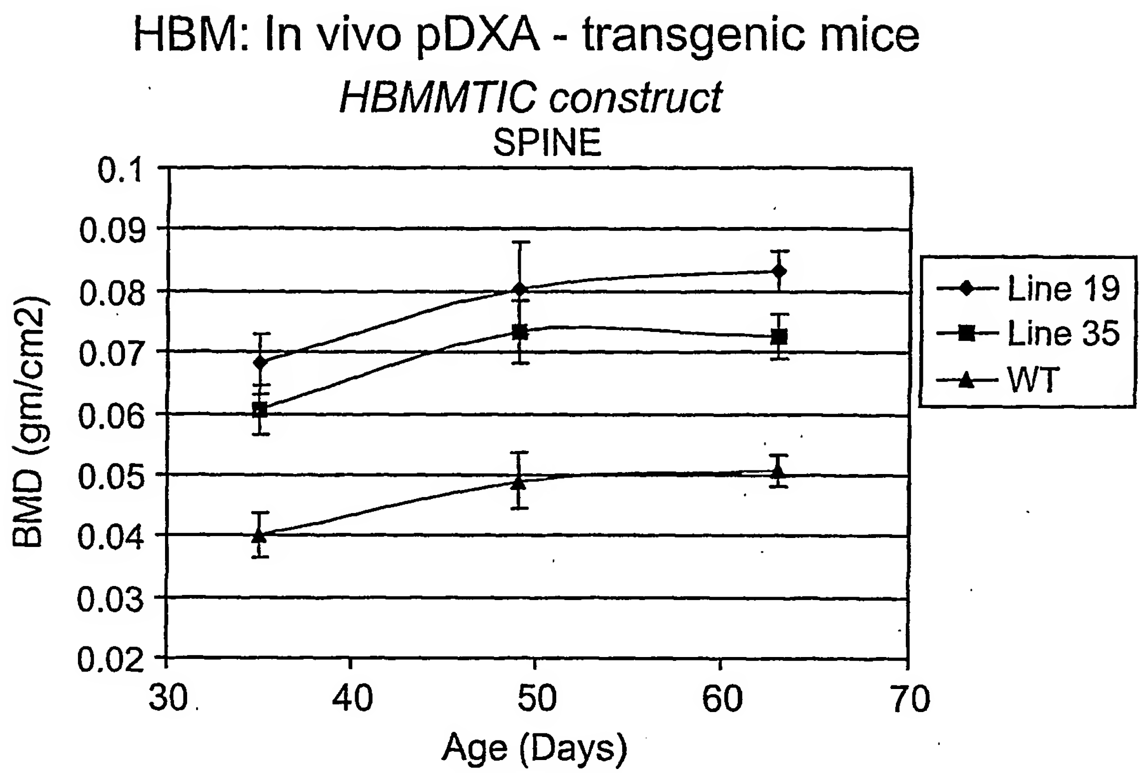


FIG. 21D

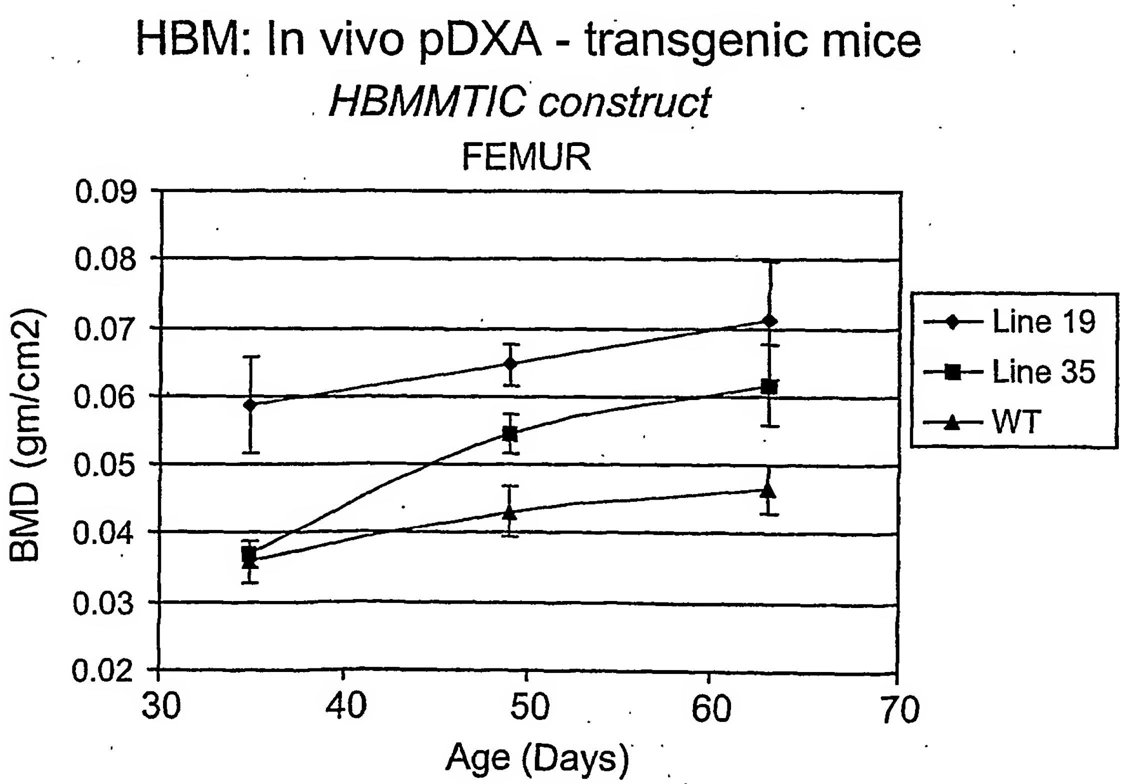


FIG. 21E

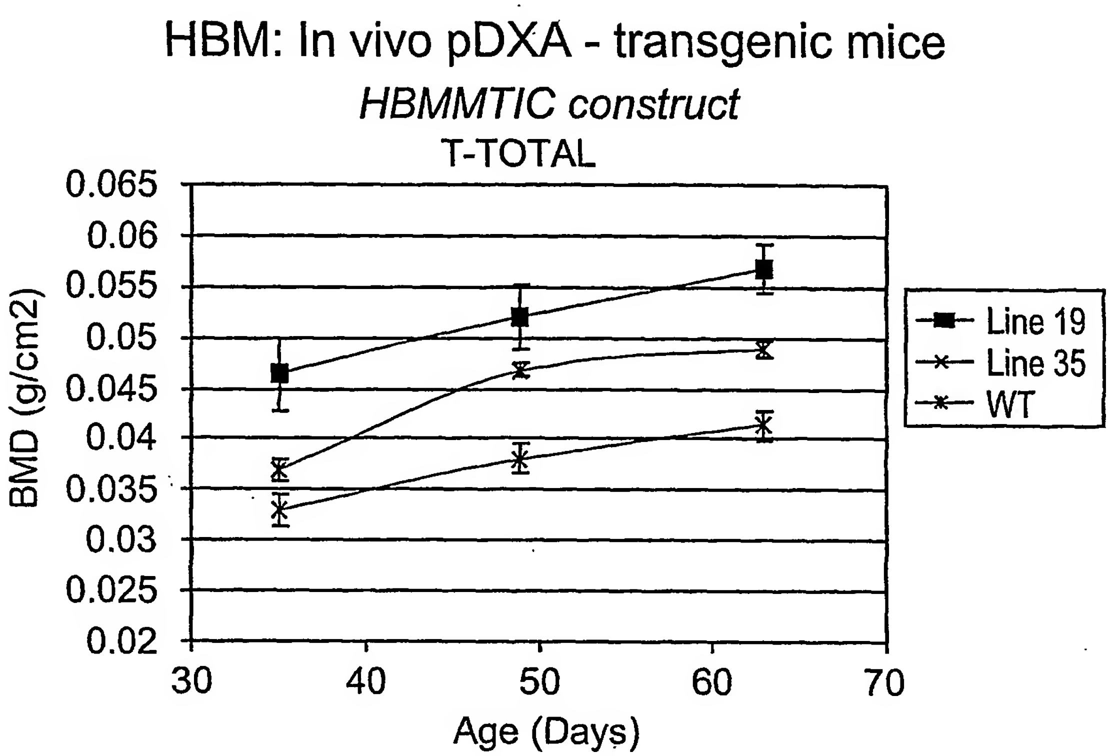

HBM: In vivo pDXA - transgenic mice
HBMMTIC construct
T-TOTAL
BMD (g/cm2)
0.065
0.06
0.055
0.05
0.045
0.04
0.035
0.03
0.025
0.02
30
40
50
60
70
Age (Days)
Line 19
Line 35
WT

FIG. 21F

HBM transgenic mice: in vivo pDXA*

BMD % changes vs WT in 5 week old animals

Line	n	Femur	Spine	Total	Tibia mRNA
HBMMCBA					
2	11	21	24	10	x7-10
13	4	11	27	5	x1-2
18	1	8	9	3	x10-11
21	1	10	12	6	0
28	15	0	30	4	x1
30	7	4	32	4	0
HBMMTIC					
19	5	63	70	41	x7-8
35	1	4	47	6	x1

** CV: Femur (2.7%); Spine (6.4%); Total (1.7%)*

FIG. 22

HBM transgenic mice: in vivo pDXA*

BMD % changes vs WT in 9 week old animals

Line	n	Femur	Spine	Total
HBMMCBA				
2	3	19	32	12
HBMMTIC				
19	2	52	64	37
35	3	32	43	18

** CV: Femur (2.7%); Spine (6.4%); Total (1.7%)*

FIG. 23

FIG. 24A

HBMGI_2AS

TCTAGACTCG AGGCGGCCGC CCATTGTGCA CTAAAGCGCC GCCGCCGCGC CATGGAGCCC
GAGTGAGCGC GGCGCGGGCC CGTCCGGCCG CCGGACAACA TGGAGGCAGC GCCGCCCGGG
CCGCCGTGGC CGCTGCTGCT GCTGCTGCTG CTGCTGCTGG CGCTGTGCGG CTGCCCGGCC
CCCGCCGCGG CCTCGCCGCT CCTGCTATTT GCCAACCGCC GGGACGTACG GCTGGTGGAC
GCCGGCGGAG TCAAGCTGGA GTCCACCATC GTGGTCAGCG GCCTGGAGGA TGCGGCCGCA
GTGGACTTCC AGTTTTCCAA GGGAGCCGTG TACTGGACAG ACGTGAGCGA GGAGGCCATC
AAGCAGACCT ACCTGAACCA GACGGGGGCC GCCGTGCAGA ACGTGGTCAT CTCCGGCCTG
GTCTCTCCCG ACGGCCTCGC CTGCGACTGG GTGGGCAAGA AGCTGTACTG GACGGACTCA
GAGACCAACC GCATCGAGGT GGCCAACCTC AATGGCACAT CCCGGAAGGT GCTCTTCTGG
CAGGACCTTG ACCAGCCGAG GGCCATCGCC TTGGACCCCG CTCACGGGTA CATGTACTGG
ACAGACTGGG TTGAGACGCC CCGGATTGAG CGGGCAGGGA TGGATGGCAG CACCCGGAAG
ATCATTGTGG ACTCGGACAT TTACTGGCCC AATGGACTGA CCATCGACCT GGAGGAGCAG
AAGCTCTACT GGGCTGACGC CAAGCTCAGC TTCATCCACC GTGCCAACCT GGACGGCTCG
TTCCGGCAGA AGGTGGTGGA GGGCAGCCTG ACGCACCCCT TCGCCCTGAC GCTCTCCGGG
GACACTCTGT ACTGGACAGA CTGGCAGACC CGCTCCATCC ATGCCTGCAA CAAGCGCACT
GGGGGGAAGA GGAAGGAGAT CCTGAGTGCC CTCTACTCAC CCATGGACAT CCAGGTGCTG
AGCCAGGAGC GGCAGCCTTT CTTCCACACT CGCTGTGAGG AGGACAATGG CGGCTGCTCC
CACCTGTGCC TGCTGTCCCC AAGCGAGCCT TTCTACACAT GCGCCTGCCC CACGGGTGTG
CAGCTGCAGG ACAACGGCAG GACGTGTAAG GCAGGAGCCG AGGAGGTGCT GCTGCTGGCC
CGGCGGACGG ACCTACGGAG GATCTCGCTG GACACGCCGG ACTTCACCGA CATCGTGCTG
CAGGTGGACG ACATCCGGCA CGCCATTGCC ATCGACTACG ACCCGCTAGA GGGCTATGTC
TACTGGACAG ATGACGAGGT GCGGGCCATC CGCAGGGCGT ACCTGGACGG GTCTGGGGCG
CAGACGCTGG TCAACACCGA GATCAACGAC CCCGATGGCA TCGCGGTCGA CTGGGTGGCC
CGAAACCTCT ACTGGACCGA CACGGGCACG GACCGCATCG AGGTGACGCG CCTCAACGGC

FIG. 24B

HBMGI_2AS

ACCTCCCGCA AGATCCTGGT GTCGGAGGAC CTGGACGAGC CCCGAGCCAT CGCACTGCAC
CCCGTGATGG GCCTCATGTA CTGGACAGAC TGGGGAGAGA ACCCTAAAAT CGAGTGTGCC
AACTTGGATG GGCAGGAGCG GCGTGTGCTG GTCAATGCCT CCCTCGGGTG GCCCAACGGC
CTGGCCCTGG ACCTGCAGGA GGGGAAGCTC TACTGGGGAG ACGCCAAGAC AGACAAGATC
GAGGTGATCA ATGTTGATGG GACGAAGAGG CGGACCCTCC TGGAGGACAA GCTCCCGCAC
ATTTTCGGGT TCACGCTGCT GGGGGACTTC ATCTACTGGA CTGACTGGCA GCGCCGCAGC
ATCGAGCGGG TGCACAAGGT CAAGGCCAGC CGGGACGTCA TCATTGACCA GCTGCCCGAC
CTGATGGGGC TCAAAGCTGT GAATGTGGCC AAGGTCGTCG GAACCAACCC GTGTGCGGAC
AGGAACGGGG GGTGCAGCCA CCTGTGCTTC TTCACACCCC ACGCAACCCG GTGTGGCTGC
CCCATCGGCC TGGAGCTGCT GAGTGACATG AAGACCTGCA TCGTGCCTGA GGCCTTCTTG
GTCTTCACCA GCAGAGCCGC CATCCACAGG ATCTCCCTCG AGACCAATAA CAACGACGTG
GCCATCCCGC TCACGGGCGT CAAGGAGGCC TCAGCCCTGG ACTTTGATGT GTCCAACAAC
CACATCTACT GGACAGACGT CAGCCTGAAG ACCATCAGCC GCGCCTTCAT GAACGGGAGC
TCGGTGGAGC ACGTGGTGGA GTTTGGCCTT GACTACCCCG AGGGCATGGC CGTTGACTGG
ATGGGCAAGA ACCTCTACTG GGCCGACACT GGGACCAACA GAATCGAAGT GGCGCGGCTG
GACGGGCAGT TCCGGCAAGT CCTCGTGTGG AGGGACTTGG ACAACCCGAG GTCGCTGGCC
CTGGATCCCA CCAAGGGCTA CATCTACTGG ACCGAGTGGG GCGGCAAGCC GAGGATCGTG
CGGGCCTTCA TGGACGGGAC CAACTGCATG ACGCTGGTGG ACAAGGTGGG CCGGGCCAAC
GACCTCACCA TTGACTACGC TGACCAGCGC CTCTACTGGA CCGACCTGGA CACCAACATG
ATCGAGTCGT CCAACATGCT GGGTCAGGAG CGGGTCGTGA TTGCCGACGA TCTCCCGCAC
CCGTTCGGTC TGACGCAGTA CAGCGATTAT ATCTACTGGA CAGACTGGAA TCTGCACAGC
ATTGAGCGGG CCGACAAGAC TAGCGGCCGG AACCGCACCC TCATCCAGGG CCACCTGGAC
TTCGTGATGG ACATCCTGGT GTTCCACTCC TCCCGCCAGG ATGGCCTCAA TGACTGTATG

FIG. 24C

HBMGI_2AS

CACAACAACG GGCAGTGTGG GCAGCTGTGC CTTGCCATCC CCGGCGGCCA CCGCTGCGGC
TGCGCCTCAC ACTACACCCT GGACCCCAGC AGCCGCAACT GCAGCCCGCC CACCACCTTC
TTGCTGTTCA GCCAGAAATC TGCCATCAGT CGGATGATCC CGGACGACCA GCACAGCCCG
GATCTCATCC TGCCCCTGCA TGGACTGAGG AACGTCAAAG CCATCGACTA TGACCCACTG
GACAAGTTCA TCTACTGGGT GGATGGGCGC CAGAACATCA AGCGAGCCAA GGACGACGGG
ACCCAGCCCT TTGTTTTGAC CTCTCTGAGC CAAGGCCAAA ACCCAGACAG GCAGCCCCAC
GACCTCAGCA TCGACATCTA CAGCCGGACA CTGTTCTGGA CGTGCGAGGC CACCAATACC
ATCAACGTCC ACAGGCTGAG CGGGGAAGCC ATGGGGGTGG TGCTGCGTGG GGACCGCGAC
AAGCCCAGGG CCATCGTCGT CAACGCGGAG CGAGGGTACC TGTACTTCAC CAACATGCAG
GACCGGGCAG CCAAGATCGA ACGCGCAGCC CTGGACGGCA CCGAGCGCGA GGTCCTCTTC
ACCACCGGCC TCATCCGCCC TGTGGCCCTG GTGGTAGACA ACACACTGGG CAAGCTGTTC
TGGGTGGACG CGGACCTGAA GCGCATTGAG AGCTGTGACC TGTCAGGGGC CAACCGCCTG
ACCCTGGAGG ACGCCAACAT CGTGCAGCCT CTGGGCCTGA CCATCCTTGG CAAGCATCTC
TACTGGATCG ACCGCCAGCA GCAGATGATC GAGCGTGTGG AGAAGACCAC CGGGGACAAG
CGGACTCGCA TCCAGGGCCG TGTCGCCCAC CTCACTGGCA TCCATGCAGT GGAGGAAGTC
AGCCTGGAGG AGTTCTCAGC CCACCCATGT GCCCGTGACA ATGGTGGCTG CTCCCACATC
TGTATTGCCA AGGGTGATGG GACACCACGG TGCTCATGCC CAGTCCACCT CGTGCTCCTG
CAGAACCTGC TGACCTGTGG AGAGCCGCCC ACCTGCTCCC CGGACCAGTT TGCATGTGCC
ACAGGGGAGA TCGACTGTAT CCCCGGGGCC TGGCGCTGTG ACGGCTTTCC CGAGTGCGAT
GACCAGAGCG ACGAGGAGGG CTGCCCCGTG TGCTCCGCCG CCCAGTTCCC CTGCGCGCGG
GGTCAGTGTG TGGACCTGCG CCTGCGCTGC GACGGCGAGG CAGACTGTCA GGACCGCTCA
GACGAGGCGG ACTGTGACGC CATCTGCCTG CCCAACCAGT TCCGGTGTGC GAGCGGCCAG
TGTGTCCTCA TCAAACAGCA GTGCGACTCC TTCCCCGACT GTATCGACGG CTCCGACGAG
CTCATGTGTG AAATCACCAA GCCGCCCTCA GACGACAGCC CGGCCCACAG CAGTGCCATC

FIG. 24D

HBMGI_2AS

GGGCCCGTCA TTGGCATCAT CCTCTCTCTC TTCGTCATGG GTGGTGTCTA TTTTGTGTGC
CAGCGCGTGG TGTGCCAGCG CTATGCGGGG GCCAACGGGC CCTTCCCGCA CGAGTATGTC
AGCGGGACCC CGCACGTGCC CCTCAATTTC ATAGCCCCGG GCGGTTCCCA GCATGGCCCC
TTCACAGGCA TCGCATGCGG AAAGTCCATG ATGAGCTCCG TGAGCCTGAT GGGGGGCCGG
GGCGGGGTGC CCCTCTACGA CCGGAACCAC GTCACAGGGG CCTCGTCCAG CAGCTCGTCC
AGCACGAAGG CCACGCTGTA CCCGCCGATC CTGAACCCGC CGCCCTCCCC GGCCACGGAC
CCCTCCCTGT ACAACATGGA CATGTTCTAC TCTTCAAACA TTCCGGCCAC TGCGAGACCG
TACAGGCCCT ACATCATTCG AGGAATGGCG CCCCCGACGA CGCCCTGCAG CACCGACGTG
TGTGACAGCG ACTACAGCGC CAGCCGCTGG AAGGCCAGCA AGTACTACCT GGATTTGAAC
TCGGACTCAG ACCCCTATCC ACCCCCACCC ACGCCCCACA GCCAGTACCT GTCGGCGGAG
GACAGCTGCC CGCCCTCGCC CGCCACCGAG AGGAGCTACT TCCATCTCTT CCCGCCCCCT
CCGTCCCCCT GCACGGACTC ATCCTGACCT CGGCCGGGCC ACTCTGGCTT CTCTGTGCCC
CTGTAAATAG TTTTAAATAT GAACAAAGAA AAAAATATAT TTTATGATTT AAAAAATAAA
TATAATTGGG ATTTTAAAAA CATGAGAAAT GTGAACTGTG ATGGGGTGGG CAGGGCTGGG
AGAACTTTGT ACAGTGGAGA AATATTTATA AACTTAATTT TGTAAAACAG AAAAAAAAAA
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCGGCCGC

FIG. 25A

ZMAXGI_3AS

TCTAGACTCG AGGCGGCCGC CCATTGTGCA CTAAAGCGCC GCCGCCGCGC CATGGAGCCC
GAGTGAGCGC GGCGCGGGCC CGTCCGGCCG CCGGACAACA TGGAGGCAGC GCCGCCCGGG
CCGCCGTGGC CGCTGCTGCT GCTGCTGCTG CTGCTGCTGG CGCTGTGCGG CTGCCCGGCC
CCCGCCGCGG CCTCGCCGCT CCTGCTATTT GCCAACCGCC GGGACGTACG GCTGGTGGAC
GCCGGCGGAG TCAAGCTGGA GTCCACCATC GTGGTCAGCG GCCTGGAGGA TGCGGCCGCA
GTGGACTTCC AGTTTTCCAA GGGAGCCGTG TACTGGACAG ACGTGAGCGA GGAGGCCATC
AAGCAGACCT ACCTGAACCA GACGGGGGCC GCCGTGCAGA ACGTGGTCAT CTCCGGCCTG
GTCTCTCCCG ACGGCCTCGC CTGCGACTGG GTGGGCAAGA AGCTGTACTG GACGGACTCA
GAGACCAACC GCATCGAGGT GGCCAACCTC AATGGCACAT CCCGGAAGGT GCTCTTCTGG
CAGGACCTTG ACCAGCCGAG GGCCATCGCC TTGGACCCCG CTCACGGGTA CATGTACTGG
ACAGACTGGG GTGAGACGCC CCGGATTGAG CGGGCAGGGA TGGATGGCAG CACCCGGAAG
ATCATTGTGG ACTCGGACAT TTACTGGCCC AATGGACTGA CCATCGACCT GGAGGAGCAG
AAGCTCTACT GGGCTGACGC CAAGCTCAGC TTCATCCACC GTGCCAACCT GGACGGCTCG
TTCCGGCAGA AGGTGGTGGA GGGCAGCCTG ACGCACCCCT TCGCCCTGAC GCTCTCCGGG
GACACTCTGT ACTGGACAGA CTGGCAGACC CGCTCCATCC ATGCCTGCAA CAAGCGCACT
GGGGGGAAGA GGAAGGAGAT CCTGAGTGCC CTCTACTCAC CCATGGACAT CCAGGTGCTG
AGCCAGGAGC GGCAGCCTTT CTTCCACACT CGCTGTGAGG AGGACAATGG CGGCTGCTCC
CACCTGTGCC TGCTGTCCCC AAGCGAGCCT TTCTACACAT GCGCCTGCCC CACGGGTGTG
CAGCTGCAGG ACAACGGCAG GACGTGTAAG GCAGGAGCCG AGGAGGTGCT GCTGCTGGCC
CGGCGGACGG ACCTACGGAG GATCTCGCTG GACACGCCGG ACTTCACCGA CATCGTGCTG
CAGGTGGACG ACATCCGGCA CGCCATTGCC ATCGACTACG ACCCGCTAGA GGGCTATGTC
TACTGGACAG ATGACGAGGT GCGGGCCATC CGCAGGGCGT ACCTGGACGG GTCTGGGGCG
CAGACGCTGG TCAACACCGA GATCAACGAC CCCGATGGCA TCGCGGTCGA CTGGGTGGCC
CGAAACCTCT ACTGGACCGA CACGGGCACG GACCGCATCG AGGTGACGCG CCTCAACGGC

FIG. 25B

ZMAXGI_3AS

ACCTCCCGCA AGATCCTGGT GTCGGAGGAC CTGGACGAGC CCCGAGCCAT CGCACTGCAC
CCCGTGATGG GCCTCATGTA CTGGACAGAC TGGGGAGAGA ACCCTAAAAT CGAGTGTGCC
AACTTGGATG GGCAGGAGCG GCGTGTGCTG GTCAATGCCT CCCTCGGGTG GCCCAACGGC
CTGGCCCTGG ACCTGCAGGA GGGGAAGCTC TACTGGGGAG ACGCCAAGAC AGACAAGATC
GAGGTGATCA ATGTTGATGG GACGAAGAGG CGGACCCTCC TGGAGGACAA GCTCCCGCAC
ATTTTCGGGT TCACGCTGCT GGGGGACTTC ATCTACTGGA CTGACTGGCA GCGCCGCAGC
ATCGAGCGGG TGCACAAGGT CAAGGCCAGC CGGGACGTCA TCATTGACCA GCTGCCCGAC
CTGATGGGGC TCAAAGCTGT GAATGTGGCC AAGGTCGTCG GAACCAACCC GTGTGCGGAC
AGGAACGGGG GGTGCAGCCA CCTGTGCTTC TTCACACCCC ACGCAACCCG GTGTGGCTGC
CCCATCGGCC TGGAGCTGCT GAGTGACATG AAGACCTGCA TCGTGCCTGA GGCCTTCTTG
GTCTTCACCA GCAGAGCCGC CATCCACAGG ATCTCCCTCG AGACCAATAA CAACGACGTG
GCCATCCCGC TCACGGGCGT CAAGGAGGCC TCAGCCCTGG ACTTTGATGT GTCCAACAAC
CACATCTACT GGACAGACGT CAGCCTGAAG ACCATCAGCC GCGCCTTCAT GAACGGGAGC
TCGGTGGAGC ACGTGGTGGA GTTTGGCCTT GACTACCCCG AGGGCATGGC CGTTGACTGG
ATGGGCAAGA ACCTCTACTG GGCCGACACT GGGACCAACA GAATCGAAGT GGCGCGGCTG
GACGGGCAGT TCCGGCAAGT CCTCGTGTGG AGGGACTTGG ACAACCCGAG GTCGCTGGCC
CTGGATCCCA CCAAGGGCTA CATCTACTGG ACCGAGTGGG GCGGCAAGCC GAGGATCGTG
CGGGCCTTCA TGGACGGGAC CAACTGCATG ACGCTGGTGG ACAAGGTGGG CCGGGCCAAC
GACCTCACCA TTGACTACGC TGACCAGCGC CTCTACTGGA CCGACCTGGA CACCAACATG
ATCGAGTCGT CCAACATGCT GGGTCAGGAG CGGGTCGTGA TTGCCGACGA TCTCCCGCAC
CCGTTCGGTC TGACGCAGTA CAGCGATTAT ATCTACTGGA CAGACTGGAA TCTGCACAGC
ATTGAGCGGG CCGACAAGAC TAGCGGCCGG AACCGCACCC TCATCCAGGG CCACCTGGAC
TTCGTGATGG ACATCCTGGT GTTCCACTCC TCCCGCCAGG ATGGCCTCAA TGACTGTATG

FIG. 25C

ZMAXGI_3AS

CACAACAACG GGCAGTGTGG GCAGCTGTGC CTTGCCATCC CCGGCGGCCA CCGCTGCGGC
TGCGCCTCAC ACTACACCCT GGACCCCAGC AGCCGCAACT GCAGCCCGCC CACCACCTTC
TTGCTGTTCA GCCAGAAATC TGCCATCAGT CGGATGATCC CGGACGACCA GCACAGCCCG
GATCTCATCC TGCCCCTGCA TGGACTGAGG AACGTCAAAG CCATCGACTA TGACCCACTG
GACAAGTTCA TCTACTGGGT GGATGGGCGC CAGAACATCA AGCGAGCCAA GGACGACGGG
ACCCAGCCCT TTGTTTTGAC CTCTCTGAGC CAAGGCCAAA ACCCAGACAG GCAGCCCCAC
GACCTCAGCA TCGACATCTA CAGCCGGACA CTGTTCTGGA CGTGCGAGGC CACCAATACC
ATCAACGTCC ACAGGCTGAG CGGGGAAGCC ATGGGGGTGG TGCTGCGTGG GGACCGCGAC
AAGCCCAGGG CCATCGTCGT CAACGCGGAG CGAGGGTACC TGTACTTCAC CAACATGCAG
GACCGGGCAG CCAAGATCGA ACGCGCAGCC CTGGACGGCA CCGAGCGCGA GGTCCTCTTC
ACCACCGGCC TCATCCGCCC TGTGGCCCTG GTGGTAGACA ACACACTGGG CAAGCTGTTC
TGGGTGGACG CGGACCTGAA GCGCATTGAG AGCTGTGACC TGTCAGGGGC CAACCGCCTG
ACCCTGGAGG ACGCCAACAT CGTGCAGCCT CTGGGCCTGA CCATCCTTGG CAAGCATCTC
TACTGGATCG ACCGCCAGCA GCAGATGATC GAGCGTGTGG AGAAGACCAC CGGGGACAAG
CGGACTCGCA TCCAGGGCCG TGTCGCCCAC CTCACTGGCA TCCATGCAGT GGAGGAAGTC
AGCCTGGAGG AGTTCTCAGC CCACCCATGT GCCCGTGACA ATGGTGGCTG CTCCCACATC
TGTATTGCCA AGGGTGATGG GACACCACGG TGCTCATGCC CAGTCCACCT CGTGCTCCTG
CAGAACCTGC TGACCTGTGG AGAGCCGCCC ACCTGCTCCC CGGACCAGTT TGCATGTGCC
ACAGGGGAGA TCGACTGTAT CCCCGGGGCC TGGCGCTGTG ACGGCTTTCC CGAGTGCGAT
GACCAGAGCG ACGAGGAGGG CTGCCCCGTG TGCTCCGCCGC CCAGTTCCCC TGCGCGCGG
GGTCAGTGTGT GGACCTGCGC CTGCGCTGCG ACGGCGAGGC AGACTGTCAG GACCGCTCA
GACGAGGCGGA CTGTGACGCC ATCTGCCTGC CCAACCAGTT CCGGTGTGCG AGCGGCCAG
TGTGTCCTCAT CAAACAGCAG TGCGACTCCT TCCCCGACTG TATCGACGGC TCCGACGAG
CTCATGTGTGA AATCACCAAG CCGCCCTCAG ACGACAGCCC GGCCCACAGC AGTGCCATC

FIG. 25D

ZMAXGI_3AS

GGGCCCGTCA TTGGCATCAT CCTCTCTCTC TTCGTCATGG GTGGTGTCTA TTTTGTGTGC
CAGCGCGTGG TGTGCCAGCG CTATGCGGGG GCCAACGGGC CCTTCCCGCA CGAGTATGTC
AGCGGGACCC CGCACGTGCC CCTCAATTTC ATAGCCCCGG GCGGTTCCCA GCATGGCCCC
TTCACAGGCA TCGCATGCGG AAAGTCCATG ATGAGCTCCG TGAGCCTGAT GGGGGGCCGG
GGCGGGGTGC CCCTCTACGA CCGGAACCAC GTCACAGGGG CCTCGTCCAG CAGCTCGTCC
AGCACGAAGG CCACGCTGTA CCCGCCGATC CTGAACCCGC CGCCCTCCCC GGCCACGGAC
CCCTCCCTGT ACAACATGGA CATGTTCTAC TCTTCAAACA TTCCGGCCAC TGCGAGACCG
TACAGGCCCT ACATCATTCG AGGAATGGCG CCCCCGACGA CGCCCTGCAG CACCGACGTG
TGTGACAGCG ACTACAGCGC CAGCCGCTGG AAGGCCAGCA AGTACTACCT GGATTTGAAC
TCGGACTCAG ACCCCTATCC ACCCCCACCC ACGCCCCACA GCCAGTACCT GTCGGCGGAG
GACAGCTGCC CGCCCTCGCC CGCCACCGAG AGGAGCTACT TCCATCTCTT CCCGCCCCCT
CCGTCCCCCT GCACGGACTC ATCCTGACCT CGGCCGGGCC ACTCTGGCTT CTCTGTGCCC
CTGTAAATAG TTTTAAATAT GAACAAAGAA AAAAATATAT TTTATGATTT AAAAAATAAA
TATAATTGGG ATTTTAAAAA CATGAGAAAT GTGAACTGTG ATGGGGTGGG CAGGGCTGGG
AGAACTTTGT ACAGTGGAGA AATATTTATA AACTTAATTT TGTAAAACAG AAAAAAAAAA
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCGGCCGC

FIG. 26A

Alignment of Human and Mouse Zmax1 (LRP5) Amino-Acid Sequences.

Top= Human, Bottom = Mouse

```
  1 MEA....APPGPPWPLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLV 46
    ||.    |||.|| |||||:     |:.: .|||||||||||||||||||
  1 METAPTRAPPPPPPPLLLLV.....LYCSLVPAAASPLLLFANRRDVRLV 45

 47 DAGGVKLESTIVVSGLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTG 96
    ||||||||||||.|||||||||||||||||||||||||||||||||||||
 46 DAGGVKLESTIVASGLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTG 95

 97 AAVQNVVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTSRKVLF 146
    ||.||:||||||||||||||||||||||||||||||||||||||||||||
 96 AAAQNIVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTSRKVLF 145

147 WQDLDQPRAIALDPAHGYMYWTDWGETPRIERAGMDGSTRKIIVDSDIYW 196
    ||||||||||||||||||||||||||.|||||||||||||||||||||||
146 WQDLDQPRAIALDPAHGYMYWTDWGEAPRIERAGMDGSTRKIIVDSDIYW 195

197 PNGLTIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHPFALTLS 246
    ||||||||||||||||||||||||||||||||||||||||||||||||||
196 PNGLTIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHPFALTLS 245

247 GDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSPMDIQVLSQERQPFFH 296
    |||||||||||||||||||:||:.||||||||||||||||||||||| ||
246 GDTLYWTDWQTRSIHACNKWTGEQRKEILSALYSPMDIQVLSQERQPPFH 295

297 TRCEEDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKAGAEEVLLL 346
    |.||||||||||||||||.||||.|||||||||||||:|||.||||||||
296 TPCEEDNGGCSHLCLLSPREPFYSCACPTGVQLQDNGKTCKTGAEEVLLL 345

347 ARRTDLRRISLDTPDFTDIVLQVDDIRHAIAIDYDPLEGYVYWTDDEVRA 396
    |||||||||||||||||||||||:||||||||||||||||||||||||||
346 ARRTDLRRISLDTPDFTDIVLQVGDIRHAIAIDYDPLEGYVYWTDDEVRA 395

397 IRRAYLDGSGAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLN 446
    ||||||||||||||||||||||||||||||||||||||||||||||||||
396 IRRAYLDGSGAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLN 445

447 GTSRKILVSEDLDEPRAIALHPVMGLMYWTDWGENPKIECANLDGQERRV 496
    ||||||||||||||||||.||||||||||||||||||||||||||.:|:|
446 GTSRKILVSEDLDEPRAIVLHPVMGLMYWTDWGENPKIECANLDGRDRHV 495

497 LVNASLGWPNGLALDLQEGKLYWGDAKTDKIEVINVDGTKRRTLLEDKLP 546
    |||.|||||||||||||||||||||||||||||||:|||||:||||||||
496 LVNTSLGWPNGLALDLQEGKLYWGDAKTDKIEVINIDGTKRKTLLEDKLP 545

547 HIFGFTLLGDFIYWTDWQRRSIERVHKVKASRDVIIDQLPDLMGLKAVNV 596
    ||||||||||||||||||||||||||||||||||||||||||||||||||
546 HIFGFTLLGDFIYWTDWQRRSIERVHKVKASRDVIIDQLPDLMGLKAVNV 595

597 AKVVGTNPCADRNGGCSHLCFFTPHATRCGCPIGLELLSDMKTCIVPEAF 646
    ||||||||||| ||||||||||||:||:|||||||||||||||||:||||
596 AKVVGTNPCADGNGGCSHLCFFTPRATKCGCPIGLELLSDMKTCIIPEAF 645

647 LVFTSRAAIHRISLETNNNDVAIPLTGVKEASALDFDVSNNHIYWTDVSL 696
    |||||||.||||||||||||||||||||||||||||||||||||||||||
646 LVFTSRATIHRISLETNNNDVAIPLTGVKEASALDFDVSNNHIYWTDVSL 695
```

FIG. 26B

Alignment of Human and Mouse Zmax1 (LRP5) Amino-Acid Sequences.

```
 697 KTISRAFMNGSSVEHVVEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVAR 746
     ||||||||||||||||:|||||||||||||||||||||||||||||||||
 696 KTISRAFMNGSSVEHVIEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVAR 745

 747 LDGQFRQVLVWRDLDNPRSLALDPTKGYIYWTEWGGKPRIVRAFMDGTNC 796
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 746 LDGQFRQVLVWRDLDNPRSLALDPTKGYIYWTEWGGKPRIVRAFMDGTNC 795

 797 MTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVVIADDLP 846
     ||||||||||||||||||||||||||||||||||||||||||:|||||||
 796 MTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERMVIADDLP 845

 847 HPFGLTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLDFVMDILVFH 896
     .|||||||||||||||||||||||||||||||||||||||||||||||||
 846 YPFGLTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLDFVMDILVFH 895

 897 SSRQDGLNDCMHNNGQCGQLCLAIPGGHRCGCASHYTLDPSSRNCSPPTT 946
     ||||||||||:|.|||||||||||||||||||||||||||||||||||.|
 896 SSRQDGLNDCVHSNGQCGQLCLAIPGGHRCGCASHYTLDPSSRNCSPPST 945

 947 FLLFSQKSAISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDG 996
     ||||||| |||||||||| ||||:||||||||||||:|||||||||||||
 946 FLLFSQKFAISRMIPDDQLSPDLVLPLHGLRNVKAINYDPLDKFIYWVDG 995

 997 RQNIKRAKDDGTQPFVLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATN 1046
     |||||||||||||| :||| ||: .|||||||||||||||||||||||||
 996 RQNIKRAKDDGTQPSMLTSPSQSLSPDRQPHDLSIDIYSRTLFWTCEATN 1045

1047 TINVHRLSGEAMGVVLRGDRDKPRAIVVNAERGYLYFTNMQDRAAKIERA 1096
     |||||||.|:||||||||||||||||.|||||||:|||||||:|||||||
1046 TINVHRLDGDAMGVVLRGDRDKPRAIAVNAERGYMYFTNMQDHAAKIERA 1095

1097 ALDGTEREVLFTTGLIRPVALVVDNTLGKLFWVDADLKRIESCDLSGANR 1146
     .||||||||||||||||||||||||.||||||||||||||||||||||||
1096 SLDGTEREVLFTTGLIRPVALVVDNALGKLFWVDADLKRIESCDLSGANR 1145

1147 LTLEDANIVQPLGLTILGKHLYWIDRQQQMIERVEKTTGDKRTRIQGRVA 1196
     |||||||||||:|||:||:|||||||||||||||||||||||||:||||.
1146 LTLEDANIVQPVGLTVLGRHLYWIDRQQQMIERVEKTTGDKRTRVQGRVT 1195

1197 HLTGIHAVEEVSLEEFSAHPCARDNGGCSHICIAKGDGTPRCSCPVHLVL 1246
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1196 HLTGIHAVEEVSLEEFSAHPCARDNGGCSHICIAKGDGTPRCSCPVHLVL 1245

1247 LQNLLTCGEPPTCSPDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGCP 1296
     ||||||||||||||||||||.|||||||||||||||||||.|||||||||
1246 LQNLLTCGEPPTCSPDQFACTTGEIDCIPGAWRCDGFPECADQSDEEGCP 1295

1297 VCSAAQFPCARGQCVDLRLRCDGEADCQDRSDEADCDAICLPNQFRCASG 1346
     ||||.|||||||||||||||||||||||||||||:|||:||||||||.||
1296 VCSASQFPCARGQCVDLRLRCDGEADCQDRSDEANCDAVCLPNQFRCTSG 1345

1347 QCVLIKQQCDSFPDCIDGSDELMCEITKPPSDDSPAHSSAIGPVIGIILS 1396
     ||||||||||||||| ||||||||||.|||||| ||||||||||||||||
1346 QCVLIKQQCDSFPDCADGSDELMCEINKPPSDDIPAHSSAIGPVIGIILS 1395

1397 LFVMGGVYFVCQRVVCQRYAGANGPFPHEYVSGTPHVPLNFIAPGGSQHG 1446
     ||||||||||||||:||||.|||.|||||||:|.||||||||||||||||
1396 LFVMGGVYFVCQRVMCQRYTGASGPFPHEYVGGAPHVPLNFIAPGGSQHG 1445
```

FIG. 26C

Alignment of Human and Mouse Zmax1 (LRP5) Amino-Acid Sequences.

```
1447 PFTGIACGKSMMSSVSLMGGRGGVPLYDRNHVTGASSSSSSSTKATLYPP 1496
     ||.||:|:||:|||:||:||||:|||||||||||||||||||||||||||
1446 PFPGIPCSKSVMSSMSLVGGRGSVPLYDRNHVTGASSSSSSSTKATLYPP 1495

1497 ILNPPPSPATDPSLYNMDMFYSSNIPATARPYRPYIIRGMAPPTTPCSTD 1546
     ||||||||||||||||:|:||||.|||||||||||:||||||||||||||
1496 ILNPPPSPATDPSLYNVDVFYSSGIPATARPYRPYVIRGMAPPTTPCSTD 1545

1547 VCDSDYSASRWKASKYYLDLNSDSDPYPPPPTPHSQYLSAEDSCPPSPAT 1596
     ||||||| ||||.||||||||||||||||||||||||||||||||||:|
1546 VCDSDYSISRWKSSKYYLDLNSDSDPYPPPPTPHSQYLSAEDSCPPSPGT 1595

1597 ERSYFHLFPPPPSPCTDSS 1615
     |||| ||||||||||||||
1596 ERSYCHLFPPPPSPCTDSS 1614
```

FIG. 27A

Alignment of Human LRP5 and LRP6

Top = LRP5, Bottom = LRP6

Underlined = region marked for antibody production

Percent Similarity: 83.542 Percent Identity: 70.901

```
   1 MEAAPPGPPWPLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGG 50
                :  :|  ||| |:  ..  |.||||:|||||:|||||..
   1 ...........MGAVLRSLLA.CSFCVLLRAAPLLLYANRRDLRLVDATN 38

  51 VKLESTIVVSGLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAVQ 100
     .| :.||||:|||||||||| ||.| :||.||||||||.| :|.|: .||
  39 GKENATIVVGGLEDAAAVDFVFSHGLIYWSDVSEEAIKRTEFNKTE.SVQ 87

 101 NVVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDL 150
     |||:|||:|||||||||:|.||||||||||||||.||:|. |||||||:|
  88 NVVVSGLLSPDGLACDWLGEKLYWTDSETNRIEVSNLDGSLRKVLFWQEL 137

 151 DQPRAIALDPAHGYMYWTDWGETPRIERAGMDGSTRKIIVDSDIYWPNGL 200
     ||||||||||. |:||||||||.|:|||||||||.| ||::|:|||||||
 138 DQPRAIALDPSSGFMYWTDWGEVPKIERAGMDGSSRFIIINSEIYWPNGL 187

 201 TIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHPFALTLSGDTL 250
     |:|.||||||||||||.|||:.||||. || ||.|||.||||||| :|.|
 188 TLDYEEQKLYWADAKLNFIHKSNLDGTNRQAVVKGSLPHPFALTLFEDIL 237

 251 YWTDWQTRSIHACNKRTGGKRKEILSALYSPMDIQVLSQERQPFFHTRCE 300
     ||||| |:|| |||| ||:  :|| |.::|||||:.:||:|||   ..|:
 238 YWTDWSTHSILACNKYTGEGLREIHSDIFSPMDIHAFSQQRQPNATNPCG 287

 301 EDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKAGAEEVLLLARRT 350
      ||||||||||:|| .||| |||||||.| :||:|||.||.|:|||||||
 288 IDNGGCSHLCLMSPVKPFYQCACPTGVKLLENGKTCKDGATELLLLARRT 337

 351 DLRRISLDTPDFTDIVLQVDDIRHAIAIDYDPLEGYVYWTDDEVRAIRRA 400
     ||||||||||||||||||::||||||||||||:|||:||||||||||||.
 338 DLRRISLDTPDFTDIVLQLEDIRHAIAIDYDPVEGYIYWTDDEVRAIRRS 387

 401 YLDGSGAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTSR 450
     ::||||.| :|..:|..||||||||||||||||||||||||||||||| |
 388 FIDGSGSQFVVTAQIAHPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTMR 437

 451 KILVSEDLDEPRAIALHPVMGLMYWTDWGENPKIECANLDGQERRVLVNA 500
     |||:||||:|||||.|.|::|.|||||||| |||| |.||| :| ||||.
 438 KILISEDLEEPRAIVLDPMVGYMYWTDWGEIPKIERAALDGSDRVVLVNT 487

 501 SLGWPNGLALDLQEGKLYWGDAKTDKIEVINVDGTKRRTLLEDKLPHIFG 550
     |||||||||||.:|||:||||||||||||:|.||| ||.|:|||:|||||
 488 SLGWPNGLALDYDEGKIYWGDAKTDKIEVMNTDGTGRRVLVEDKIPHIFG 537

 551 FTLLGDFIYWTDWQRRSIERVHKVKASRDVIIDQLPDLMGLKAVNVAKVV 600
     ||||||::||||||||||||||| .|.|:||||||||||||||.|| :|:
 538 FTLLGDYVYWTDWQRRSIERVHKRSAEREVIIDQLPDLMGLKATNVHRVI 587

 601 GTNPCADRNGGCSHLCFFTPHATRCGCPIGLELLSDMKTCIVPEAFLVFT 650
     |.||||: ||||||||:: |:: ||:||||:||:|||||||||||||:|.
 588 GSNPCAEENGGCSHLCLYRPQGLRCACPIGFELISDMKTCIVPEAFLLFS 637
```

FIG. 27B
Alignment of Human LRP5 and LRP6

```
 651 SRAAIHRISLETNNNDVAIPLTGVKEASALDFDVSNNHIYWTDVSLKTIS 700
     .||.|:|||||||||:|||||||||||||||||||.:|:|||||:|||||
 638 RRADIRRISLETNNNNVAIPLTGVKEASALDFDVTDNRIYWTDISLKTIS 687

 701 RAFMNGSSVEHVVEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVARLDGQ 750
     |||||||.:||||||||||||||||||:||||||||||||||||.:||||
 688 RAFMNGSALEHVVEFGLDYPEGMAVDWLGKNLYWADTGTNRIEVSKLDGQ 737

 751 FRQVLVWRDLDNPRSLALDPTKGYIYWTEWGGKPRIVRAFMDGTNCMTLV 800
      ||||||:|||.||.|||||..|::|||||||||:| || |||.:  |||
 738 HRQVLVWKDLDSPRALALDPAEGFMYWTEWGGKPKIDRAAMDGSERTTLV 787

 801 DKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVVIADDLPHPFG 850
     ..|||||:||||||..||||||||||:|||||||| :| |||||||||||
 788 PNVGRANGLTIDYAKRRLYWTDLDTNLIESSNMLGLNREVIADDLPHPFG 837

 851 LTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLDFVMDILVFHSSRQ 900
     |||| ||||||||. :|||||:||||.|||:||||||:||||||||||||
 838 LTQYQDYIYWTDWSRRSIERANKTSGQNRTIIQGHLDYVMDILVFHSSRQ 887

 901 DGLNDCMHNNGQCGQLCLAIP.GGHRCGCASHYTLDPSSRNCSPPTTFLL 949
     .|:|:|  .||:|::||||:| ||  |||:.||.|::..|.||:||||||
 888 SGWNECASSNGHCSHLCLAVPVGGFVCGCPAHYSLNADNRTCSAPTTFLL 937

 950 FSQKSAISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQN 999
     |||||||.||: |:|:|||:|||:|:||||:||||||||| :||:|:|||
 938 FSQKSAINRMVIDEQQSPDIILPIHSLRNVRAIDYDPLDKQLYWIDSRQN 987

1000 .IKRAKDDGTQPF.VLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATNT 1047
      |::|.:||.|.| |:.|  .:|| : ||.||||||||| ::|||||||.
 988 MIRKAQEDGSQGFTVVVSSVPSQNLEIQPYDLSIDIYSRYIYWTCEATNV 1037

1048 INVHRLSGEAMGVVLRGDRDKPRAIVVNAERGYLYFTNMQDRAAKIERAA 1097
     ||| ||.| .:||||:|:.|:|||||||:|:||:||||:|:|.:||||||
1038 INVTRLDGRSVGVVLKGEQDRPRAIVVNPEKGYMYFTNLQERSPKIERAA 1087

1098 LDGTEREVLFTTGLIRPVALVVDNTLGKLFWVDADLKRIESCDLSGANRL 1147
     |||||||||| .|| :|:||.:|. ||||||.|.||:||||:|||||||:
1088 LDGTEREVLFFSGLSKPIALALDSRLGKLFWADSDLRRIESSDLSGANRI 1137

1148 TLEDANIVQPLGLTILGKHLYWIDRQQQMIERVEKTTGDKRTRIQGRVAH 1197
     .|||.||:||:|||::::.||||||:||||||:::.|  : ||::|.|:|:
1138 VLEDSNILQPVGLTVFENWLYWIDKQQQMIEKIDMTGREGRTKVQARIAQ 1187

1198 LTGIHAVEEVSLEEFSAHPCARDNGGCSHICIAKGDGTPRCSCPVHLVLL 1247
     |.:||||.|:.|:|:..||||.|||||||||:.|||||.|||||:|||||
1188 LSDIHAVKELNLQEYRQHPCAQDNGGCSHICLVKGDGTTRCSCPMHLVLL 1237

1248 QNLLTCGEPPTCSPDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGCPV 1297
     |: |.|||||||||:||.| ||||||||.|||||||.||:|:||| .|||
1238 QDELSCGEPPTCSPQQFTCFTGEIDCIPVAWRCDGFTECEDHSDELNCPV 1287

1298 CSAAQFPCARGQCVDLRLRCDGEADCQDRSDEADCDAICLPNQFRCASGQ 1347
     ||..||.||.|||:|  |||:|:|:|||:||| :|:.:|| :|||||.||
1288 CSESQFQCASGQCIDGALRCNGDANCQDKSDEKNCEVLCLIDQFRCANGQ 1337

1348 CVLIKQQCDSFPDCIDGSDELMCEITKPPSDDSPAHSSAIGPVIGIILSL 1397
     |:   ..||   ||| | |||| |  |..|   .|. ...:|.|||:|:.:
1338 CIGKHKKCDHNVDCSDKSDELDCYPTEEP...APQATNTVGSVIGVIVTI 1384
```

FIG. 27C

Alignment of Human LRP5 and LRP6

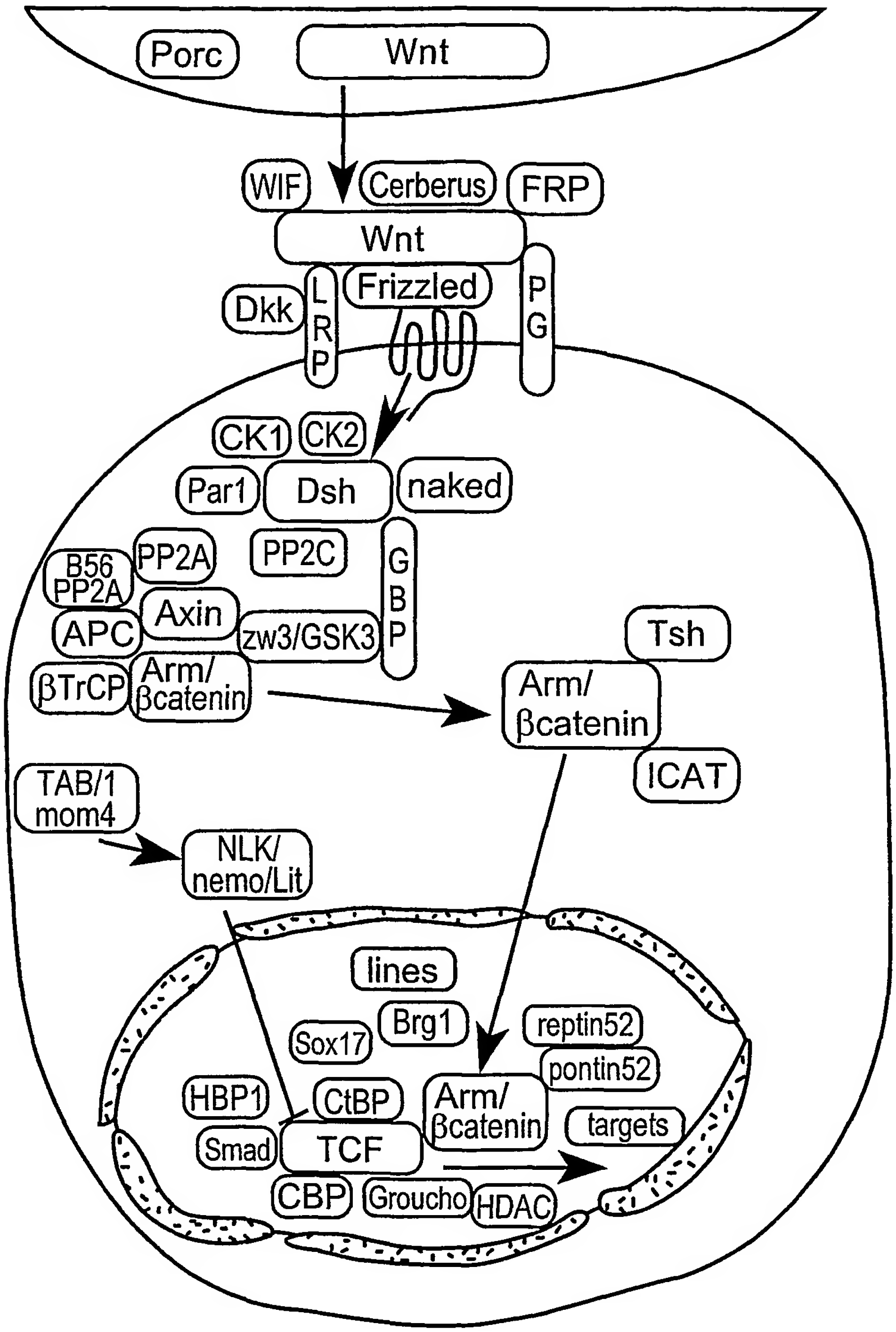
```
1398 FVMGGVYFVCQRVVCQRYAGANGPFPHEYVS.GTPHVPLNFIAPGGSQHG 1446
     || |.|||:|||::|.|  |..:.:.::||  |.: |||.:::..:|  |
1385 FVSGTVYFICQRMLCPRMKGDGETMTNDYVVHGPASVPLGYVPHPSSLSG 1434

1447 PFTGIACGKSMMSSVSLMGGRGGVPLYDRNHVTGASSSSSSSTKATLYPP 1496
     .:.|:. ||||:||:|:|||.:|.| |||.||||||||||||||:|.:|:
1435 SLPGMSRGKSMISSLSIMGGSSGPP.YDRAHVTGASSSSSSSTKGTYFPA 1483

1497 ILNPPPSPATDPSLYNMDMFYSSNIPATAR..PYRPYIIRGMAPPTTPCS 1544
     ||||||||||:.| |.|:: |||| |.| |  .|||| .| :||||||||
1484 ILNPPPSPATERSHYTMEFGYSSNSPSTHRSYSYRPYSYRHFAPPTTPCS 1533

1545 TDVCDSDYSASRWKAS.....KYYLDLNSDSDPYPPPPTPHSQYLSAE.. 1587
     ||||||||.:||:..|      |  ||| ||:| |||||||:|||||||  
1534 TDVCDSDYAPSRRMTSVATAKGYTSDLNYDSEPVPPPPTPRSQYLSAEEN 1583

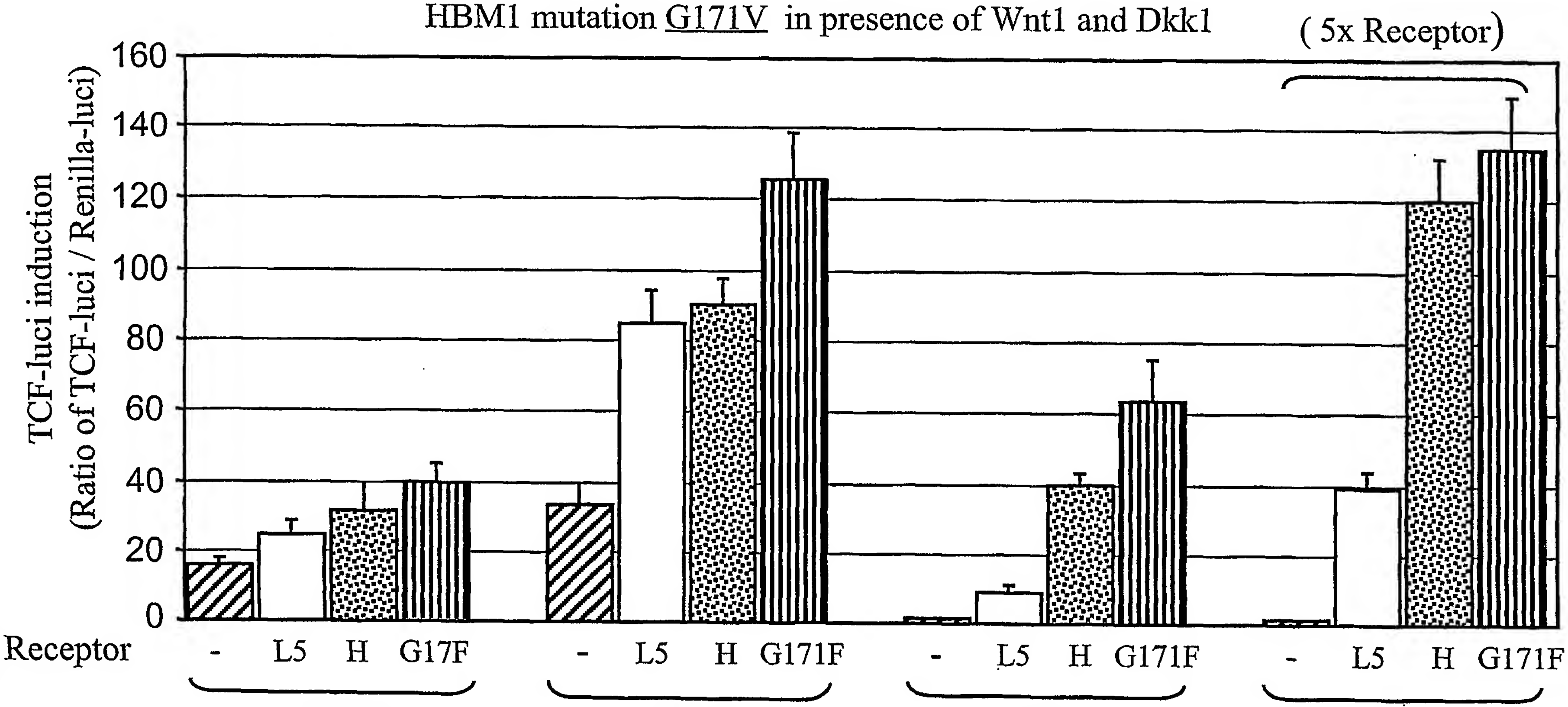
1588 .DSCPPSPATERSY.FHLFPPPPSPCTDSS 1615
      :|||||| |||||  ||:|||||||||||
1584 YESCPPSPYTERSYSHHLYPPPPSPCTDSS 1613
```



Model of Wnt signaling

FIG. 28

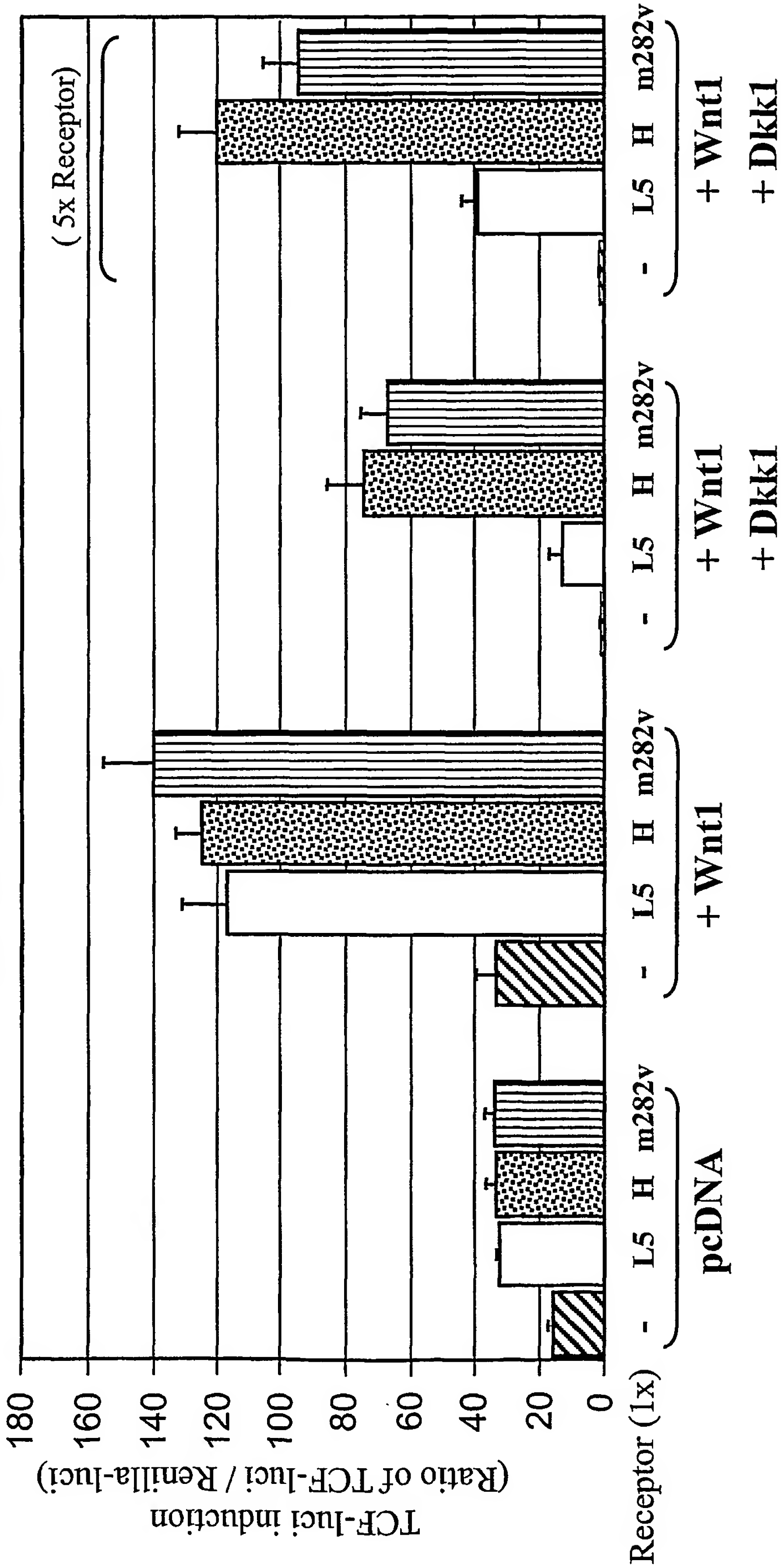
LRP 5 mutation G171F results in greater TCF-activation than with HBM1 mutation G171V in presence of Wnt1 and Dkk1



• G171F mutation involves the ringed R group (F) alteration and leads to marginally greater TCF-luci activation than that with HBM1 mutation G171V.

FIG. 29

LRP5-blade1 Mutant M282V leads to HBM1 type TCF-signal with Wnt1 and Dkk1 in U2-OS cells



• In blade 1, propeller 1, M282 is at the accessible interior position.
• It is conserved in propellers 1-3

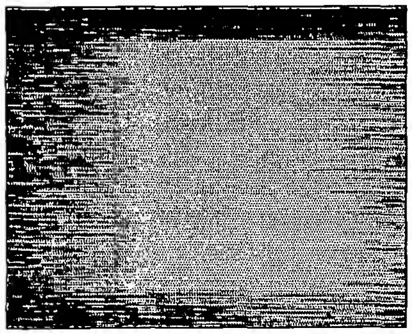
FIG. 30

Gene	Genbank Accession #	Protein Accession #
granulin	M75161	AAA58617
similar to cys/His rich protein	BC004544	AAH04544
IGF-BINDING PROTEIN 6	M69054	AAA88070
latent TGFb binding protein 4	AF051344	AAC39879
NOTCH 2	AF315356	AAG37073
fibulin 1	X53743	CAA37772
MDC15 (ADAM15)	U46005	AAC51112
DKFZp761G02121(notch1 Ca++ binding like)	AL137311	CAB70690
chordin	AF076612	AAC69835
fibronectin 1	U42594	AAD00019
MG50(melanoma associated antigen)	AF200348	AAF06354
unknown (notch 4-like)	AX068260	CAC27245
Slit 1	AB017167	BAA35184
tomoregulin (agarin repeat homology)	AB004064	BAA90820
sprouty 1	AF041037	AAC39566
sprouty 2	AF039843	AAC04258
NOV1	X96584	CAA65403
agrin	AF016903	AAC39776
fibrillin 1	L13923	AAB02036
thrombospondin1	X04665	CAA28370
ADAM19	AF134707	AAF22162
Nafl alpha	AJ011895	CAA09855
laminin alpha 5	Z95636	CAB09137
CRIM1	AF167706	AAF34409
nidogen	M30269	AAA59932
fibulin-2	X82494	CAA57876
thrombospondin 2	L12350	AAA03703
KIAA1323	AB037744	BAA92561
fibrillin-2	U03272	AAA18950
MEGF9	AB011542	BAA32470
integrin beta 1	X07979	CAA30790
matrilin-2 precursor	U69263	AAC51260
tenascin	X56160	A32160

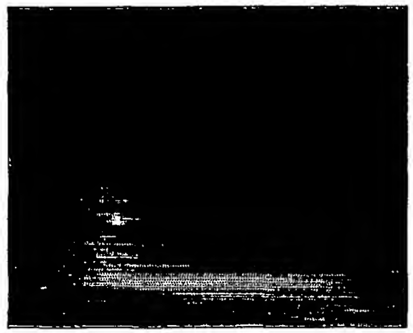
FIG. 31

FIG. 32

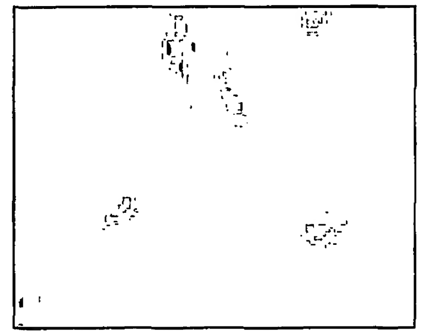
Affinity Purified 69546/47



Non-infected

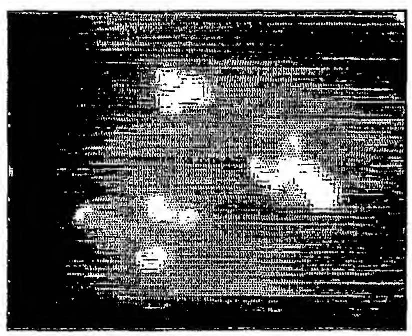


LRP5 virus infected, fluorescence

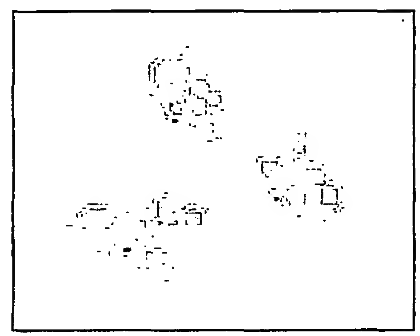


LRP5 virus infected, phase

Non-infected



HBM virus infected, fluorescence



HBM virus infected, phase

Antibody to: aa 165-177 (Mutation)

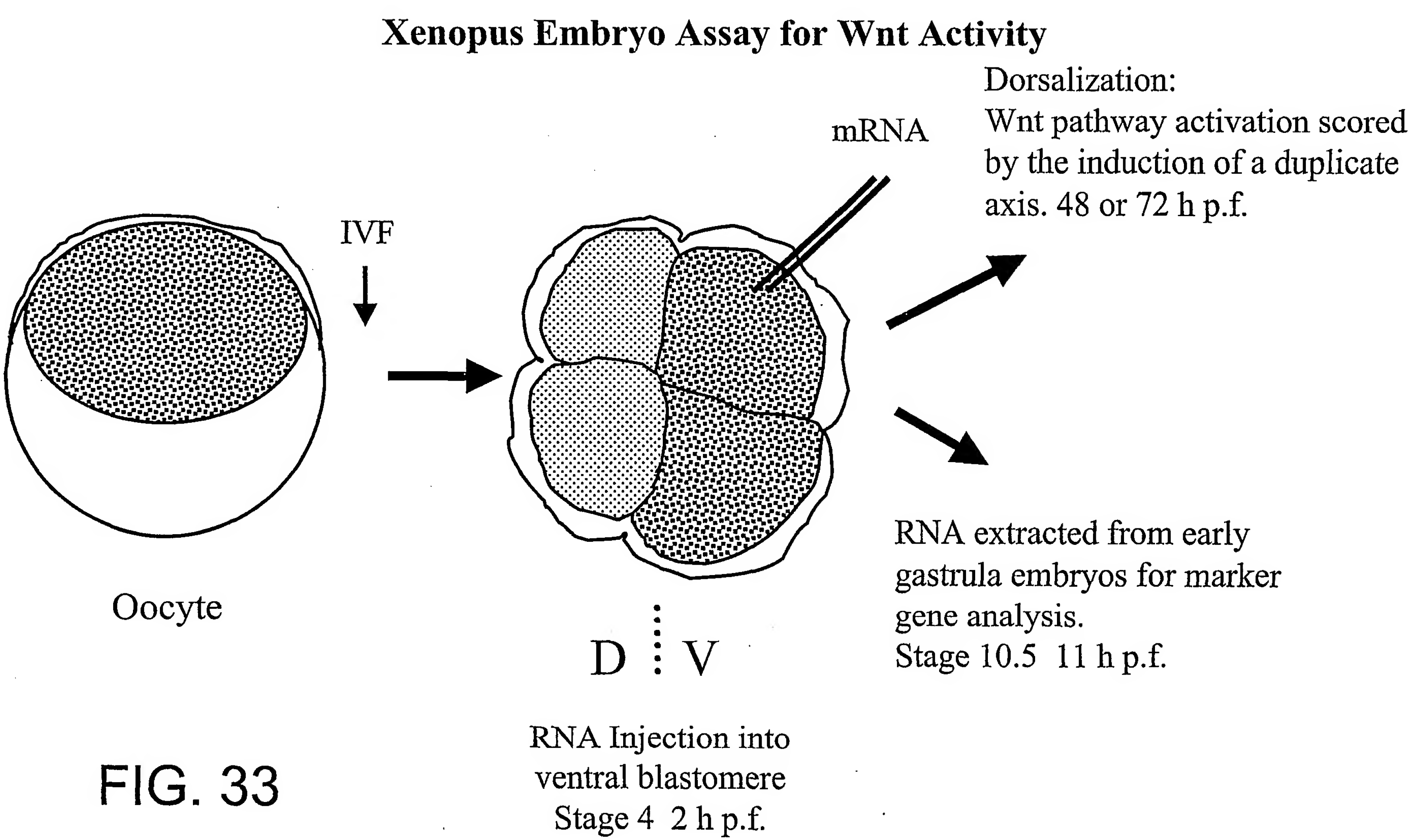

Xenopus Embryo Assay for Wnt Activity
Oocyte
IVF
mRNA
D
V
RNA Injection into ventral blastomere Stage 4 2 h p.f.
Dorsalization:
Wnt pathway activation scored by the induction of a duplicate axis. 48 or 72 h p.f.
RNA extracted from early gastrula embryos for marker gene analysis.
Stage 10.5 11 h p.f.

FIG. 33

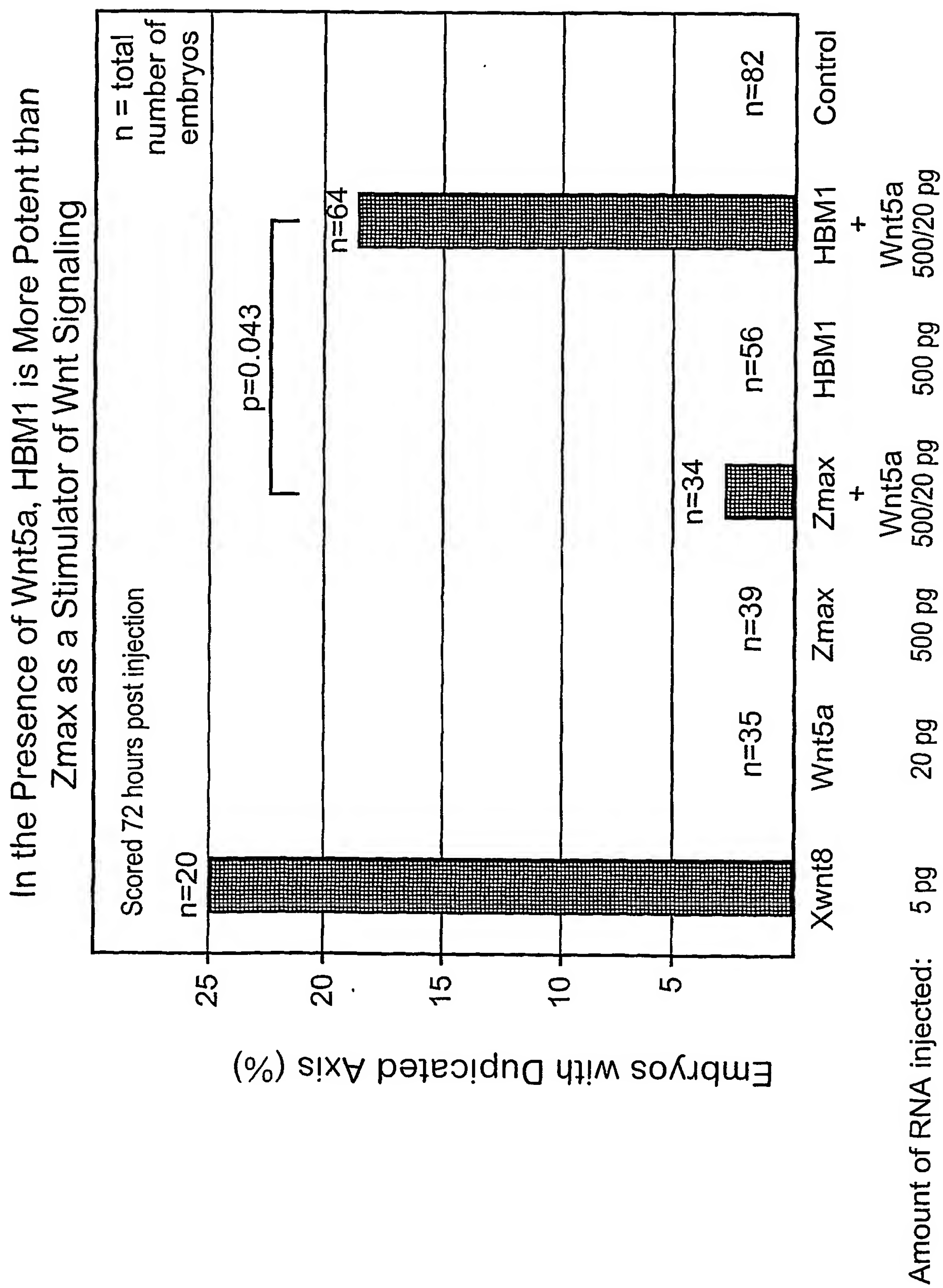

In the Presence of Wnt5a, HBM1 is More Potent than Zmax as a Stimulator of Wnt Signaling
Scored 72 hours post injection
n = total number of embryos
Embryos with Duplicated Axis (%)
25
20
15
10
5
n=20
n=35
n=39
n=34
n=56
n=64
n=82
p=0.043
Xwnt8
Wnt5a
Zmax
Zmax + Wnt5a
HBM1
HBM1 + Wnt5a
Control
Amount of RNA injected:
5 pg
20 pg
500 pg
500/20 pg
500 pg
500/20 pg

FIG. 34

Both Zmax and HBM1, in the presence of Wnt5a, induce secondary axis formation in Xenopus (photos at 48 hrs post-injection)

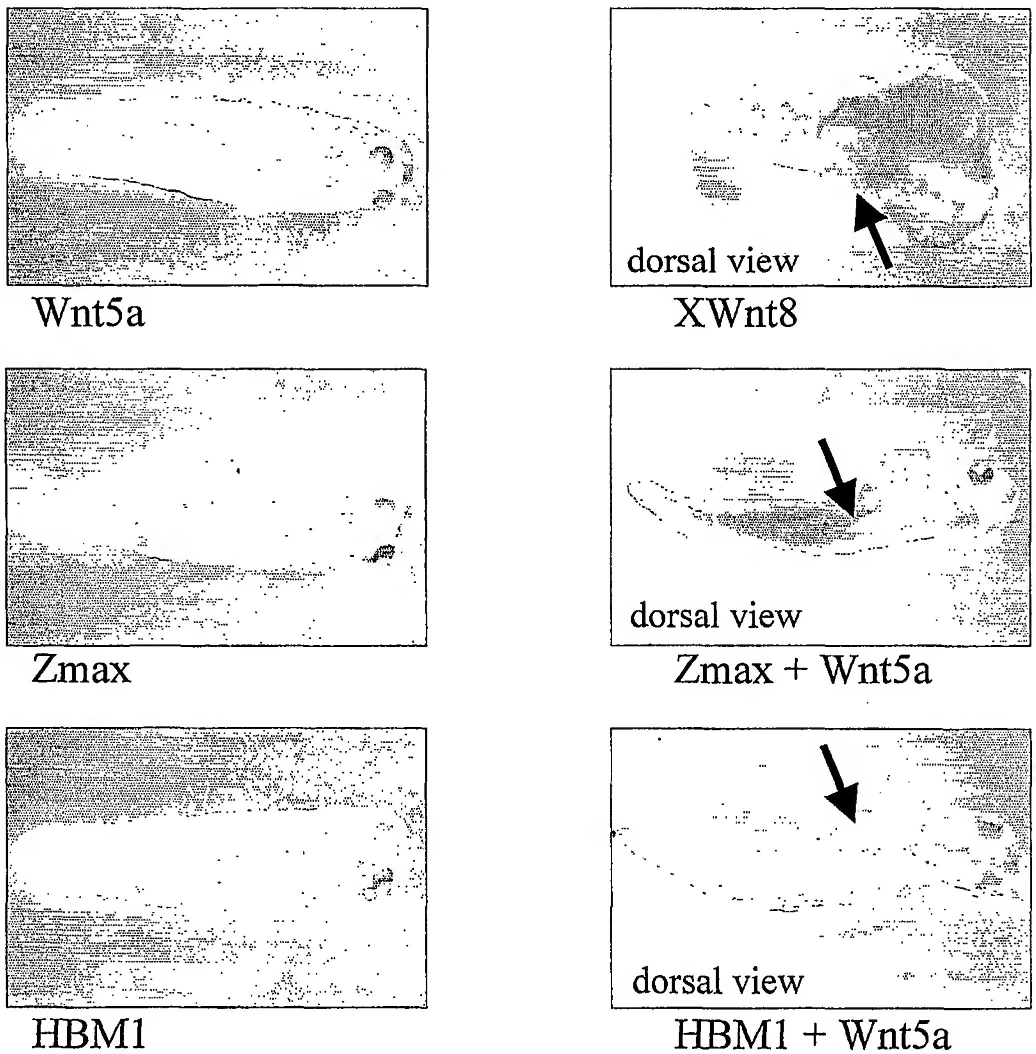


FIG. 35

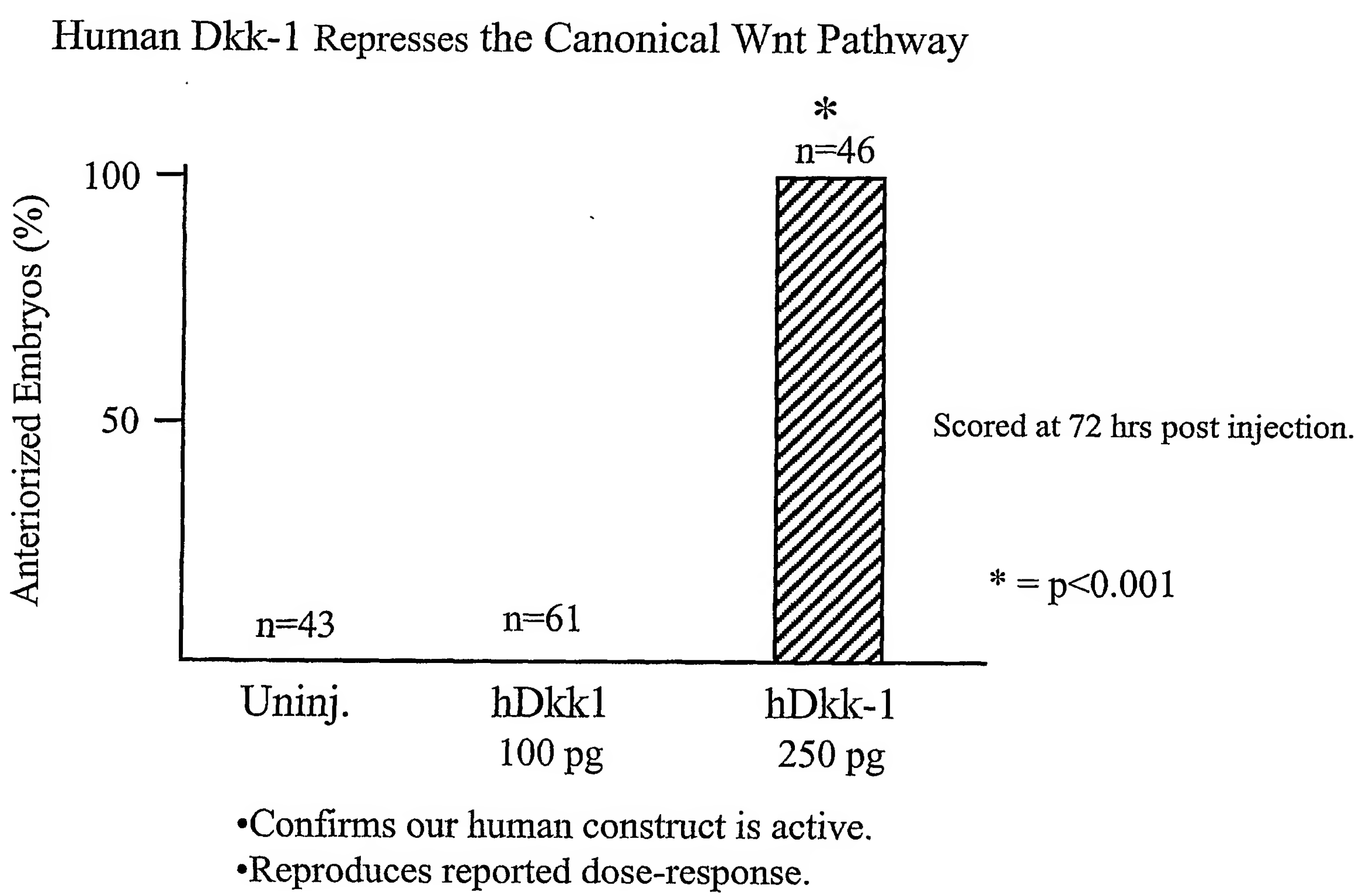

Human Dkk-1 Represses the Canonical Wnt Pathway
*
n=46
100
50
Anteriorized Embryos (%)
n=43
n=61
Uninj.
hDkk1
100 pg
hDkk-1
250 pg
Scored at 72 hrs post injection.
* = p<0.001
•Confirms our human construct is active.
•Reproduces reported dose-response.

FIG. 36

hDkk1 Represses Zmax- but Not HBM1-Mediated Wnt Signaling

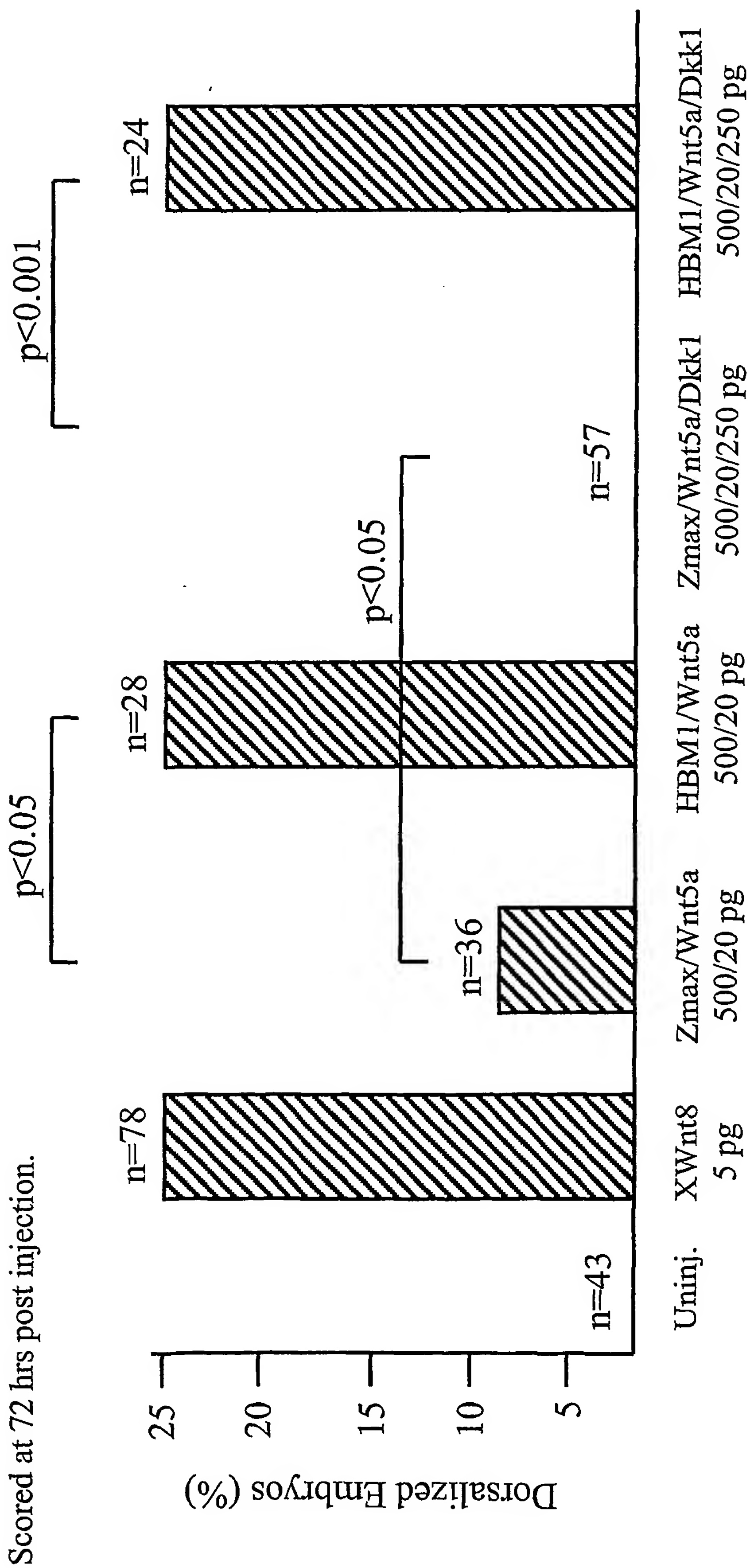


FIG. 37

zmaxLBD
1,4
screen X
peptide
library

Peptide Number	Peptide Sequence	No. of Hits
9	VVLCSRCGRLWRWSCG	1
12	EVRQVTCIRCRRGFLL	1
13	GGGGMWEAWSCYACG	1
14	GWRWCGRCGALWWRRV	3

FIG. 38

Listed are the pcDNA3.1 construct names followed by the DNA sequence

OST258 (control for OST 259-OST262 and OST264,OST265)
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCC

OST259
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCATGAGCGATAAAATTATTCACCTGA
CTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGAATTCCGTGGTTCTGTGTTCGCGTTG
TGGGCGTTTGTGGCGGTGGTCGTGTGGGACTAGTGGTCCGTGCAAAATGATCG
CCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCA
AAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGG
GTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAA
GCGGCCGC

OST260
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCATGAGCGATAAAATTATTCACCTGA
CTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGAATTCCGGGTGGCGGTGGTGTGGTCG
GTGTGGGGCTTTGTGGTGGCGGCGTGTTACTAGTGGTCCGTGCAAAATGATCG
CCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCA
AAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGG
GTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAA
GCGGCCGC

OST261
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCATGAGCGATAAAATTATTCACCTGA
CTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGAATTCCGAGGTGCGGCAGGTTACGTG
TATTAGGTGTCGTCGGGGTTTTCTGTTGACTAGTGGTCCGTGCAAAATGATCG
CCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCA

FIG. 39A

AAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGG
GTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAA
GCGGCCGC

OST262
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCATGAGCGATAAAATTATTCACCTGA
CTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGAATTCCGGTGGTGGGGGATGATTTG
GGAGGCTTGGAGTTGTTATGCGTGTGGGACTAGTGGTCCGTGCAAAATGATCG
CCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCA
AAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGG
GTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAA
GCGGCCGC

OST263
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCATGAGCGATAAAATTATTCACCTGA
CTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGAATTCCTTGTGGATTGGGCCGGGTGA
TCAGGGTCTGTTTCGGCGTTTTGTTTTTACTAGTGGTCCGTGCAAAATGATCG
CCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCA
AAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGG
GTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAA
GCGGCCGC

OST264
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCGTGTCTTCTGATCAAAATCATTTCC
GAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACC
TTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGT
GTTGTGCTAGACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGT
CAAGTGTGTACCAAGCATAGGAGAAAAGGCTCTCATGGACTAGAAATATTCCA
GCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGAAAGATCACCATC
AAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGAGACACTAAGCGGCCGC

FIG. 39B

OST265
AAGCTTGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTG
GGTTCCAGGTTCCACTGGTGACGGATCCTGCGCTAGTCCCACCCGCGGAGGGG
ACGCGGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATG
CGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTC
TTCTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCT
TTGGTAATGATCATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCT
TCAAAAATGTATCACACCAAAGGACAAGAAGGTTCTGTTTGTCTCCGGTCATC
AGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGTCCAAGATCTGTA
AACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCTCT
CATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCTA
AGCGGCCGC

OST266
AAGCTTGCCACCATGGGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGT
GGTGCGGTCCGAATTCCTATGCGTGGTTGTTTTCTTGTAGTAGGTGTAGGTGG
TGGTTGCCTTGGACTAGTGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
AATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATC
AAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGG
TCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAAGCGGCCGC

OST267
AAGCTTGCCACCATGGGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGT
GGTGCGGTCCGAATTCCATTTGTGAGGTTGTGAGGTTGTGGAGTCGGTATCCT
TGGTCTTGGGTGACTAGTGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
AATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATC
AAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGG
TCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAAGCGGCCGC

FIG. 39C

OST268
AAGCTTGCCACCATGGGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGT
GGTGCGGTCCGAATTCCGGTTGTACTAGTGCGGTGTGTGGTGCTTGGGCTGAG
GCGGGTAGGTTTTATTGTACTAGTGGTCCGTGCAAAATGATCGCCCCGATTCT
GGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACA
TCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACT
CTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTC
TAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAAGCGGCCGC

OST269 (irrelevant control peptide for OST266-OST268)
AAGCTTGCCACCATGGGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGT
GGTGCGGTCCGAATTCCTTGTGGATTGGGCCGGGTGATCAGGGTCTGTTTCGG
CGTTTTGTTTTTACTAGTGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
AATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATC
AAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGG
TCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTAAGCGGCCGC

FIG. 39D

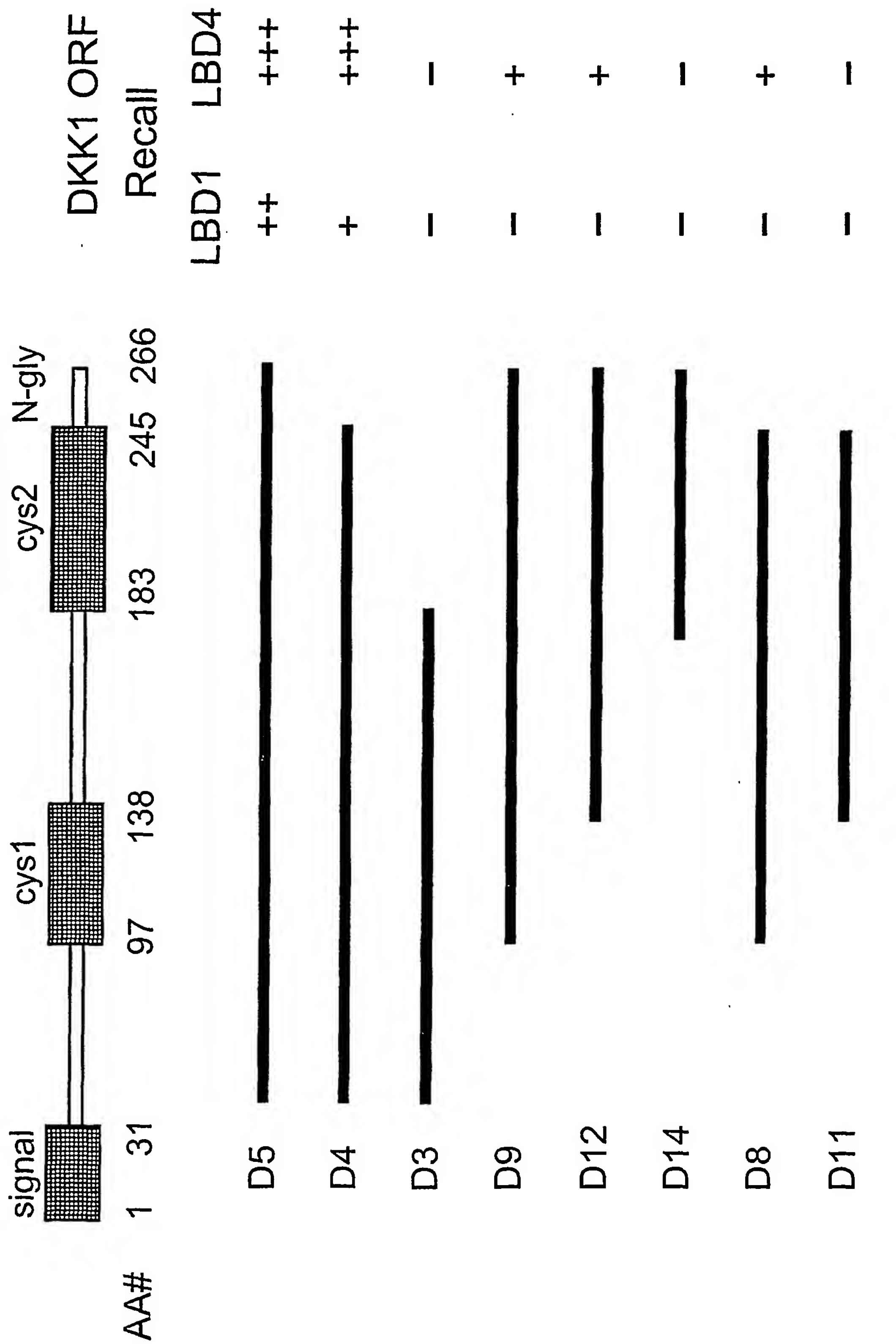

DKK1 ORF
Recall
LBD1 LBD4
AA#
signal
cys1
cys2
N-gly
1
31
97
138
183
245
266
D5 ++ +++
D4 + +++
D3 - -
D9 - +
D12 - +
D14 - -
D8 - +
D11 - -

FIG. 40

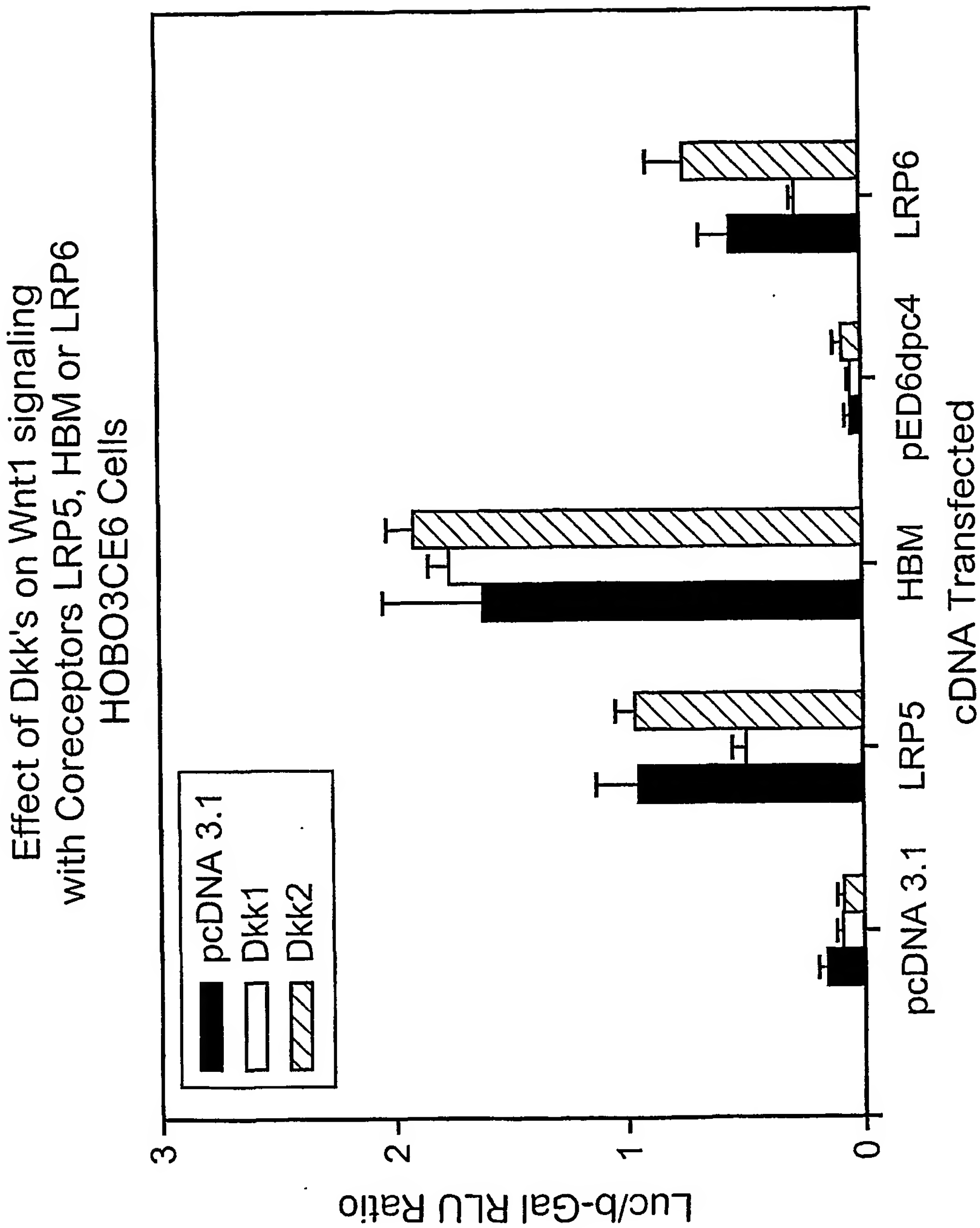

Effect of Dkk's on Wnt1 signaling
with Coreceptors LRP5, HBM or LRP6
HOBO3CE6 Cells
pcDNA 3.1
Dkk1
Dkk2
Luc/b-Gal RLU Ratio
0
1
2
3
pcDNA 3.1
LRP5
HBM
pED6dpc4
LRP6
cDNA Transfected

FIG. 41

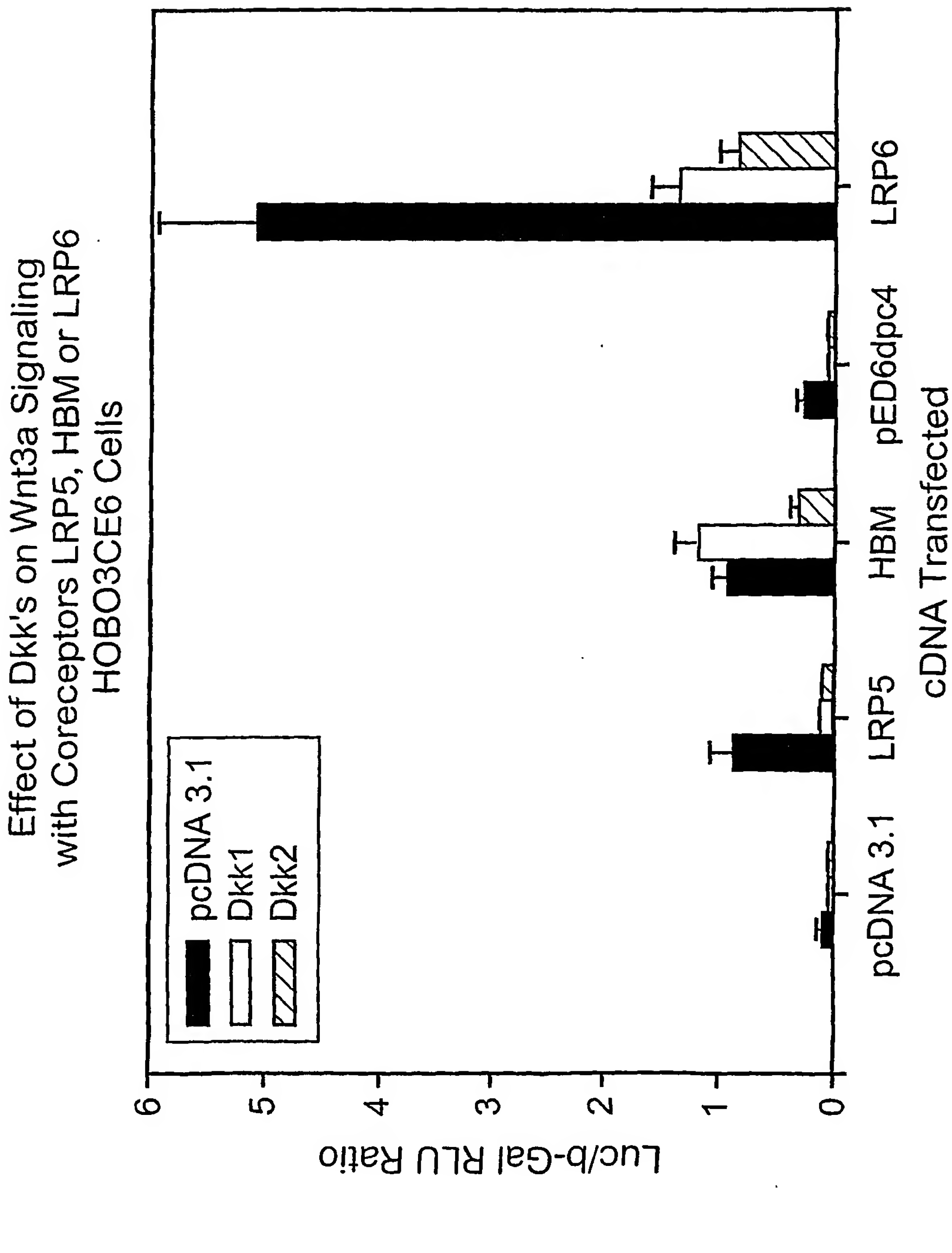

Effect of Dkk's on Wnt3a Signaling
with Coreceptors LRP5, HBM or LRP6
HOBO3CE6 Cells
pcDNA 3.1
Dkk1
Dkk2
Luc/b-Gal RLU Ratio
0
1
2
3
4
5
6
pcDNA 3.1
LRP5
HBM
pED6dpc4
LRP6
cDNA Transfected

FIG. 42

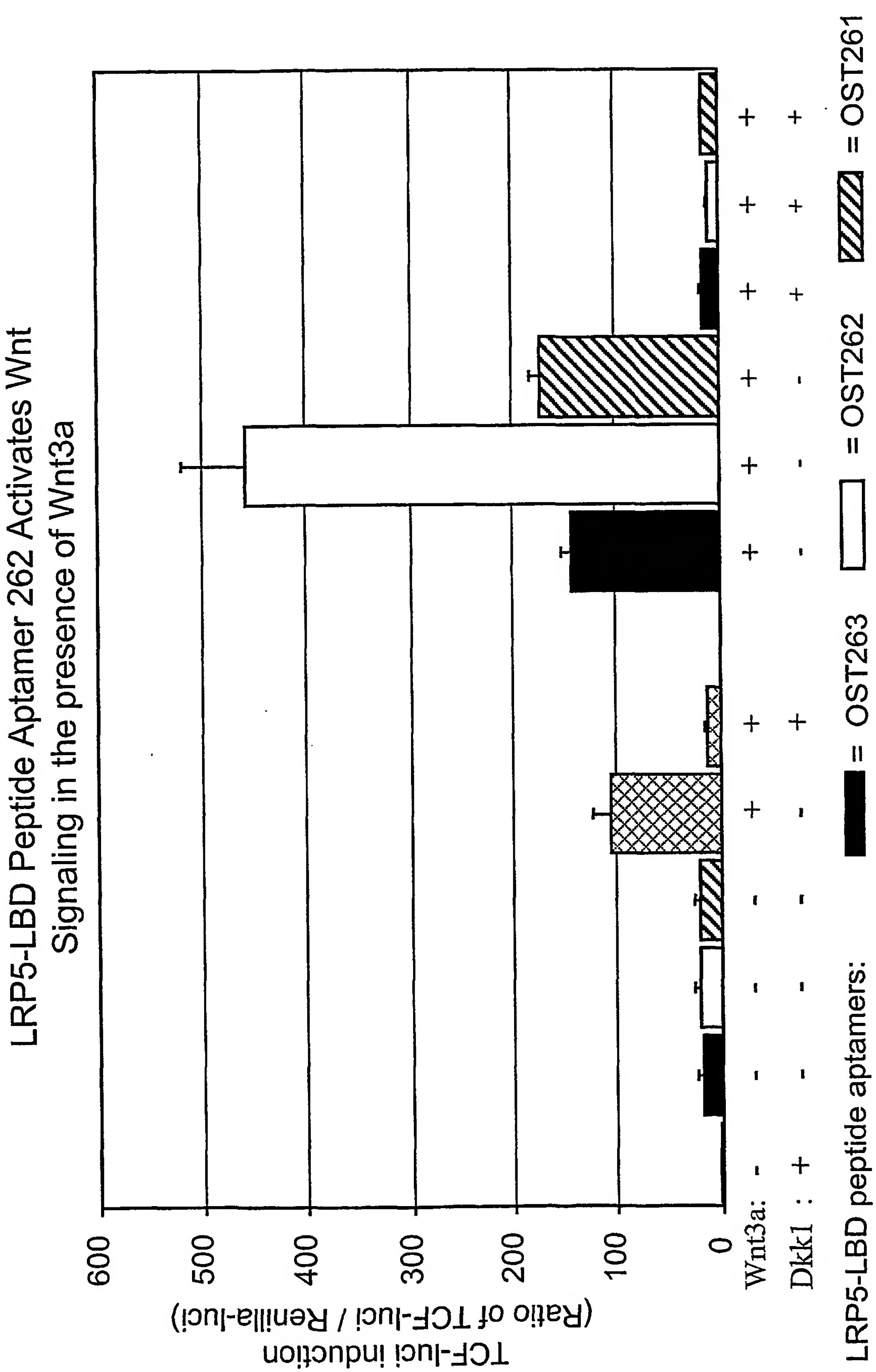

LRP5-LBD Peptide Aptamer 262 Activates Wnt
Signaling in the presence of Wnt3a
TCF-luci induction
(Ratio of TCF-luci / Renilla-luci)
600
500
400
300
200
100
0
Wnt3a: - - - - + + + + + + + +
Dkk1 : + - - - - + - - - + + +
LRP5-LBD peptide aptamers:
= OST263
= OST262
= OST261

FIG. 43

Listed below are the amino acid sequences corresponding to the pcDNA3.1 constructs in Appendix 1A

OST258
METDTLLLWVLLLWVPGSTGDGS

OST259
METDTLLLWVLLLWVPGSTGDGSMSDKIIHLTDDSFDTDVLKADGAILVDFWA
EWCGPNSVVLCSRCGRLWRWSCGTSGPCKMIAPILDEIADEYQGKLTVAKLNI
DQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

OST260
METDTLLLWVLLLWVPGSTGDGSMSDKIIHLTDDSFDTDVLKADGAILVDFWA
EWCGPNSGWRWCGRCGALWWRRVTSGPCKMIAPILDEIADEYQGKLTVAKLNI
DQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

OST261
METDTLLLWVLLLWVPGSTGDGSMSDKIIHLTDDSFDTDVLKADGAILVDFWA
EWCGPNSEVRQVTCIRCRRGFLLTSGPCKMIAPILDEIADEYQGKLTVAKLNI
DQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

OST262
METDTLLLWVLLLWVPGSTGDGSMSDKIIHLTDDSFDTDVLKADGAILVDFWA
EWCGPNSGGGGMIWEAWSCYACGTSGPCKMIAPILDEIADEYQGKLTVAKLNI
DQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

OST263
METDTLLLWVLLLWVPGSTGDGSMSDKIIHLTDDSFDTDVLKADGAILVDFWA
EWCGPNSLWIGPGDQGLFRRFVFTSGPCKMIAPILDEIADEYQGKLTVAKLNI
DQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

OST264
METDTLLLWVLLLWVPGSTGDGSVSSDQNHFRGEIEETITESFGNDHSTLDGY
SRRTTLSSKMYHTKGQEGSVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCT
KHRRKGSHGLEIFQRCYCGEGLSCRIQKDHHQASNSSRLHTCQRH

FIG. 44A

OST265
METDTLLLWVLLLWVPGSTGDGSCASPTRGGDAGVQICLACRKRRKRCMRHAM
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMY
HTKGQEGSVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLE
IFQRCYCGEGLSC.

OST266
MGDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPNSYAWLFSCSRCRWWLPW
TSGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKN
GEVAATKVGALSKGQLKEFLDANLA

OST267
MGDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPNSICEVVRLWSRYPWSWV
TSGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKN
GEVAATKVGALSKGQLKEFLDANLA

OST268
MGDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPNSGCTSAVCGAWAEAGRF
YCTSGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLF
KNGEVAATKVGALSKGQLKEFLDANLA

OST269
MGDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPNSLWIGPGDQGLFRRFVF
TSGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKN
GEVAATKVGALSKGQLKEFLDANLA

FIG. 44B

FIG. 45

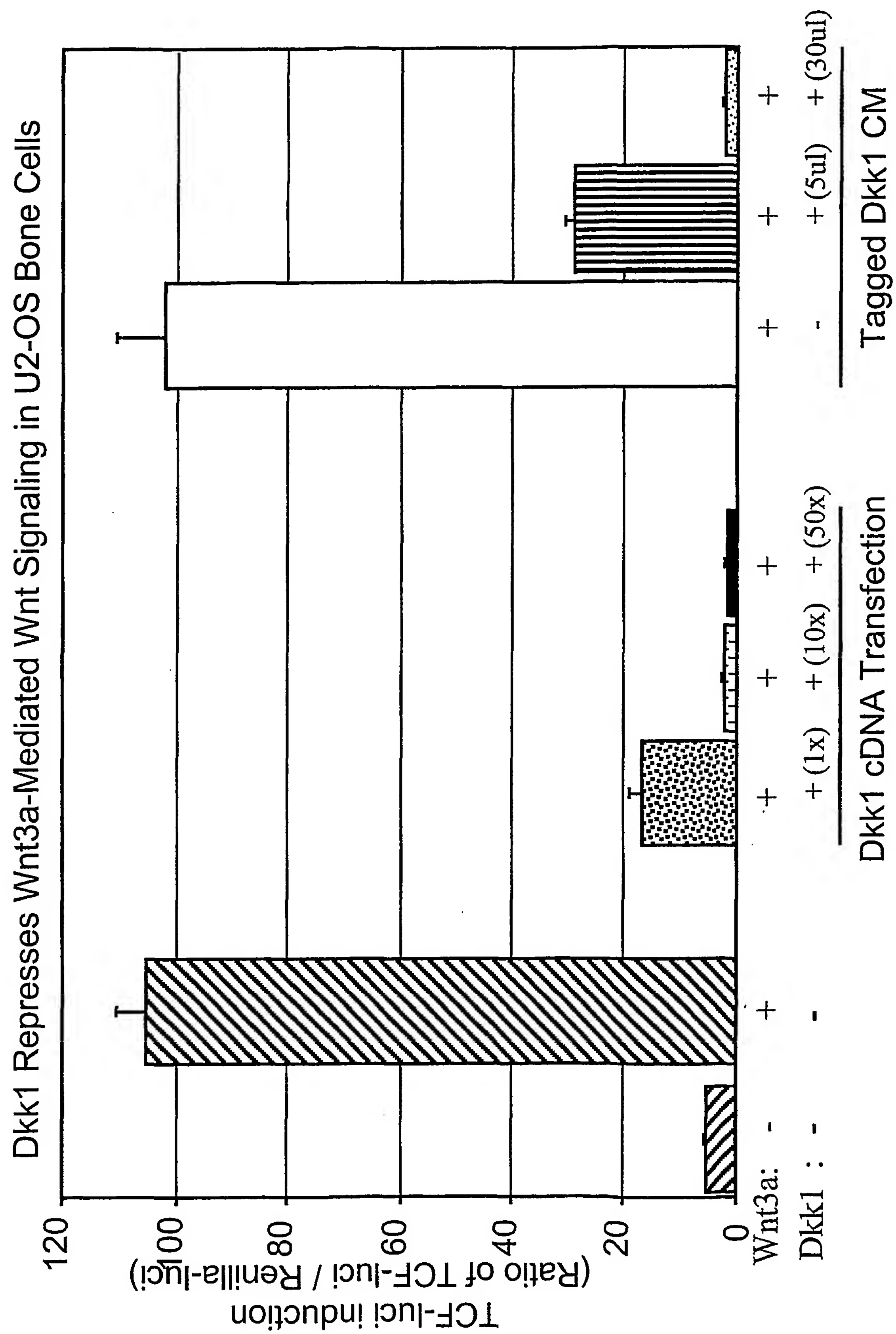
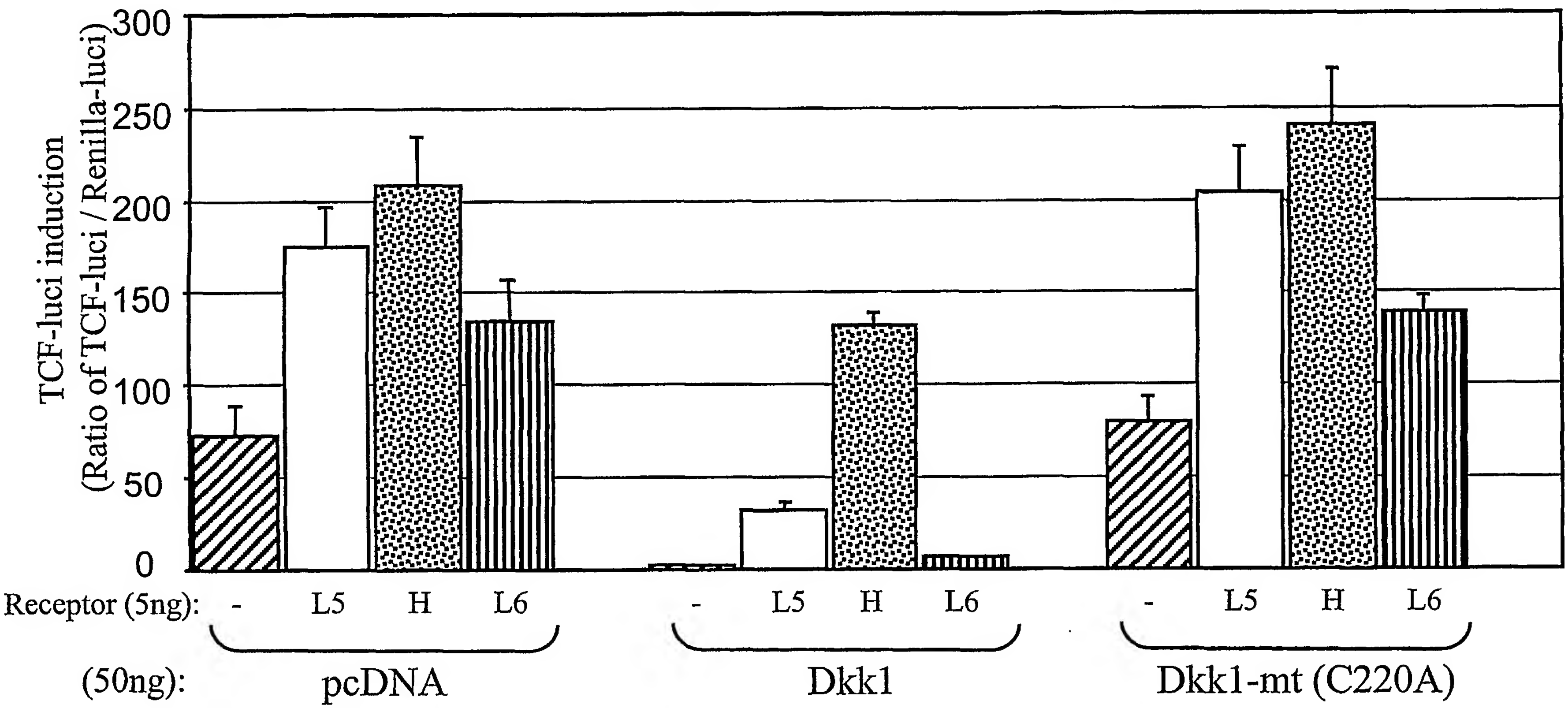

Dkk1 Represses Wnt3a-Mediated Wnt Signaling in U2-OS Bone Cells
TCF-luci induction
(Ratio of TCF-luci / Renilla-luci)
120
100
80
60
40
20
0
Wnt3a: - + + + + + + +
Dkk1 : - - + (1x) + (10x) + (50x) - + (5ul) + (30ul)
Dkk1 cDNA Transfection
Tagged Dkk1 CM

FIG. 46

Wnt1 - HBM generated TCF-luci is not efficiently inhibited by Dkk1 in U2-OS bone cells.



- With Wnt1 the TCF-signal generated by LRP5 is greater than that of LRP6.
- LRP5/6 -Wnt1 induced TCF- is efficiently blocked byDkk1

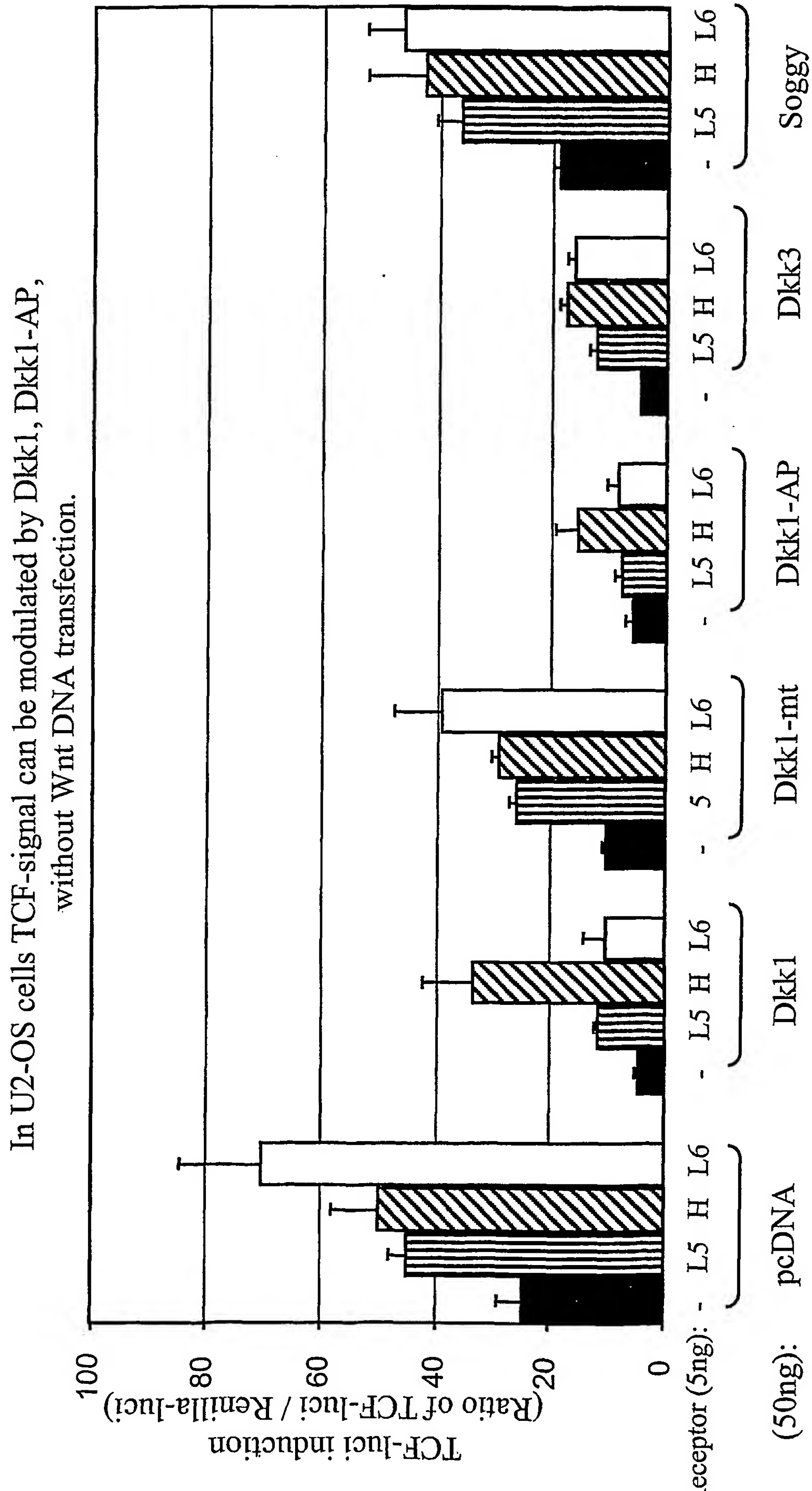

In U2-OS cells TCF-signal can be modulated by Dkk1, Dkk1-AP,
without Wnt DNA transfection.
TCF-luci induction
(Ratio of TCF-luci / Renilla-luci)
100
80
60
40
20
0
Receptor (5ng): - L5 H L6 - L5 H L6 - 5 H L6 - L5 H L6 - L5 H L6 - L5 H L6
(50ng): pcDNA Dkk1 Dkk1-mt Dkk1-AP Dkk3 Soggy

FIG. 47

FIG. 48

Aptamers 261 and 262 from the LRP5-LBD Activate Wnt Signaling in Xenopus

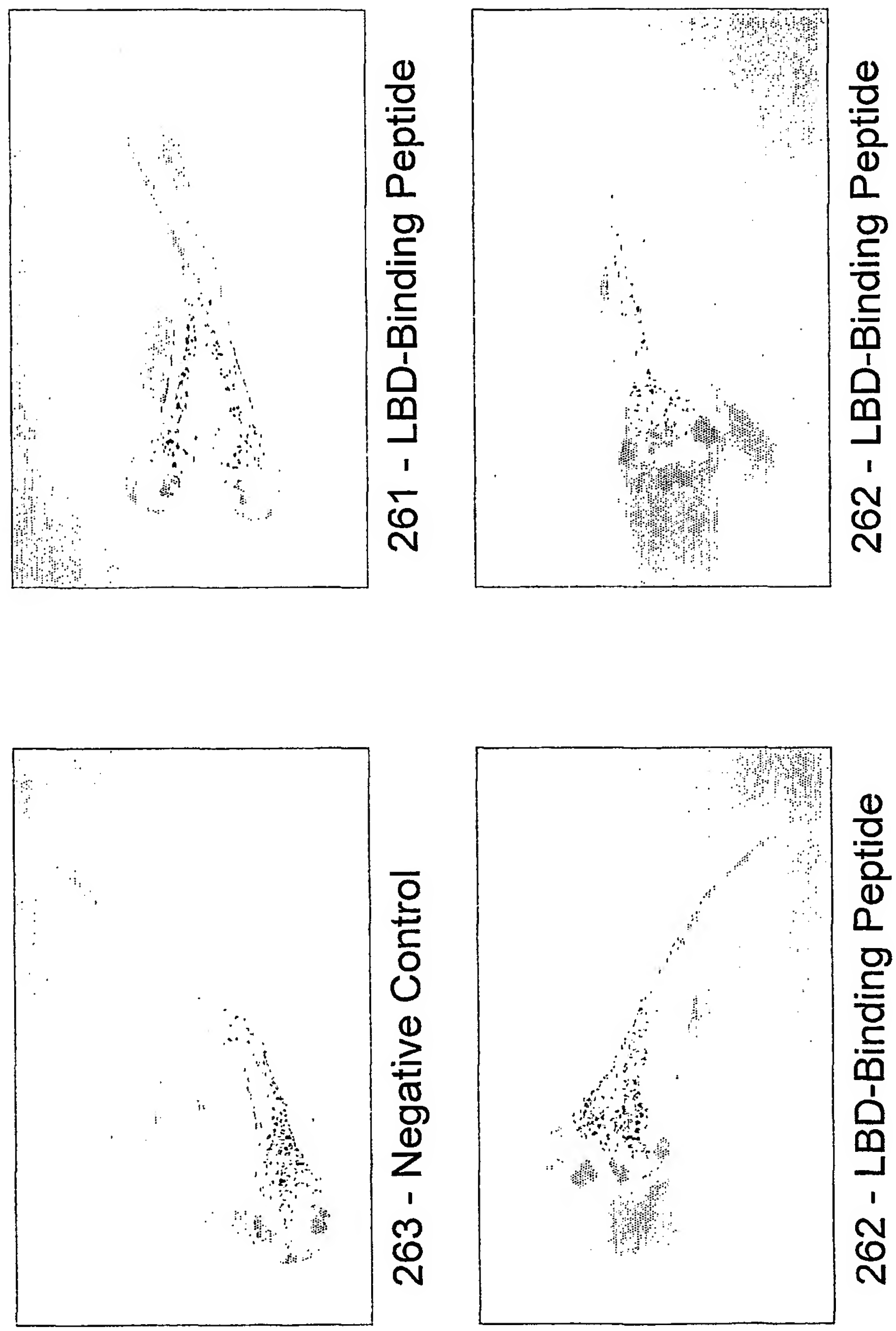
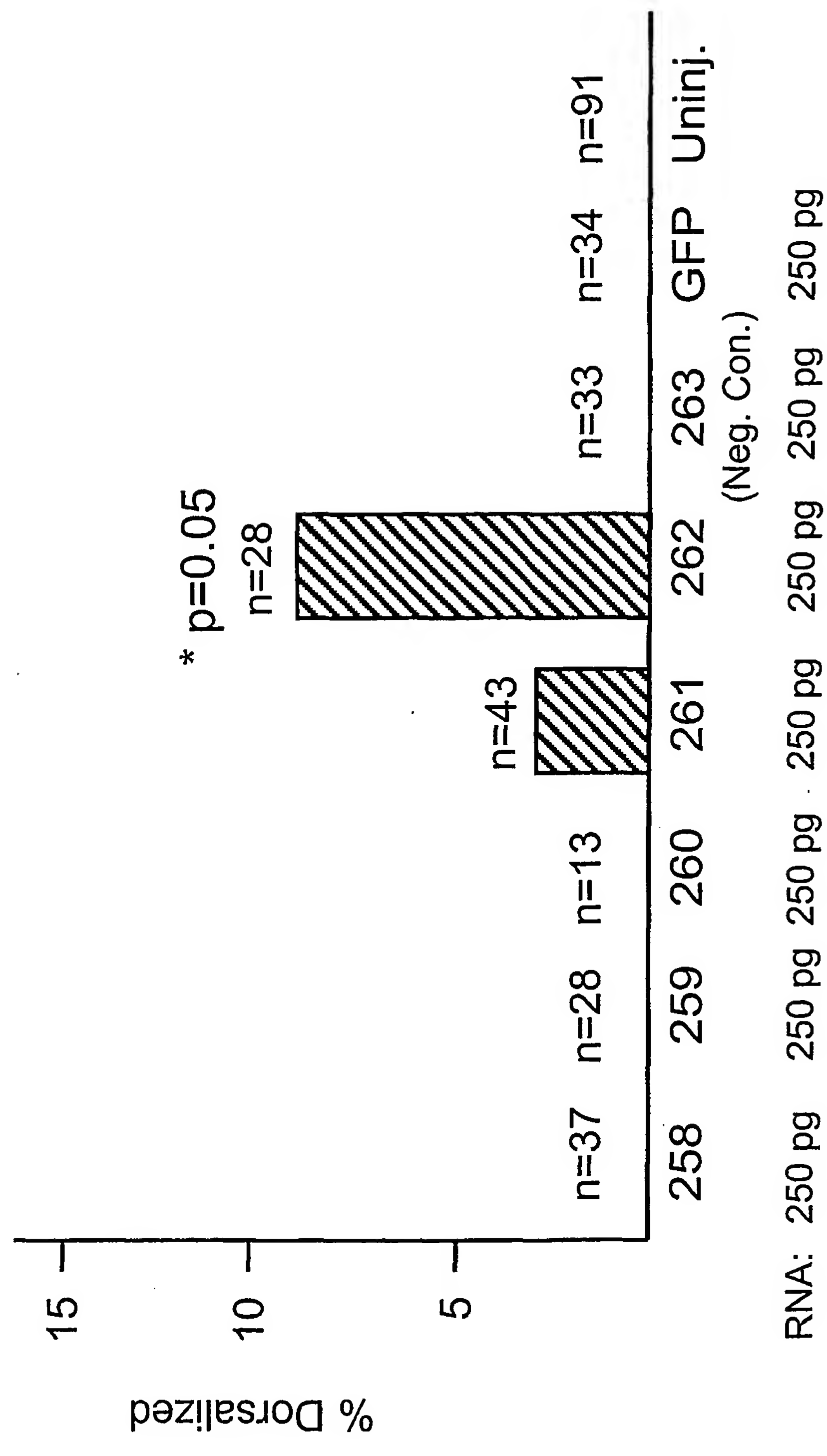


FIG. 49

LRP5 Peptide Aptamers 261 and 262 Induce Wnt Signaling



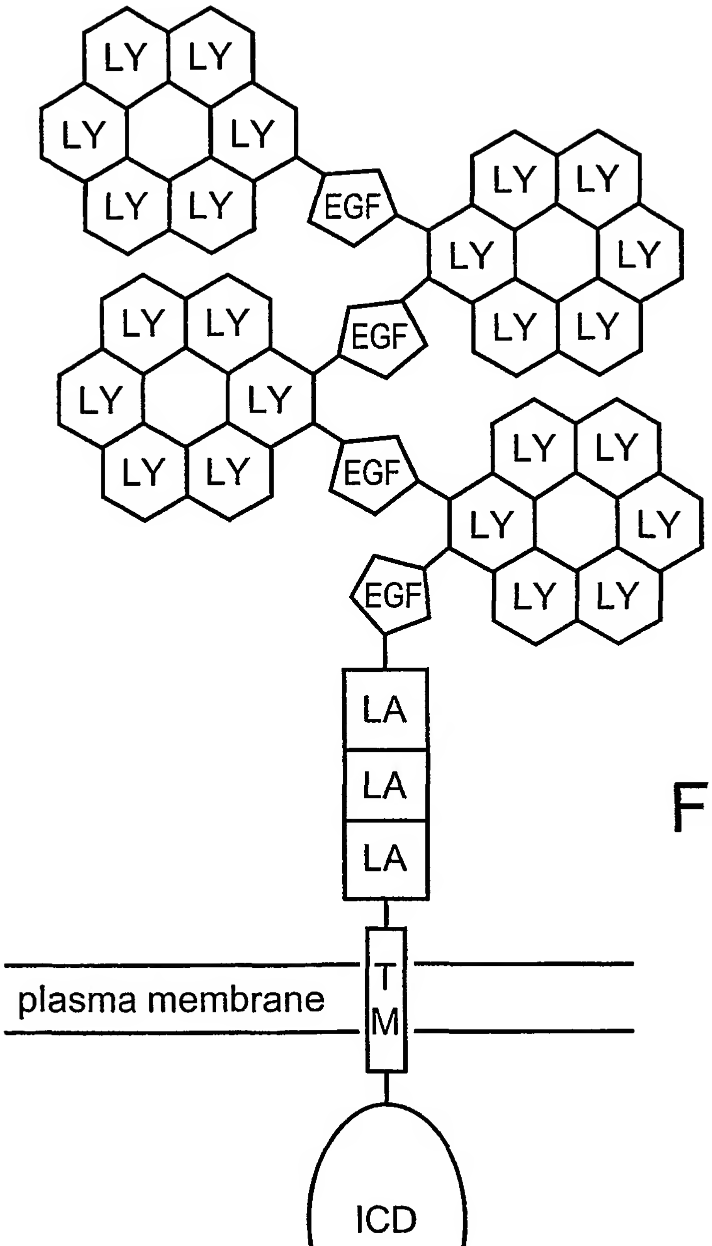


FIG. 50

LY propeller blade (YWTD "domain"/repeat 1-43-45 aa ae ea./~265/prop.])
EGF epidermal growth factor-like domain [~42 aa]
LA LDL receptor class A module [~38 aa]
TM transmembrane helix [22 aa]
ICD intracellular domain [107 aa]

Blades 1 @ = **BOLD DOUBLE UNDERLINE UPPERCASE** Blades 2 @ = lower case – dashed box

Blades 3 @ = BOLD UPPERCASE BOX Blades 4 @ = double underline lower case

Blades 5 @ = BOLD UPPERCASE DASHED UNDERLINE Blades 6 @ = double underline bold lower case

Top loops @ **bold lower case** Bottom loops @ **BOLD UPPER CASE**

```
AF064984m_ywtd6a     -ASPLLLFANRRDVRLVDAGGVKL----ESTIVASGLEDAAAVDFQFSKGAVYWTDVSEE
AF077847m_ywtd6a     -ASPLLLFANRRDVRLVDAGGVKL----ESTIVASGLEDAAAVDFQFSKGAVYWTDVSEE
AF077820h_ywtd6a     -ASPLLLFANRRDVRLVDAGGVKL----ESTIVVSGLEDAAAVDFQFSKGAVYWTDVSEE
AF074264h_ywtd6a     --APLLLYANRRDLRLVDATNGKE----NATIVVGGLEDAAAVDFVFSHGLIYWSDVSEE
AF074265m_ywtd6a     --APLLLYANRRDLRLVDATNGKE----NATIVVGGLEDAAAVDFVFGHGLIYWSDVSEE
1lpx                 DEEPFLIFANryYLRKLNLDGS------NYTLLKQglnnavaldfDYREQmiywtdvttq
af064984m_ywtd6c     -PEAFLVFTSRATIHRISLETNNN----DVAIPLTGVKEASALDFDVSNNHIYWTDVSLK
af077820h_ywtd6c     -PEAFLVFTSRAAIHRISLETNNN----DVAIPLTGVKEASALDFDVSNNHIYWTDVSLK
af074264h_ywtd6c     -PEAFLLFSRRADIRRISLETNNN----NVAIPLTGVKEASALDFDVTDNRIYWTDISLK
af074265m_ywtd6c     -PEAFLLFSRRADIRRISLETNNN----NVAIPLTGVKEASALDFDVTDNRIYWTDISLK
af064984m_ywtd6b     GAEEVLLLARRTDLRRISLDTPDF---TDIVLQVGDIRHAIAIDYDPLEGYVYWTDDEVR
af077820h_ywtd6b     ---EVLLLARRTDLRRISLDTPDF---TDIVLQVDDIRHAIAIDYDPLEGYVYWTDDEVR
af074264h_ywtd6b     GATELLLLARRTDLRRISLDTPDF---TDIVLQLEDIRHAIAIDYDPVEGYIYWTDDEVR
af074265m_ywtd6b     GATELLLLARRTDLRRISLDTPDF---TDIVLQLEDIRHAIAIDYDPVEGYIYWTDDEVR
1ndx                 PPGTHLLFAQtgKIERLPLEGNTMRKTEAKAFLHvpakviiglafDCVDKmvywtditep
af064984m_ywtd6d     -PSTFLLFSQKFAISRMIPDDQLS---PDLVLPLHGLRNVKAINYDPLDKFIYWVDGRQN
af077820h_ywtd6d     -PTTFLLFSQKSAISRMIPDDQHS---PDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQN
```

FIG. 51A

```
af074264h_ywtd6d   -PTTFLLFSQKSAINRMVIDEQQS---PDIILPIHSLRNVRAIDYDPLDKQLYWIDSRQN
af074265m_ywtd6d   -PSTFLLFSQKSAINRMVIDEQQS---PDIILPIHSLRNVRAIDYDPLDKQLYWIDSRQN
DSC_SEC            -CCCEEHHHHCCCCCEEECCCCCC----CEEEEECCCCCEEEEEECCCCCEEEEECCCHH
PROB_H             -11243598544444321211110----00000243444310001111111000011257
PROB_E             -00256301010111665321111----29999611011569975422135888632211
PROB_C             -99611211556555124578889----81111256655231134577864222467642
AF064984m_ywtd6a   AIKQTYLNQTG----AAAQNIVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTS
AF077847m_ywtd6a   AIKQTYLNQTG----AAAQNIVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTS
AF077820h_ywtd6a   AIKQTYLNQTG----AAVQNVVISGLVSPDGLACDWVGKKLYWTDSETNRIEVANLNGTS
AF074264h_ywtd6a   AIKRTEFNKT-----ESVQNVVVSGLLSPDGLACDWLGEKLYWTDSETNRIEVSNLDGSL
AF074265m_ywtd6a   AIKRTEFNKS-----ESVQNVVVSGLLSPDGLACDWLGEKLYWTDSETNRIEVSNLDGSL
1lpx               gsmirrmhING----snvqvlhrtglsnPDGLAVDWVGGNLYWCdkgrdTIEVSKLNGAY
af064984m_ywtd6c   TISRAFMNGS------SVEHVIEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVARLDGQF
af077820h_ywtd6c   TISRAFMNGS------SVEHVVEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVARLDGQF
af074264h_ywtd6c   TISRAFMNGS------ALEHVVEFGLDYPEGMAVDWLGKNLYWADTGTNRIEVSKLDGQH
af074265m_ywtd6c   TISRAFMNGS------ALEHVVEFGLDYPEGMAVDWLGKNLYWADTGTNRIEVSKLDGQH
af064984m_ywtd6b   AIRRAYLDGS------GAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTS
af077820h_ywtd6b   AIRRAYLDGS------GAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTS
af074264h_ywtd6b   AIRRSFIDGS------GSQFVVTAQIAHPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTM
af074265m_ywtd6b   AIRRSFIDGS------GSQFVVTAQIAHPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTM
1ndx               sigrasLHGG------EpttiirqdlgsPEGIAVDHLGRNIFWTDsnldrIEVAKLDGTQ
af064984m_ywtd6d   -IKRAKDDGTQPS-MLTSPSQSLSPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLDGDA
af077820h_ywtd6d   -IKRAKDDGTQPF-VLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLSGEA
af074264h_ywtd6d   MIRKAQEDGSQGFTVVVSSVPSQNLEIQPYDLSIDIYSRYIYWTCEATNVINVTRLDGRS
```

FIG. 51B

```
af074265m_ywtd6d    SIRKAHEDGGQGFNVVANSVANQNLEIQPYDLSIDIYSRYIYWTCEATNVIDVTRLDGRS
DSC_SEC             HHHHEEECCCC----CCCEEEEEECCCCCCEEEEECCCCEEEECCCCCEEEEEECCCCC
PROB_H              99953211111----1131000011111111001332220001111111000221112
PROB_E              00135652111----12379999642111125796532336775110016999963000 1
PROB_C              11022247888----874211113578888743132465543348899831111259997
                                               *
AF064984m_ywtd6a    RKVLFWQDLDQPRAIALDPAHGYMYWTDWG-EAPRIERAGMDGSTRKIIVDSDIYWPNGL
AF077847m_ywtd6a    RKVLFWQDLDQPRAIALDPAHGYMYWTDWG-EAPRIERAGMDGSTRKIIVDSDIYWPNGL
AF077820h_ywtd6a    RKVLFWQDLDQPRAIALDPAHGYMYWTDWG-ETPRIERAGMDGSTRKIIVDSDIYWPNGL
AF074264h_ywtd6a    RKVLFWQELDQPRAIALDPSSGFMYWTDWG-EVPKIERAGMDGSSRFIIINSEIYWPNGL
AF074265m_ywtd6a    RKVLFWQELDQPRAIALDPSSGFMYWTDWG-EVPKIERAGMDGSSRFVIINTEIYWPNGL
1lpx                RTVLVNsglrePRALVVDVQNGYLYWTDwg-dhsLIGKIGMDGTNRSVIVdtkitwPNGL
af064984m_ywtd6c    RQVLVWRDLDNPRSLALDPTKGYIYWTEWG-GKPRIVRAFMDGTNCMTLVD-KVGRANDL
af077820h_ywtd6c    RQVLVWRDLDNPRSLALDPTKGYIYWTEWG-GKPRIVRAFMDGTNCMTLVD-KVGRANDL
af074264h_ywtd6c    RQVLVWKDLDSPRALALDPAEGFMYWTEWG-GKPKIDRAAMDGSERTTLVP-NVGRANGL
af074265m_ywtd6c    RQVLVWKDLDSPRALALDPAEGFMYWTEWG-GKPKIDRAAMDGSERTTLVP-NVGRANGL
af064984m_ywtd6b    RKILVSEDLDEPRAIVLHPVMGLMYWTDWG-ENPKIECANLDGRDRHVLVNTSLGWPNGL
af077820h_ywtd6b    RKILVSEDLDEPRAIALHPVMGLMYWTDWG-ENPKIECANLDGQERRVLVNASLGWPNGL
af074264h_ywtd6b    RKILISEDLEEPRAIVLDPMVGYMYWTDWG-EIPKIERAALDGSDRVVLVNTSLGWPNGL
af074265m_ywtd6b    RKILISEDLEEPRAIVLDPMVGYMYWTDWG-EIPKIERAALDGSDRVVLVNTSLGWPNGL
1ndx                RRVLfetdlvnPRGIVTDSVRGNLYWTDwnrdnpKIETSYMDGTNRRILVqddlglPNGL
af064984m_ywtd6d    MGVVLRGDRDKPRAIAVNAERGYMYFTNMQDHAAKIERASLDGTEREVLFTTGLIRPVAL
af077820h_ywtd6d    MGVVLRGDRDKPRAIVVNAERGYLYFTNMQDRAAKIERAALDGTEREVLFTTGLIRPVAL
af074264h_ywtd6d    VGVVLKGEQDRPRAIVVNPEKGYMYFTNLQERSPKIERAALDGTEREVLFFSGLSKPIAL
```

FIG. 51C

af074265m_ywtd6d	VGVVLKGEQDRPRAIVVNPEKGYMYFTNLQERSPKIERAALDGTEREVLFFSGLSKPIAL
DSC_SEC	CEEEEECCCCCCCEEECCCCCEEEEECCC-CCCHHHHCCCCCCEEEEEECCCCCCCC
PROB_H	3311024332134411112211100011111-1125475642111220000000011112
PROB_E	3599961110011176511001599962000-0012323211000149999822211123
PROB_C	4200125668965523487898411137990-9973312257999741111288898887 5
AF064984m_ywtd6a	TIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSI
AF077847m_ywtd6a	TIDLEEQKLYWADAKLSFIHHANLDGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSI
AF077820h_ywtd6a	TIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSI
AF074264h_ywtd6a	TLDYEEQKLYWADAKLNFIHKSNLDGTNRQAVVKGSLPHPFALTLFEDILYWTDWSTHSI
AF074265m_ywtd6a	TLDYQERKLYWADAKLNFIHKSNLDGTNRQAVVKGSLPHPFALTLFEDTLYWTDWNTHSI
1lpx	**TLDYINSRIYWADaredYIEFASLDGSNRHTVLSqdiphifaltlFEDyiywtdwetksi**
af064984m_ywtd6c	TIDYADQRLYWTDLDTNMIESSNMLGQER-MVIADDLPYPFGLTQYSDYIYWTDWNLHSI
af077820h_ywtd6c	TIDYADQRLYWTDLDTNMIESSNMLGQER-VVIADDLPHPFGLTQYSDYIYWTDWNLHSI
af074264h_ywtd6c	TIDYAKRRLYWTDLDTNLIESSNMLGLNR-EVIADDLPHPFGLTQYQDYIYWTDWSRRSI
af074265m_ywtd6c	TIDYAKRRLYWTDLDTNLIESSDMLGLNR-EVIADDLPHPFGLTQYQDYIYWTDWSRRSI
af064984m_ywtd6b	ALDLQEGKLYWGDAKTDKIEVINIDGTKRKTLLEDKLPHIFGFTLLGDFIYWTDWQRRSI
af077820h_ywtd6b	ALDLQEGKLYWGDAKTDKIEVINVDGTKRRTLLEDKLPHIFGFTLLGDFIYWTDWQRRSI
af074264h_ywtd6b	ALDYDEGKIYWGDAKTDKIEVMNTDGTGRRVLVEDKIPHIFGFTLLGDYVYWTDWQRRSI
af074265m_ywtd6b	ALDYDEGTIYWGDAKTDKIEVMNTDGTGRRVLVEDKIPHIFGFTLLGDYVYWTDWQRRSI
1ndx	**HFDAFSSQLCWVDagtnRAECLNPSQPSRRKALeg-lqypfavtSYGKnlyftdwkmnsv**
af064984m_ywtd6d	VVDNALGKLFWVDADLKRIESCDLSGANRLTLEDANIVQPVGLTVLGRHLYWIDRQQQMI
af077820h_ywtd6d	VVDNTLGKLFWVDADLKRIESCDLSGANRLTLEDANIVQPLGLTILGKHLYWIDRQQQMI
af074264h_ywtd6d	ALDSRLGKLFWADSDLRRIESSDLSGANRIVLEDSNILQPVGLTVFENWLYWIDKQQQMI
af074265m_ywtd6d	ALDSKLGKLFWADSDLRRIESSDLSGANRIVLEDSNILQPVGLTVFENWLYWIDKQQQMI
DSC_SEC	CCCCCCCCEEEECCCCCEEEEECCCCCCCCEEECCCCCCCCEEECCCCCEEECCCCCHHH

FIG. 51D

```
PROB_H              113444331001111244332112112241101211111110021122111122224577
PROB_E              443111137995221215556521000114896321111245663211366642110111
PROB_C              554555642114778651222477998755113578888754445787533356776422
AF064984m_ywtd6a    HACNKWTGEQRKEILSALYSPMDIQVLSQERQPPFHT
AF077847m_ywtd6a    HACNKWTGEQRKEILSALYSPMDIQVLSQERQPPFHT
AF077820h_ywtd6a    HACNKRTGGKRKEILSALYSPMDIQVLSQERQPFFHT
AF074264h_ywtd6a    LACNKYTGEGLREIHSDIFSPMDIHAFSQQRQPNA--
AF074265m_ywtd6a    LACNKYTGEGLREIHSNIFSPMDIHAFSQQRQPNA--
1lpx                nrahKTTGanktllistlhrPMDIHIYHPYR------
af064984m_ywtd6c    ERADKTSGRNRTLIQGHLDFVMDILVFHSSRQDGL--
af077820h_ywtd6c    ERADKTSGRNRTLIQGHLDFVMDILVFHSSRQDGL--
af074264h_ywtd6c    ERANKTSGQNRTIIQGHLDYVMDILVFHSSRQSG---
af074265m_ywtd6c    ERANKTSGQNRTIIQGHLDYVMDILVFHSSRQAG---
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DSC_SEC             HHHCCCCCCCCEEEEECCCCCCEEEEECCCCCCCCCC
PROB_H              7664422112321122322221111123322111101
PROB_E              1211121001368864322122566663321221111
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FIG. 51E

Possible Effect of Functional Mutations on Side Chain Interactions

Wild Type Mutant

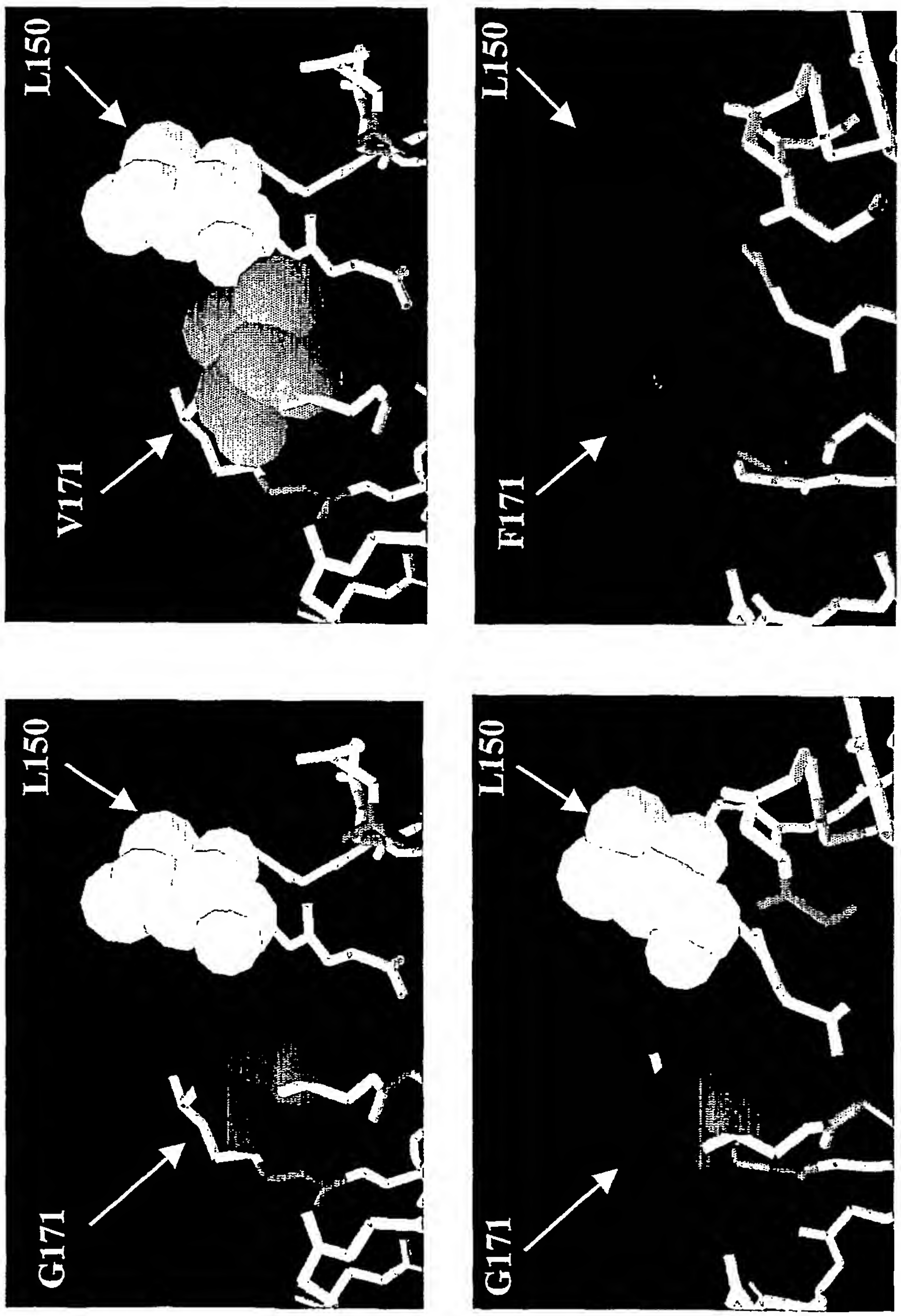

FIG. 52

Homology Model of LRP5's 2nd Propeller Domain
Propeller 2 Contains Two OPPG mutations

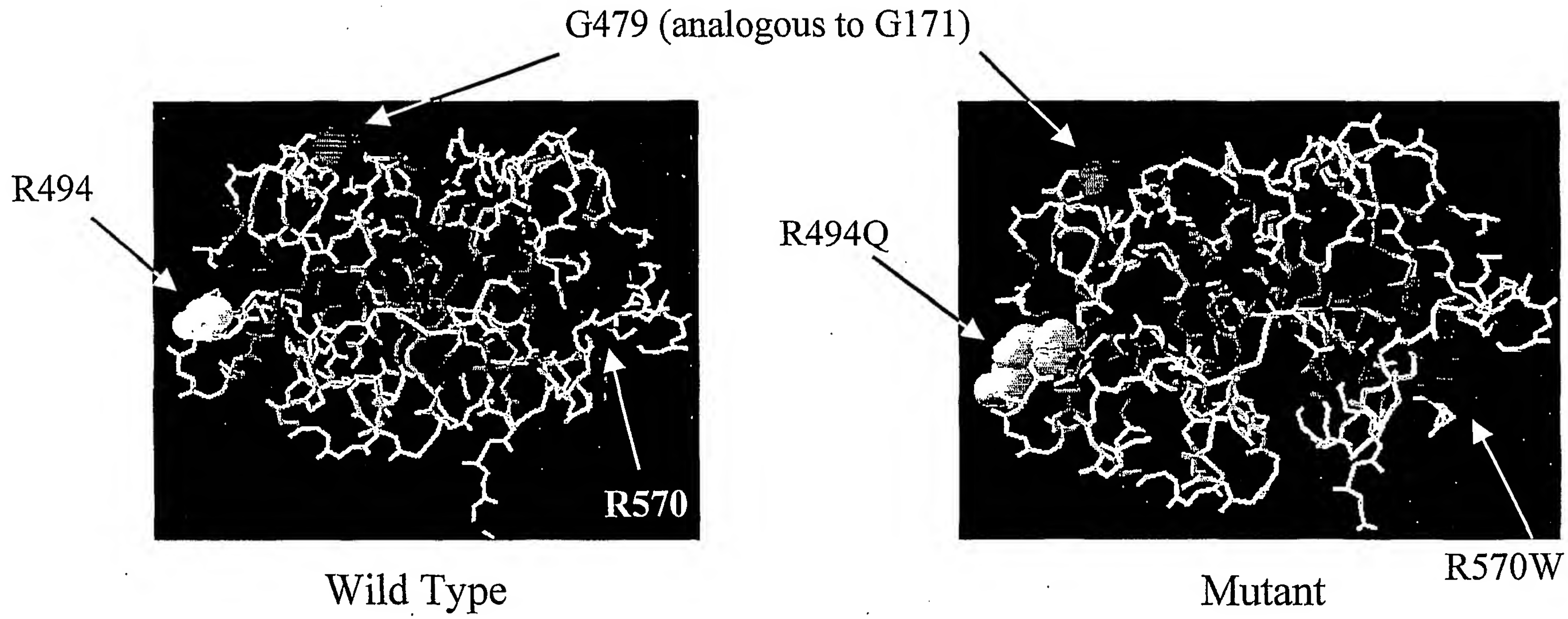

FIG. 53A

Homology Model of LRP5's 2nd Propeller Domain
Propeller 2 Contains Two OPPG mutations

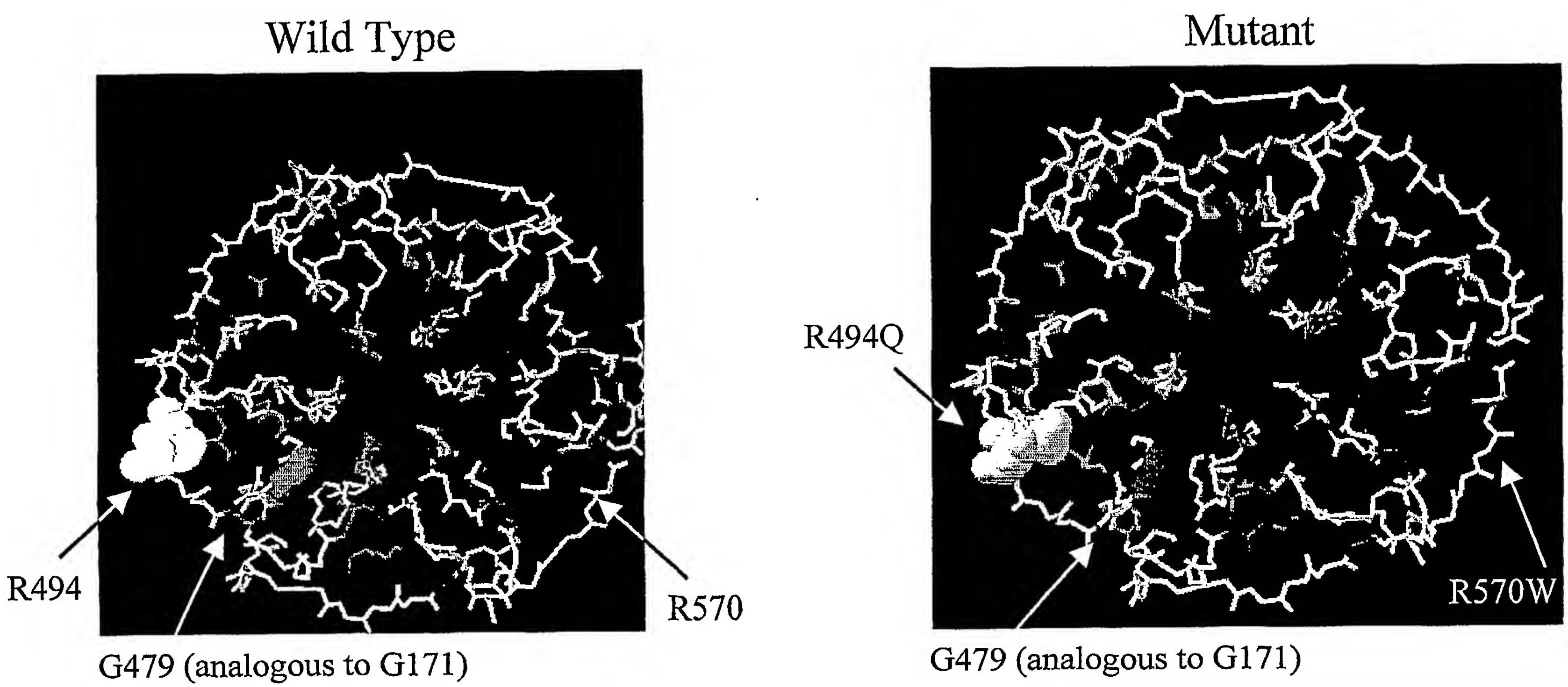

FIG. 53B

Homology Model of LRP5's 3rd Propeller Domain
Propeller 3 Contains One OPPG mutations

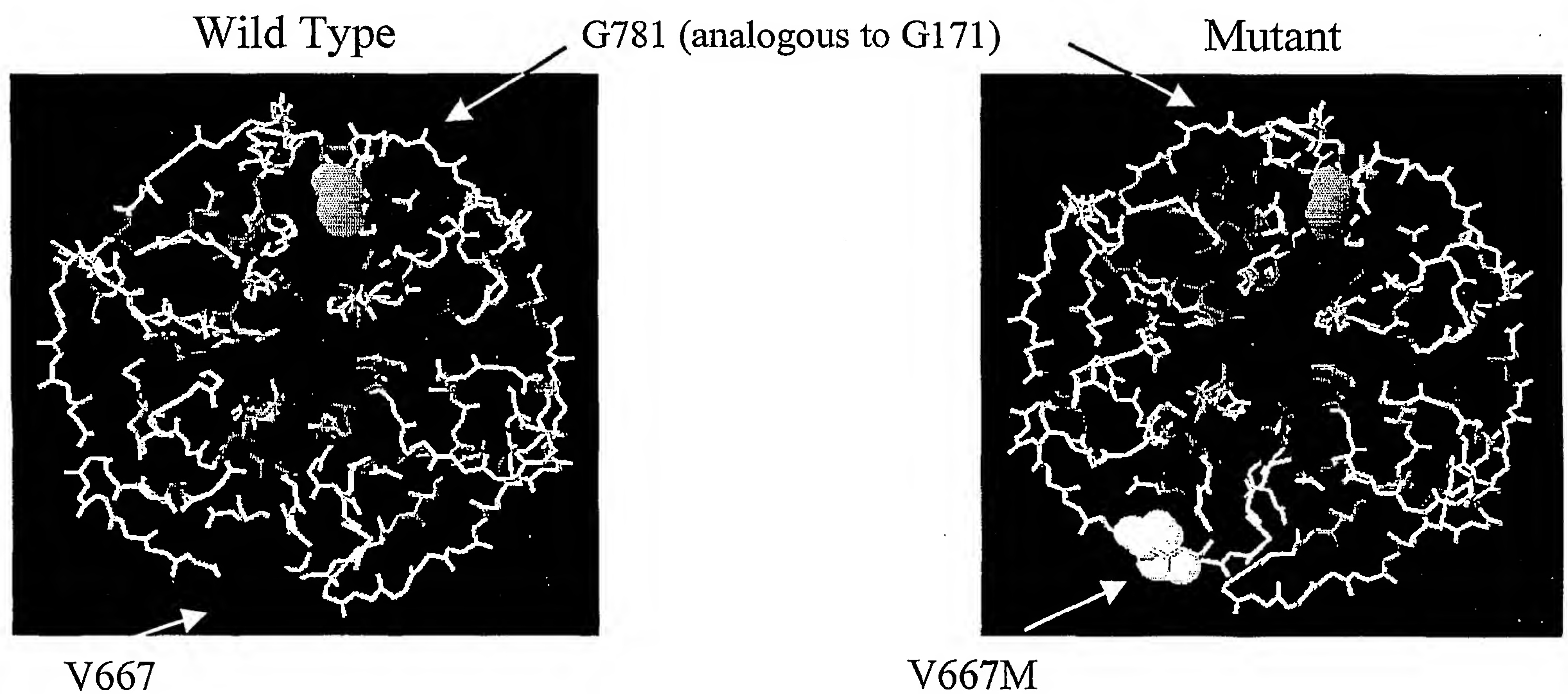

FIG. 53C

SEQUENCE LISTING

<110> Allen, Kristina M.
Yaworsky, Paul
Morales, Arturo J.
Graham, James R.
Anisowicz, Anthony
Liu, Wei

<120> HBM Variants that Modulate Bone Mass and Lipid Levels

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<151> 2001-05-11

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Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
1 5 10
ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc 157
Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
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gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc cgg gac gta cgg ctg 205
Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
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gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc 253
Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
50 55 60
ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
65 70 75
tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac 349
Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn

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Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
    95                      100                     105
ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg          445
Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr
110                     115                     120                     125
gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc          493
Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser
                    130                     135                     140
cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc          541
Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala
                145                     150                     155
ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg ggt gag acg          589
Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr
        160                     165                     170
ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att          637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile
    175                     180                     185
gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag          685
Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu
190                     195                     200                     205
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Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu
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acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca          829
Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
        240                     245                     250
gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg          877
Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly
    255                     260                     265
aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag          925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln
270                     275                     280                     285
gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag          973
Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu
                    290                     295                     300
gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct         1021
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro
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ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc         1069
Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly
        320                     325                     330
agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg         1117
Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg
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acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc         1165
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
350                     355                     360                     365
gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac         1213
Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp
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ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc 1261
Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile
385 390 395
cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc 1309
Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr
400 405 410
gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac 1357
Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn
415 420 425
ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc 1405
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu
430 435 440 445
aac ggc acc tcc cgc aag atc ctg gtg tcg gag gac ctg gac gag ccc 1453
Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro
450 455 460
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac 1501
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp
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Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu
480 485 490
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Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala
495 500 505
ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac 1645
Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp
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Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu
530 535 540
gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc 1741
Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe
545 550 555
atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag 1789
Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys
560 565 570
gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg 1837
Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met
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Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys
590 595 600 605
gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac 1933
Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His
610 615 620
gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg 1981
Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met
625 630 635
aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc 2029
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala
640 645 650
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Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile

655 660 665
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Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser
670 675 680 685
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Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg
690 695 700
gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt 2221
Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu
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gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac 2269
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Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly
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Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu
830 835 840 845
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Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr
850 855 860
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Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg
865 870 875
aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg 2749
Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu
880 885 890
gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac 2797
Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn
895 900 905
aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc 2845
Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg
910 915 920 925
tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc 2893
Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys
930 935 940
agc ccg ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt 2941
Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser

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Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu
        960                     965                     970
cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag        3037
His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys
    975                     980                     985
ttc atc tac tgg gtg gat ggg cgc cag aac atc aag cga gcc aag gac        3085
Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp
990                     995                     1000                    1005
gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac        3133
Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn
                1010                    1015                    1020
cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca        3181
Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr
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ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg        3229
Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu
        1040                    1045                    1050
agc ggg gaa gcc atg ggg gtg gtg ctg cgt ggg gac cgc gac aag ccc        3277
Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro
    1055                    1060                    1065
agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac        3325
Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn
1070                    1075                    1080                    1085
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Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu
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Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu
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Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys
1150                    1155                    1160                    1165
cat ctc tac tgg atc gac cgc cag cag cag atg atc gag cgt gtg gag        3613
His Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu
                1170                    1175                    1180
aag acc acc ggg gac aag cgg act cgc atc cag ggc cgt gtc gcc cac        3661
Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His
            1185                    1190                    1195
ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca        3709
Leu Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser
        1200                    1205                    1210
gcc cac cca tgt gcc cgt gac aat ggt ggc tgc tcc cac atc tgt att        3757
Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile
    1215                    1220                    1225
gcc aag ggt gat ggg aca cca cgg tgc tca tgc cca gtc cac ctc gtg        3805
Ala Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val
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1250 1255 1260
gac cag ttt gca tgt gcc aca ggg gag atc gac tgt atc ccc ggg gcc 3901
Asp Gln Phe Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala
1265 1270 1275
tgg cgc tgt gac ggc ttt ccc gag tgc gat gac cag agc gac gag gag 3949
Trp Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu
1280 1285 1290
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Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln
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Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp
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Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe
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Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro
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Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe
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Val Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro
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Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe
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Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr
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Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile

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agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat        4765
Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp
1550                   1555                   1560                   1565
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Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser
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Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu
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agg agc tac ttc cat ctc ttc ccg ccc cct ccg tcc ccc tgc acg gac        4909
Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp
        1600                   1605                   1610
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Ser Ser
    1615
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taaaaacatg agaaatgtga actgtgatgg ggtgggcagg gctgggagaa ctttgtacag     5085
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           Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
           1               5                   10
ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc        157
Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
    15                  20                  25
gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc cgg gac gta cgg ctg        205
Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
30                  35                  40                  45
gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc        253
Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
                50                  55                  60
ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg        301
Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
            65                  70                  75
tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac        349
Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
        80                  85                  90
cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct        397
Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
    95                  100                 105
ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg        445
Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr
110                 115                 120                 125
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gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc 493
Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser
130 135 140

cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc 541
Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala
145 150 155

ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg gtt gag acg 589
Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr
160 165 170

ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att 637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile
175 180 185

gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag 685
Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu
190 195 200 205

gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt 733
Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg
210 215 220

gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg 781
Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu
225 230 235

acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca 829
Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
240 245 250

gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg 877
Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly
255 260 265

aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag 925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln
270 275 280 285

gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag 973
Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu
290 295 300

gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct 1021
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro
305 310 315

ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc 1069
Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly
320 325 330

agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg 1117
Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg
335 340 345

acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc 1165
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
350 355 360 365

gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac 1213
Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp
370 375 380

ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc 1261
Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile
385 390 395

cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc 1309
Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr
400 405 410

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gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac      1357
Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn
    415                 420                 425
ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc      1405
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu
430                 435                 440                 445
aac ggc acc tcc cgc aag atc ctg gtg tcg gag gac ctg gac gag ccc      1453
Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro
                450                 455                 460
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac      1501
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp
            465                 470                 475
tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag      1549
Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu
        480                 485                 490
cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc      1597
Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala
    495                 500                 505
ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac      1645
Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp
510                 515                 520                 525
aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg      1693
Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu
                530                 535                 540
gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc      1741
Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe
            545                 550                 555
atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag      1789
Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys
        560                 565                 570
gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg      1837
Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met
    575                 580                 585
ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt      1885
Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys
590                 595                 600                 605
gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac      1933
Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His
                610                 615                 620
gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg      1981
Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met
            625                 630                 635
aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc      2029
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala
        640                 645                 650
gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc      2077
Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile
    655                 660                 665
ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc      2125
Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser
670                 675                 680                 685
aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc      2173
Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg
                690                 695                 700
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gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt 2221
Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu
705 710 715

gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac 2269
Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr
720 725 730

tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg 2317
Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly
735 740 745

cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg 2365
Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser
750 755 760 765

ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc 2413
Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly
770 775 780

ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg 2461
Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met
785 790 795

acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac 2509
Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr
800 805 810

gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag 2557
Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu
815 820 825

tcg tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc 2605
Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu
830 835 840 845

ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca 2653
Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr
850 855 860

gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg 2701
Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg
865 870 875

aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg 2749
Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu
880 885 890

gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac 2797
Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn
895 900 905

aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc 2845
Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg
910 915 920 925

tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc 2893
Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys
930 935 940

agc ccg ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt 2941
Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser
945 950 955

cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg 2989
Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu
960 965 970

cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag 3037
His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys
975 980 985

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ttc atc tac tgg gtg gat ggg cgc cag aac atc aag cga gcc aag gac        3085
Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp
990                 995                 1000                1005
gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac        3133
Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn
                1010                1015                1020
cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca        3181
Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr
            1025                1030                1035
ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg        3229
Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu
        1040                1045                1050
agc ggg gaa gcc atg ggg gtg gtg ctg cgt ggg gac cgc gac aag ccc        3277
Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro
    1055                1060                1065
agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac        3325
Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn
1070                1075                1080                1085
atg cag gac cgg gca gcc aag atc gaa cgc gca gcc ctg gac ggc acc        3373
Met Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr
                1090                1095                1100
gag cgc gag gtc ctc ttc acc acc ggc ctc atc cgc cct gtg gcc ctg        3421
Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu
            1105                1110                1115
gtg gtg gac aac aca ctg ggc aag ctg ttc tgg gtg gac gcg gac ctg        3469
Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu
        1120                1125                1130
aag cgc att gag agc tgt gac ctg tca ggg gcc aac cgc ctg acc ctg        3517
Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu
    1135                1140                1145
gag gac gcc aac atc gtg cag cct ctg ggc ctg acc atc ctt ggc aag        3565
Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys
1150                1155                1160                1165
cat ctc tac tgg atc gac cgc cag cag cag atg atc gag cgt gtg gag        3613
His Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu
                1170                1175                1180
aag acc acc ggg gac aag cgg act cgc atc cag ggc cgt gtc gcc cac        3661
Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His
            1185                1190                1195
ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca        3709
Leu Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser
        1200                1205                1210
gcc cac cca tgt gcc cgt gac aat ggt ggc tgc tcc cac atc tgt att        3757
Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile
    1215                1220                1225
gcc aag ggt gat ggg aca cca cgg tgc tca tgc cca gtc cac ctc gtg        3805
Ala Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val
1230                1235                1240                1245
ctc ctg cag aac ctg ctg acc tgt gga gag ccg ccc acc tgc tcc ccg        3853
Leu Leu Gln Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro
                1250                1255                1260
gac cag ttt gca tgt gcc aca ggg gag atc gac tgt atc ccc ggg gcc        3901
Asp Gln Phe Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala
            1265                1270                1275
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tgg cgc tgt gac ggc ttt ccc gag tgc gat gac cag agc gac gag gag      3949
Trp Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu
        1280                1285                1290
ggc tgc ccc gtg tgc tcc gcc gcc cag ttc ccc tgc gcg cgg ggt cag      3997
Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln
    1295                1300                1305
tgt gtg gac ctg cgc ctg cgc tgc gac ggc gag gca gac tgt cag gac      4045
Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp
1310                1315                1320                1325
cgc tca gac gag gtg gac tgt gac gcc atc tgc ctg ccc aac cag ttc      4093
Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe
                1330                1335                1340
cgg tgt gcg agc ggc cag tgt gtc ctc atc aaa cag cag tgc gac tcc      4141
Arg Cys Ala Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser
            1345                1350                1355
ttc ccc gac tgt atc gac ggc tcc gac gag ctc atg tgt gaa atc acc      4189
Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr
        1360                1365                1370
aag ccg ccc tca gac gac agc ccg gcc cac agc agt gcc atc ggg ccc      4237
Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro
    1375                1380                1385
gtc att ggc atc atc ctc tct ctc ttc gtc atg ggt ggt gtc tat ttt      4285
Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe
1390                1395                1400                1405
gtg tgc cag cgc gtg gtg tgc cag cgc tat gcg ggg gcc aac ggg ccc      4333
Val Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro
                1410                1415                1420
ttc ccg cac gag tat gtc agc ggg acc ccg cac gtg ccc ctc aat ttc      4381
Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe
            1425                1430                1435
ata gcc ccg ggc ggt tcc cag cat ggc ccc ttc aca ggc atc gca tgc      4429
Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys
        1440                1445                1450
gga aag tcc atg atg agc tcc gtg agc ctg atg ggg ggc cgg ggc ggg      4477
Gly Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly
    1455                1460                1465
gtg ccc ctc tac gac cgg aac cac gtc aca ggg gcc tcg tcc agc agc      4525
Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser
1470                1475                1480                1485
tcg tcc agc acg aag gcc acg ctg tac ccg ccg atc ctg aac ccg ccg      4573
Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro
                1490                1495                1500
ccc tcc ccg gcc acg gac ccc tcc ctg tac aac atg gac atg ttc tac      4621
Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr
            1505                1510                1515
tct tca aac att ccg gcc act gcg aga ccg tac agg ccc tac atc att      4669
Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile
        1520                1525                1530
cga gga atg gcg ccc ccg acg acg ccc tgc agc acc gac gtg tgt gac      4717
Arg Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp
    1535                1540                1545
agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat      4765
Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp
1550                1555                1560                1565
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 ttg aac tcg gac tca gac ccc tat cca ccc cca ccc acg ccc cac agc        4813
 Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser
                 1570                1575                1580
 cag tac ctg tcg gcg gag gac agc tgc ccg ccc tcg ccc gcc acc gag        4861
 Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu
             1585                1590                1595
 agg agc tac ttc cat ctc ttc ccg ccc cct ccg tcc ccc tgc acg gac        4909
 Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp
         1600                1605                1610
 tca tcc tgacctcggc cgggccactc tggcttctct gtgcccctgt aaatagtttt         4965
 Ser Ser
     1615
aaatatgaac aaagaaaaaa atatatttta tgatttaaaa aataaatata attgggattt       5025
taaaaacatg agaaatgtga actgtgatgg ggtgggcagg gctgggagaa ctttgtacag       5085
tggagaaata tttataaact taattttgta aaaca                                 5120

&lt;210&gt; 3
&lt;211&gt; 1615
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;400&gt; 3
Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu Leu Leu Leu
1               5                   10                  15
 Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala Ala Ala Ser
             20                  25                  30
 Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala
         35                  40                  45
 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
     50                  55                  60
 Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
 65                  70                  75                  80
 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
                 85                  90                  95
 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
             100                 105                 110
 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
         115                 120                 125
 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
     130                 135                 140
 Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
 145                 150                 155                 160
 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
                 165                 170                 175
 Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
             180                 185                 190
 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
         195                 200                 205
 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
     210                 215                 220
 Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
 225                 230                 235                 240
 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
                 245                 250                 255
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Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys
            260                 265                 270
Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser
        275                 280                 285
Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
    290                 295                 300
Gly Trp Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr
305                 310                 315                 320
Cys Ala Cys Pro Thr Gly Val Gln Met Gln Asp Asn Gly Arg Thr Cys
                325                 330                 335
Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg Thr Asp Leu
            340                 345                 350
Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln
        355                 360                 365
Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
    370                 375                 380
Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala
385                 390                 395                 400
Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn
                405                 410                 415
Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp
            420                 425                 430
Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr
        435                 440                 445
Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
    450                 455                 460
Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu
465                 470                 475                 480
Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val
                485                 490                 495
Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu
            500                 505                 510
Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
        515                 520                 525
Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
    530                 535                 540
Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp
545                 550                 555                 560
Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala
                565                 570                 575
Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
            580                 585                 590
Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
        595                 600                 605
Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
    610                 615                 620
Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
625                 630                 635                 640
Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His
                645                 650                 655
Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile Pro Leu Thr
            660                 665                 670
Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His
        675                 680                 685
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Ile Tyr Trp Thr Asp Val Ser Leu Lys Asn Ile Ser Arg Ala Phe Met
690 695 700
Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro
705 710 715 720
Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp
725 730 735
Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg
740 745 750
Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu
755 760 765
Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro
770 775 780
Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val
785 790 795 800
Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln
805 810 815
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agtttggcct tgactacccc gagggcatgg ccgttgactg gatgggcaag aacctctact 120
gggccgacac tgggaccaac agaatcgaag tggcgcggct ggacgggcag ttccggcaag 180
tcctcgtgtg gagggacttg gacaacccga ggtcgctggc cctggatccc accaaggggt 240
aagtgtttgc ctgtc 255

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<212> DNA
<213> Homo sapiens

<400> 50
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ttcatggacg ggaccaactg catgacgctg gtggacaagg tgggccgggc caacgacctc 120
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tcgtccaaca tgctgggtga gggccgggct 210

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<211> 352
<212> DNA
<213> Homo sapiens

<400> 51
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tgacgcagta cagcgattat atctactgga cagactggaa tctgcacagc attgagcggg 120
ccgacaagac tagcggccgg aaccgcaccc tcatccaggg ccacctggac ttcgtgatgg 180
acatcctggt gttccactcc tcccgccagg atggcctcaa tgactgtatg cacaacaacg 240
ggcagtgtgg gcagctgtgc cttgccatcc ccggcggcca ccgctgcggc tgcgcctcac 300

actacaccct ggaccccagc agccgcaact gcagccgtaa gtgcctcatg gt 352

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<212> DNA
<213> Homo sapiens

<400> 52
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atcccggacg accagcacag cccggatctc atcctgcccc tgcatggact gaggaacgtc 120
aaagccatcg actatgaccc actggacaag ttcatctact gggtggatgg gcgccagaac 180
atcaagcgag ccaaggacga cgggacccag gcaggtgccc tgtgg 225

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<211> 235
<212> DNA
<213> Homo sapiens

<400> 53
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gccccacgac ctcagcatcg acatctacag ccggacactg ttctggacgt gcgaggccac 120
caataccatc aacgtccaca ggctgagcgg ggaagccatg gggtggtgc tgcgtgggga 180
ccgcgacaag cccagggcca tcgtcgtcaa cgcggagcga gggtaggagg ccaac 235

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<212> DNA
<213> Homo sapiens

<400> 54
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cgcgcagccc tggacggcac cgagcgcgag gtcctcttca ccaccggcct catccgccct 120
gtggccctgg tggtggacaa cacactgggc aagctgttct gggtggacgc ggacctgaag 180
cgcattgaga gctgtgacct gtcaggtacg cgccccgg 218

<210> 55
<211> 234
<212> DNA
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<400> 55
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gcctgaccat ccttggcaag catctctact ggatcgaccg ccagcagcag atgatcgagc 120
gtgtggagaa gaccaccggg gacaagcgga ctcgcatcca gggccgtgtc gcccacctca 180
ctggcatcca tgcagtggag gaagtcagcc tggaggagtt ctgtacgtgg gggc 234

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<211> 157
<212> DNA
<213> Homo sapiens

<400> 56
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ttgccaaggg tgatgggaca ccacggtgct catgcccagt ccacctcgtg ctcctgcaga 120

acctgctgac ctgtggaggt aggtgtgacc taggtgc 157

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<211> 272
<212> DNA
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<400> 57
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tgaccagagc gacgaggagg gctgccccgt gtgctccgcc gcccagttcc cctgcgcgcg 180
gggtcagtgt gtggacctgc gcctgcgctg cgacggcgag gcagactgtc aggaccgctc 240
agacgaggtg gactgtgacg gtgaggccct cc 272

<210> 58
<211> 134
<212> DNA
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catcaaacag cagtgcgact ccttccccga ctgtatcgac ggctccgacg agctcatgtg 120
tggtgagcca gctt 134

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<211> 274
<212> DNA
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tgtgccagcg cgtggtgtgc cagcgctatg cgggggccaa cgggcccttc ccgcacgagt 180
atgtcagcgg gaccccgcac gtgcccctca atttcatagc cccgggcggt tcccagcatg 240
gccccttcac aggtaaggag cctgagatat ggaa 274

<210> 60
<211> 164
<212> DNA
<213> Homo sapiens

<400> 60
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gccggggcgg ggtgcccctc tacgaccgga accacgtcac aggggcctcg tccagcagct 120
cgtccagcac gaaggccacg ctgtacccgc cggtgagggg cggg 164

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<211> 130
<212> DNA
<213> Homo sapiens

<400> 61
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acatggacat gttctactct tcaaacattc cggccactgc gagaccgtac aggtaggaca 120

tcccctgcag 130

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<212> DNA
<213> Homo sapiens

<400> 62
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gccagcaagt actacctgga tttgaactcg gactcagacc cctatccacc cccacccacg 180
ccccacagcc agtacctgtc ggcggaggac agctgcccgc cctcgcccgc caccgagagg 240
agctacttcc atctcttccc gccccctccg tccccctgca cggactcatc ctgacctcgg 300
ccgggccact ctggcttctc tgtgcccctg taaatagttt taaatatgaa caaagaaaaa 360
aatatatttt atgatttaaa aaataaatat aattgggatt ttaaaaacat gagaaatgtg 420
aactgtgatg gggtgggcag ggctgggaga actttgtaca gtggagaaat atttataaac 480
ttaattttgt aaaaca 496

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<220>
<223> Artificial Sequence is a primer.

<400> 63
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<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence is a primer.

<400> 64
aaaactgtgg gtgcttctgg 20

<210> 65
<211> 21
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<220>
<223> Artificial Sequence is a primer.

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<210> 66
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<212> DNA
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<220>
<223> Artificial Sequence is a primer.

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<400> 67
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<210> 68
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<400> 68
ttcagaagca cttggctgg 19

<210> 69
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<400> 69
ctcagtgcca tgaagatgga 20

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<400> 70
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<400> 73
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<400> 74
gccctctgtc ctgacttcag g 21

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<400> 75
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<400> 76
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<210> 77
<211> 24
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<213> Homo sapiens

<400> 77
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<210> 78
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<400> 78
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<210> 79
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<213> Homo sapiens

<400> 79
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<210> 80
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<400> 81
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<400> 82
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<400> 83
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<400> 92
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<400> 95
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<400> 108
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<220>
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<220>
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Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
545                 550                 555                 560
Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
                565                 570                 575
Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
            580                 585                 590
Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
        595                 600                 605
Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
    610                 615                 620
Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
625                 630                 635                 640
Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
                645                 650                 655
Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
            660                 665                 670
```

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
675 680 685
Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
690 695 700
His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705 710 715 720
Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
725 730 735
Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
740 745 750
Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro
755 760 765
Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn
770 775 780
Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp
785 790 795 800
Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met
805 810 815
Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser
820 825 830
Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu
835 840 845
Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met
850 855 860
Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met
865 870 875 880
Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
885 890

<210> 667
<211> 197
<212> PRT
<213> Homo sapiens

<400> 667
Met Met Phe Pro Gln Ser Arg His Ser Gly Ser Ser His Leu Pro Gln
1 5 10 15
Gln Leu Lys Phe Thr Thr Ser Asp Ser Cys Asp Arg Ile Lys Asp Glu
20 25 30
Phe Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp
35 40 45
Lys Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr
50 55 60
Tyr Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu
65 70 75 80
Ile Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu
85 90 95
Ser Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys
100 105 110
Gln Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln
115 120 125
Ala His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro
130 135 140
Leu Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly

145 150 155 160
Thr Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser
165 170 175
Lys Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp
180 185 190
Gly Glu Lys Ser Asp
195

<210> 668
<211> 739
<212> PRT
<213> Homo sapiens

<400> 668
Gly Asp Lys Glu Pro Thr Glu Thr Ile Gly Asp Leu Ser Ile Cys Leu
1 5 10 15
Asp Gly Leu Gln Leu Glu Ser Glu Val Val Thr Asn Gly Glu Thr Thr
20 25 30
Cys Ser Glu Ser Ala Ser Gln Asn Asp Asp Gly Ser Arg Ser Lys Asp
35 40 45
Glu Thr Arg Val Ser Thr Asn Gly Ser Asp Asp Pro Glu Asp Ala Gly
50 55 60
Ala Gly Glu Asn Arg Arg Val Ser Gly Asn Asn Ser Pro Ser Leu Ser
65 70 75 80
Asn Gly Gly Phe Lys Pro Ser Arg Pro Pro Arg Pro Ser Arg Pro Pro
85 90 95
Pro Pro Thr Pro Arg Arg Pro Ala Ser Val Asn Gly Ser Pro Ser Ala
100 105 110
Thr Ser Glu Ser Asp Gly Ser Ser Thr Gly Ser Leu Pro Pro Thr Asn
115 120 125
Thr Asn Thr Asn Thr Ser Glu Gly Ala Thr Ser Gly Leu Ile Ile Pro
130 135 140
Leu Thr Ile Ser Gly Gly Ser Gly Pro Arg Pro Leu Asn Pro Val Thr
145 150 155 160
Gln Ala Pro Leu Pro Pro Gly Trp Glu Gln Arg Val Asp Gln His Gly
165 170 175
Arg Val Tyr Tyr Val Asp His Val Glu Lys Arg Thr Thr Trp Asp Arg
180 185 190
Pro Glu Pro Leu Pro Pro Gly Trp Glu Arg Arg Val Asp Asn Met Gly
195 200 205
Arg Ile Tyr Tyr Val Asp His Phe Thr Arg Thr Thr Thr Trp Gln Arg
210 215 220
Pro Thr Leu Glu Ser Val Arg Asn Tyr Glu Gln Trp Gln Leu Gln Arg
225 230 235 240
Ser Gln Leu Gln Gly Ala Met Gln Gln Phe Asn Gln Arg Phe Ile Tyr
245 250 255
Gly Asn Gln Asp Leu Phe Ala Thr Ser Gln Ser Lys Glu Phe Asp Pro
260 265 270
Leu Gly Pro Leu Pro Pro Gly Trp Glu Lys Arg Thr Asp Ser Asn Gly
275 280 285
Arg Val Tyr Phe Val Asn His Asn Thr Arg Ile Thr Gln Trp Glu Asp
290 295 300
Pro Arg Ser Gln Gly Gln Leu Asn Glu Lys Pro Leu Pro Glu Gly Trp
305 310 315 320

Glu Met Arg Phe Thr Val Asp Gly Ile Pro Tyr Phe Val Asp His Asn
                325   330   335
Arg Arg Thr Thr Thr Tyr Ile Asp Pro Arg Thr Gly Lys Ser Ala Leu
            340   345   350
Asp Asn Gly Pro Gln Ile Ala Tyr Val Arg Asp Phe Lys Ala Lys Val
        355   360   365
Gln Tyr Phe Arg Phe Trp Cys Gln Gln Leu Ala Met Pro Gln His Ile
    370   375   380
Lys Ile Thr Val Thr Arg Lys Thr Leu Phe Glu Asp Ser Phe Gln Gln
385   390   395   400
Ile Met Ser Phe Ser Pro Gln Asp Leu Arg Arg Arg Leu Trp Val Ile
                405   410   415
Phe Pro Gly Glu Glu Gly Leu Asp Tyr Gly Gly Val Ala Arg Glu Trp
            420   425   430
Phe Phe Leu Leu Ser His Glu Val Leu Asn Pro Met Tyr Cys Leu Phe
        435   440   445
Glu Tyr Ala Gly Lys Asp Asn Tyr Cys Leu Gln Ile Asn Pro Ala Ser
    450   455   460
Tyr Ile Asn Pro Asp His Leu Lys Tyr Phe Arg Phe Ile Gly Arg Phe
465   470   475   480
Ile Ala Met Ala Leu Phe His Gly Lys Phe Ile Asp Thr Gly Phe Ser
                485   490   495
Leu Pro Phe Tyr Lys Arg Ile Leu Asn Lys Pro Val Gly Leu Lys Asp
            500   505   510
Leu Glu Ser Ile Asp Pro Glu Phe Tyr Asn Ser Leu Ile Trp Val Lys
        515   520   525
Glu Asn Asn Ile Glu Glu Cys Asp Leu Glu Met Tyr Phe Ser Val Asp
    530   535   540
Lys Glu Ile Leu Gly Glu Ile Lys Ser His Asp Leu Lys Pro Asn Gly
545   550   555   560
Gly Asn Ile Leu Val Thr Glu Glu Asn Lys Glu Glu Tyr Ile Arg Met
                565   570   575
Val Ala Glu Trp Arg Leu Ser Arg Gly Val Glu Glu Gln Thr Gln Ala
            580   585   590
Phe Phe Glu Gly Phe Asn Glu Ile Leu Pro Gln Gln Tyr Leu Gln Tyr
        595   600   605
Phe Asp Ala Lys Glu Leu Glu Val Leu Leu Cys Gly Met Gln Glu Ile
    610   615   620
Asp Leu Asn Asp Trp Gln Arg His Ala Ile Tyr Arg His Tyr Ala Arg
625   630   635   640
Thr Ser Lys Gln Ile Met Trp Phe Trp Gln Phe Val Lys Glu Ile Asp
                645   650   655
Asn Glu Lys Arg Met Arg Leu Leu Gln Phe Val Thr Gly Thr Cys Arg
            660   665   670
Leu Pro Val Gly Gly Phe Ala Asp Leu Met Gly Ser Asn Gly Pro Gln
        675   680   685
Lys Phe Cys Ile Glu Lys Val Gly Lys Glu Asn Trp Leu Pro Arg Ser
    690   695   700
His Thr Cys Phe Asn Arg Leu Asp Leu Pro Pro Tyr Lys Ser Tyr Glu
705   710   715   720
Gln Leu Lys Glu Lys Leu Leu Phe Ala Ile Glu Glu Thr Glu Gly Phe
                725   730   735
Gly Gln Glu

<210> 669
<211> 431
<212> PRT
<213> Homo sapiens

<400> 669
Gly Pro Pro Pro Thr Arg Ala Leu Pro Leu Pro Gln Ser Leu Pro Pro
1 5 10 15
Asp Phe Arg Leu Glu Pro Thr Ala Pro Ala Leu Ser Pro Arg Ser Ser
20 25 30
Phe Ala Ser Ser Ser Ala Ser Asp Ala Ser Lys Pro Ser Ser Pro Arg
35 40 45
Gly Ser Leu Leu Leu Asp Gly Ala Gly Ala Gly Gly Ala Gly Gly Ser
50 55 60
Arg Pro Cys Ser Asn Arg Thr Ser Gly Ile Ser Met Gly Tyr Asp Gln
65 70 75 80
Arg His Gly Ser Pro Leu Pro Ala Gly Pro Cys Leu Phe Gly Pro Pro
85 90 95
Leu Ala Gly Ala Pro Ala Gly Tyr Ser Pro Gly Gly Val Pro Ser Ala
100 105 110
Tyr Pro Glu Leu His Ala Ala Leu Asp Arg Leu Tyr Ala Gln Arg Pro
115 120 125
Ala Gly Phe Gly Cys Gln Glu Ser Arg His Ser Tyr Pro Pro Ala Leu
130 135 140
Gly Ser Pro Gly Ala Leu Ala Gly Ala Arg Val Gly Ala Ala Gly Pro
145 150 155 160
Leu Glu Arg Arg Gly Ala Gln Pro Gly Arg His Ser Val Thr Gly Tyr
165 170 175
Gly Asp Cys Ala Val Gly Ala Arg Tyr Gln Asp Glu Leu Thr Ala Leu
180 185 190
Leu Arg Leu Thr Val Gly Thr Gly Gly Arg Glu Ala Gly Ala Arg Gly
195 200 205
Glu Pro Ser Gly Ile Glu Pro Ser Gly Leu Glu Glu Pro Pro Gly Pro
210 215 220
Phe Val Pro Glu Ala Ala Arg Ala Arg Met Arg Glu Pro Glu Ala Arg
225 230 235 240
Glu Asp Tyr Phe Gly Thr Cys Ile Lys Cys Asn Lys Gly Ile Tyr Gly
245 250 255
Gln Ser Asn Ala Cys Gln Ala Leu Asp Ser Leu Tyr His Thr Gln Cys
260 265 270
Phe Val Cys Cys Ser Cys Gly Arg Thr Leu Arg Cys Lys Ala Phe Tyr
275 280 285
Ser Val Asn Gly Ser Val Tyr Cys Glu Glu Asp Tyr Leu Phe Ser Gly
290 295 300
Phe Gln Glu Ala Ala Glu Lys Cys Cys Val Cys Gly His Leu Ile Leu
305 310 315 320
Glu Lys Ile Leu Gln Ala Met Gly Lys Ser Tyr His Pro Gly Cys Phe
325 330 335
Arg Cys Ile Val Cys Asn Lys Cys Leu Asp Gly Ile Pro Phe Thr Val
340 345 350
Asp Phe Ser Asn Gln Val Tyr Cys Val Thr Asp Tyr His Lys Asn Tyr
355 360 365
Ala Pro Lys Cys Ala Ala Cys Gly Gln Pro Ile Leu Pro Ser Glu Gly
370 375 380

Cys Glu Asp Ile Val Arg Val Ile Ser Met Asp Arg Asp Tyr His Phe
385 390 395 400
Glu Cys Tyr His Cys Glu Asp Cys Arg Met Gln Leu Ser Asp Glu Glu
405 410 415
Gly Cys Cys Cys Phe Pro Leu Asp Gly His Leu Leu Cys His Gly
420 425 430

<210> 670
<211> 900
<212> PRT
<213> Homo sapiens

<400> 670
Gly Pro Gly Ser Arg His His Arg Ala Arg Asp Arg Leu Ile His Phe
1 5 10 15
Gly Ala Val Ser Thr Asp Val Leu Gly Cys Ser Ala His Cys Ser Leu
20 25 30
Thr Gln Ser Pro Lys Met Asn Ile Gln Glu Gln Gly Phe Pro Leu Asp
35 40 45
Leu Gly Ala Ser Phe Thr Glu Asp Ala Pro Arg Pro Pro Val Pro Gly
50 55 60
Glu Glu Gly Glu Leu Val Ser Thr Asp Pro Arg Pro Ala Ser Tyr Ser
65 70 75 80
Phe Cys Ser Gly Lys Gly Val Gly Ile Lys Gly Glu Thr Ser Thr Ala
85 90 95
Thr Pro Arg Arg Ser Asp Leu Asp Leu Gly Tyr Glu Pro Glu Gly Ser
100 105 110
Ala Ser Pro Thr Pro Pro Tyr Leu Lys Trp Ala Glu Ser Leu His Ser
115 120 125
Leu Leu Asp Asp Gln Asp Gly Ile Ser Leu Phe Arg Thr Phe Leu Lys
130 135 140
Gln Glu Gly Cys Ala Asp Leu Leu Asp Phe Trp Phe Ala Cys Thr Gly
145 150 155 160
Phe Arg Lys Leu Glu Pro Cys Asp Ser Asn Glu Glu Lys Arg Leu Lys
165 170 175
Leu Ala Arg Ala Ile Tyr Arg Lys Tyr Ile Leu Asp Asn Asn Gly Ile
180 185 190
Val Ser Arg Gln Thr Lys Pro Ala Thr Lys Ser Phe Ile Lys Gly Cys
195 200 205
Ile Met Lys Gln Leu Ile Asp Pro Ala Met Phe Asp Gln Ala Gln Thr
210 215 220
Glu Ile Gln Ala Thr Met Glu Glu Asn Thr Tyr Pro Ser Phe Leu Lys
225 230 235 240
Ser Asp Ile Tyr Leu Glu Tyr Thr Arg Thr Gly Ser Glu Ser Pro Lys
245 250 255
Val Cys Ser Asp Gln Ser Ser Gly Ser Gly Thr Gly Lys Gly Ile Ser
260 265 270
Gly Tyr Leu Pro Thr Leu Asn Glu Asp Glu Glu Trp Lys Cys Asp Gln
275 280 285
Asp Met Asp Glu Asp Asp Gly Arg Asp Ala Ala Pro Pro Gly Arg Leu
290 295 300
Pro Gln Lys Leu Leu Leu Glu Thr Ala Ala Pro Arg Val Ser Ser Ser
305 310 315 320
Arg Arg Tyr Ser Glu Gly Arg Glu Phe Arg Tyr Gly Ser Trp Arg Glu

325 330 335
Pro Val Asn Pro Tyr Tyr Val Asn Ala Gly Tyr Ala Leu Ala Pro Ala
340 345 350
Thr Ser Ala Asn Asp Ser Glu Gln Gln Ser Leu Ser Ser Asp Ala Asp
355 360 365
Thr Leu Ser Leu Thr Asp Ser Ser Val Asp Gly Ile Pro Pro Tyr Arg
370 375 380
Ile Arg Lys Gln His Arg Arg Glu Met Gln Glu Ser Ala Gln Val Asn
385 390 395 400
Gly Arg Val Pro Leu Pro His Ile Pro Arg Thr Tyr Arg Val Pro Lys
405 410 415
Glu Val Arg Val Glu Pro Gln Lys Phe Ala Glu Glu Leu Ile His Arg
420 425 430
Leu Glu Ala Val Gln Arg Thr Arg Glu Ala Glu Glu Lys Leu Glu Glu
435 440 445
Arg Leu Lys Arg Val Arg Met Glu Glu Glu Gly Glu Asp Gly Asp Pro
450 455 460
Ser Ser Gly Pro Pro Gly Pro Cys His Lys Leu Pro Pro Ala Pro Ala
465 470 475 480
Trp His His Phe Pro Pro Arg Leu Cys Trp Thr Trp Ala Cys Ala Gly
485 490 495
Leu Arg Asp Ala His Glu Glu Asn Pro Glu Ser Ile Leu Asp Glu His
500 505 510
Val Gln Arg Val Leu Arg Thr Thr Gly Arg Gln Ser Pro Gly Pro Gly
515 520 525
His Arg Ser Pro Asp Ser Gly His Val Ala Lys Met Pro Val Ala Leu
530 535 540
Gly Gly Ala Ala Ser Gly His Gly Lys His Val Pro Lys Ser Gly Ala
545 550 555 560
Lys Leu Asp Ala Ala Gly Leu His His His Arg His Val His His His
565 570 575
Val His His Ser Thr Ala Arg Pro Lys Glu Gln Val Glu Ala Glu Ala
580 585 590
Thr Arg Arg Ala Gln Ser Ser Phe Ala Trp Gly Leu Glu Pro His Ser
595 600 605
His Gly Ala Arg Ser Arg Gly Tyr Ser Glu Ser Val Gly Ala Ala Pro
610 615 620
Asn Ala Ser Asp Gly Leu Ala His Ser Gly Lys Val Gly Val Ala Cys
625 630 635 640
Lys Arg Asn Ala Lys Lys Ala Glu Ser Gly Lys Ser Ala Ser Thr Glu
645 650 655
Val Pro Gly Ala Ser Glu Asp Ala Glu Lys Asn Gln Lys Ile Met Gln
660 665 670
Trp Ile Ile Glu Gly Glu Lys Glu Ile Ser Arg His Arg Arg Thr Gly
675 680 685
His Gly Ser Ser Gly Thr Arg Lys Pro Gln Pro His Glu Asn Ser Arg
690 695 700
Pro Leu Ser Leu Glu His Pro Trp Ala Gly Pro Gln Leu Arg Thr Ser
705 710 715 720
Val Gln Pro Ser His Leu Phe Ile Gln Asp Pro Thr Met Pro Pro His
725 730 735
Pro Ala Pro Asn Pro Leu Thr Gln Leu Glu Glu Ala Arg Arg Arg Leu
740 745 750
Glu Glu Glu Glu Lys Arg Ala Ser Arg Ala Pro Ser Lys Gln Arg Tyr

```
        755                     760                     765
Val Gln Glu Val Met Arg Arg Gly Arg Ala Cys Val Arg Pro Ala Cys
    770                     775                     780
Ala Pro Val Leu His Val Val Pro Ala Val Ser Asp Met Glu Leu Ser
785                     790                     795                 800
Glu Thr Glu Thr Arg Ser Gln Arg Lys Val Gly Gly Gly Ser Ala Gln
                805                     810                     815
Pro Cys Asp Ser Ile Val Val Ala Tyr Tyr Phe Cys Gly Glu Pro Ile
            820                     825                     830
Pro Tyr Arg Thr Leu Val Arg Gly Arg Ala Val Thr Leu Gly Gln Phe
        835                     840                     845
Lys Glu Leu Leu Thr Lys Lys Gly Ser Tyr Arg Tyr Tyr Phe Lys Lys
    850                     855                     860
Val Ser Asp Glu Phe Asp Cys Gly Val Val Phe Glu Glu Val Arg Glu
865                     870                     875                 880
Asp Glu Ala Val Leu Pro Val Phe Glu Glu Lys Ile Ile Gly Lys Val
                885                     890                     895
Glu Lys Val Asp
            900

<210> 671
<211> 591
<212> PRT
<213> Homo sapiens

<400> 671
Met Val Pro Val Ala Val Thr Ala Ala Val Ala Pro Val Leu Ser Ile
 1               5                  10                  15
Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile Lys Lys Gln Leu Leu Leu
            20                  25                  30
Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu Leu His Ser Ser Lys Trp
        35                  40                  45
Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala Leu Pro Leu Ala Glu Leu
    50                  55                  60
Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp Ala Gln Asp Met Asp Ala
65                  70                  75                  80
Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val Lys Glu Tyr Asp Arg Ala
                85                  90                  95
Ala His Phe Leu His Gly Cys Asn Ser Lys Lys Ala Tyr Phe Leu Tyr
            100                 105                 110
Met Tyr Ser Arg Tyr Leu Ser Gly Glu Lys Lys Lys Asp Asp Glu Thr
        115                 120                 125
Val Asp Ser Leu Gly Pro Leu Glu Lys Gly Gln Val Lys Asn Glu Ala
    130                 135                 140
Leu Arg Glu Leu Arg Val Glu Leu Ser Lys Lys His Gln Ala Arg Glu
145                 150                 155                 160
Leu Asp Gly Phe Gly Leu Tyr Leu Tyr Gly Val Val Leu Arg Lys Leu
                165                 170                 175
Asp Leu Val Lys Glu Ala Ile Asp Val Phe Val Glu Ala Thr His Val
            180                 185                 190
Leu Pro Leu His Trp Gly Ala Trp Leu Glu Leu Cys Asn Leu Ile Thr
        195                 200                 205
Asp Lys Glu Met Leu Lys Phe Leu Ser Leu Pro Asp Thr Trp Met Lys
    210                 215                 220
```

```
Glu Phe Phe Leu Ala His Ile Tyr Thr Glu Leu Gln Leu Ile Glu Glu
225                 230                 235                 240
Ala Leu Gln Lys Tyr Gln Asn Leu Ile Asp Val Gly Phe Ser Lys Ser
                245                 250                 255
Ser Tyr Ile Val Ser Gln Ile Ala Val Ala Tyr His Asn Ile Arg Asp
            260                 265                 270
Ile Asp Lys Ala Leu Ser Ile Phe Asn Glu Leu Arg Lys Gln Asp Pro
        275                 280                 285
Tyr Arg Ile Glu Asn Met Asp Thr Phe Ser Asn Leu Leu Tyr Val Arg
    290                 295                 300
Ser Met Lys Ser Glu Leu Ser Tyr Leu Ala His Asn Leu Cys Glu Ile
305                 310                 315                 320
Asp Lys Tyr Arg Val Glu Thr Cys Cys Val Ile Gly Asn Tyr Tyr Ser
                325                 330                 335
Leu Arg Ser Gln His Glu Lys Ala Ala Leu Tyr Phe Gln Arg Ala Leu
            340                 345                 350
Lys Leu Asn Pro Arg Tyr Leu Gly Ala Trp Thr Leu Met Gly His Glu
        355                 360                 365
Tyr Met Glu Met Lys Asn Thr Ser Ala Ala Ile Gln Ala Tyr Arg His
    370                 375                 380
Ala Ile Glu Val Asn Lys Arg Asp Tyr Arg Ala Trp Tyr Gly Leu Gly
385                 390                 395                 400
Gln Thr Tyr Glu Ile Leu Lys Met Pro Phe Tyr Cys Leu Tyr Tyr Tyr
                405                 410                 415
Arg Arg Ala His Gln Leu Arg Pro Asn Asp Ser Arg Met Leu Val Ala
            420                 425                 430
Leu Gly Glu Cys Tyr Glu Lys Leu Asn Gln Leu Val Glu Ala Lys Lys
        435                 440                 445
Cys Tyr Trp Arg Ala Tyr Ala Val Gly Asp Val Glu Lys Met Ala Leu
    450                 455                 460
Val Lys Leu Ala Lys Leu His Glu Gln Leu Thr Glu Ser Glu Gln Ala
465                 470                 475                 480
Ala Gln Cys Tyr Ile Lys Tyr Ile Gln Asp Ile Tyr Ser Cys Gly Glu
                485                 490                 495
Ile Val Glu His Leu Glu Glu Ser Thr Ala Phe Arg Tyr Leu Ala Gln
            500                 505                 510
Tyr Tyr Phe Lys Cys Lys Leu Trp Asp Glu Ala Ser Thr Cys Ala Gln
        515                 520                 525
Lys Cys Cys Ala Phe Asn Asp Thr Arg Glu Glu Gly Lys Ala Leu Leu
    530                 535                 540
Arg Gln Ile Leu Gln Leu Arg Asn Gln Gly Glu Thr Pro Thr Thr Glu
545                 550                 555                 560
Val Pro Ala Pro Phe Phe Leu Pro Ala Ser Leu Ser Ala Asn Asn Thr
                565                 570                 575
Pro Thr Arg Arg Val Ser Pro Leu Asn Leu Ser Ser Val Thr Pro
            580                 585                 590
```

<210> 672
<211> 914
<212> PRT
<213> Homo sapiens

<400> 672

```
Val Tyr Gln Val Leu Leu Val Gly Ser Thr Leu Leu Lys Glu Val Pro
```

```
1               5                   10                  15
Ser Gly Leu Gln Leu Glu Gln Leu Pro Ser Gln Ser Leu Leu Thr His
            20                  25                  30
Ile Pro Thr Ala Gly Leu Pro Thr Ser Leu Gly Gly Gly Leu Pro Tyr
        35                  40                  45
Cys His Gln Ala Trp Leu Asp Phe Arg Arg Arg Leu Glu Ala Leu Leu
    50                  55                  60
Gln Asn Cys Gln Ala Ala Cys Ala Leu Leu Gln Gly Ala Ile Glu Ser
65                  70                  75                  80
Val Lys Ala Val Pro Gln Pro Met Glu Pro Gly Glu Val Gly Gln Leu
                85                  90                  95
Leu Gln Gln Thr Glu Val Leu Met Gln Gln Val Leu Asp Ser Pro Trp
            100                 105                 110
Leu Ala Trp Leu Gln Cys Gln Gly Gly Arg Glu Leu Thr Trp Leu Lys
        115                 120                 125
Gln Glu Val Pro Glu Val Thr Leu Ser Pro Asp Tyr Arg Thr Ala Met
    130                 135                 140
Asp Lys Ala Asp Glu Leu Tyr Asp Arg Val Asp Gly Leu Leu His Gln
145                 150                 155                 160
Leu Thr Leu Gln Ser Asn Gln Arg Ile Gln Ala Leu Glu Leu Val Gln
                165                 170                 175
Thr Leu Glu Ala Arg Glu Ser Gly Leu His Gln Ile Glu Val Trp Leu
            180                 185                 190
Gln Gln Val Gly Trp Pro Ala Leu Glu Glu Ala Gly Glu Pro Ser Leu
        195                 200                 205
Asp Met Leu Leu Gln Ala Gln Gly Ser Phe Gln Glu Leu Tyr Gln Val
    210                 215                 220
Ala Gln Glu Gln Val Arg Gln Gly Glu Lys Phe Leu Gln Pro Leu Thr
225                 230                 235                 240
Gly Trp Glu Ala Ala Glu Leu Asp Pro Pro Gly Ala Arg Phe Leu Ala
                245                 250                 255
Leu Arg Ala Gln Leu Thr Glu Phe Ser Arg Ala Leu Ala Gln Arg Cys
            260                 265                 270
Gln Arg Leu Ala Asp Ala Glu Arg Leu Phe Gln Leu Phe Arg Glu Ala
        275                 280                 285
Leu Thr Trp Ala Glu Glu Gly Gln Arg Val Leu Ala Glu Leu Glu Gln
    290                 295                 300
Glu Arg Pro Gly Val Val Leu Gln Gln Leu Gln Leu His Trp Thr Arg
305                 310                 315                 320
His Pro Asp Leu Pro Pro Ala His Phe Arg Lys Met Trp Ala Leu Ala
                325                 330                 335
Thr Gly Leu Gly Ser Glu Ala Ile Arg Gln Glu Cys Arg Trp Ala Trp
            340                 345                 350
Ala Arg Cys Gln Asp Thr Trp Leu Ala Leu Asp Gln Lys Leu Glu Ala
        355                 360                 365
Ser Leu Lys Leu Pro Pro Val Gly Ser Thr Ala Ser Leu Cys Val Ser
    370                 375                 380
Gln Val Pro Ala Ala Pro Ala His Pro Pro Leu Arg Lys Ala Tyr Ser
385                 390                 395                 400
Phe Asp Arg Asn Leu Gly Gln Ser Leu Ser Glu Pro Ala Cys His Cys
                405                 410                 415
His His Ala Ala Thr Ile Ala Ala Cys Arg Arg Pro Glu Ala Gly Gly
            420                 425                 430
Gly Ala Leu Pro Gln Ala Ser Pro Thr Val Pro Pro Pro Gly Ser Ser
```

435 440 445
Asp Pro Arg Ser Leu Asn Arg Leu Gln Leu Val Leu Ala Glu Met Val
450 455 460
Ala Thr Glu Arg Glu Tyr Val Arg Ala Leu Glu Tyr Thr Met Glu Asn
465 470 475 480
Tyr Phe Pro Glu Leu Asp Arg Pro Asp Val Pro Gln Gly Leu Arg Gly
485 490 495
Gln Arg Ala His Leu Phe Gly Asn Leu Glu Lys Leu Arg Asp Phe His
500 505 510
Cys His Phe Phe Leu Arg Glu Leu Glu Ala Cys Thr Arg His Pro Pro
515 520 525
Arg Val Ala Tyr Ala Phe Leu Arg His Arg Val Gln Phe Gly Met Tyr
530 535 540
Ala Leu Tyr Ser Lys Asn Lys Pro Arg Ser Asp Ala Leu Met Ser Ser
545 550 555 560
Tyr Gly His Thr Phe Phe Lys Asp Lys Gln Gln Ala Leu Gly Asp His
565 570 575
Leu Asp Leu Ala Ser Tyr Leu Leu Lys Pro Ile Gln Arg Met Gly Lys
580 585 590
Tyr Ala Leu Leu Leu Gln Glu Leu Ala Arg Ala Cys Gly Gly Pro Thr
595 600 605
Gln Glu Leu Ser Ala Leu Arg Glu Ala Gln Ser Leu Val His Phe Gln
610 615 620
Leu Arg His Gly Asn Asp Leu Leu Ala Met Asp Ala Ile Gln Gly Cys
625 630 635 640
Asp Val Asn Leu Lys Glu Gln Gly Gln Leu Val Arg Gln Asp Glu Phe
645 650 655
Val Val Arg Thr Gly Arg His Lys Ser Val Arg Arg Ile Phe Leu Phe
660 665 670
Glu Glu Leu Leu Leu Phe Ser Lys Pro Arg His Gly Pro Thr Gly Val
675 680 685
Asp Thr Phe Ala Tyr Lys Arg Ser Phe Lys Met Ala Asp Leu Gly Leu
690 695 700
Thr Glu Cys Cys Gly Asn Ser Asn Leu Arg Phe Glu Ile Trp Phe Arg
705 710 715 720
Arg Arg Lys Ala Arg Asp Thr Phe Val Leu Gln Ala Ser Ser Leu Ala
725 730 735
Ile Lys Gln Ala Trp Thr Ala Asp Ile Ser His Leu Leu Trp Arg Gln
740 745 750
Ala Val His Asn Lys Glu Val Arg Met Ala Glu Met Val Ser Met Gly
755 760 765
Val Gly Asn Lys Ala Phe Arg Asp Ile Ala Pro Ser Glu Glu Ala Ile
770 775 780
Asn Asp Arg Thr Val Asn Tyr Val Leu Lys Cys Arg Glu Val Arg Ser
785 790 795 800
Arg Ala Ser Ile Ala Val Ala Pro Phe Asp His Asp Ser Leu Tyr Leu
805 810 815
Gly Ala Ser Asn Ser Leu Pro Gly Asp Pro Ala Ser Cys Ser Val Leu
820 825 830
Gly Ser Leu Asn Leu His Leu Tyr Arg Asp Pro Ala Leu Leu Gly Leu
835 840 845
Arg Cys Pro Leu Tyr Pro Ser Phe Leu Glu Glu Ala Ala Leu Glu Ala
850 855 860
Glu Ala Glu Leu Gly Gly Gln Pro Ser Leu Thr Ala Glu Asp Ser Glu

```
865                 870                 875                 880
Ile Ser Ser Gln Cys Pro Ser Ala Ser Gly Ser Ser Gly Ser Asp Ser
                885                 890                 895
Ser Cys Val Ser Gly Gln Ala Leu Gly Arg Gly Leu Glu Asp Leu Pro
            900                 905                 910
Cys Val
```

<210> 673
<211> 277
<212> PRT
<213> Homo sapiens

<400> 673

```
Leu Asn Tyr Leu Leu Glu Ser Arg Leu Glu Ala Ala Ala His Cys Ala
 1               5                  10                  15
Leu Lys Gln Gly Ile Ala Thr Ala Ser Leu Leu Pro Ala Gln Leu Gln
            20                  25                  30
Pro Ala Val Leu Thr Val Val Thr Cys His Val Val Val Ser Val His
        35                  40                  45
Gly His His Thr Asp Gly Cys Leu Ala Ala Leu Cys Arg Glu Asp Arg
    50                  55                  60
Thr Gly Thr Gly Gly Ala Phe Trp Cys Lys Asn Arg Val Ile Val Ser
65                  70                  75                  80
His Ala Val Asp Val Val Leu His Val His Gly Glu Gly Asn Pro Val
                85                  90                  95
Gln Ala Leu Ile Ala His Gly Ala Pro Glu Ala Ala Trp Val Val Gly
            100                 105                 110
Leu Ala Gln Gly Leu Gln Asp His Phe His Asp Glu Met Ser Thr His
        115                 120                 125
Ala Ala Phe Val Gly Arg Leu Leu Glu Pro Gly Val Gln Glu Val Leu
    130                 135                 140
Leu Ala Val His Phe Leu Thr His Val Val Glu Arg Leu Pro Thr Glu
145                 150                 155                 160
Ser Ser Pro Thr Arg Val Ala Gly Glu Ala Val Ser Val Ile Lys Thr
                165                 170                 175
Pro His Cys Leu Ala Arg Leu Leu Gly Ser Val Asp Ala Lys Pro Thr
            180                 185                 190
Leu Asp Ala Asn Ala Glu Val Val Pro Arg Arg Ala Arg Leu Glu Arg
        195                 200                 205
Pro Leu Gln Leu Pro Gly Glu Arg Leu Gln Pro Pro Leu Gly Arg Ala
    210                 215                 220
Trp Ala Ala Leu Pro Ala Arg Gly Gln Arg Glu Cys Arg Gln Arg Glu
225                 230                 235                 240
Gly Gly Arg Pro Arg Arg Leu Arg Gly Ala Ser Gly Arg Gly Ala Gly
                245                 250                 255
Ala Gly Arg Glu Glu Val Ser Val Gly Phe Ser Ala Gln Trp Glu Phe
            260                 265                 270
Gly Ser Gly Arg His
        275
```

<210> 674
<211> 1120
<212> PRT

<213> Homo sapiens

<400> 674

```
Met Trp Arg Val Lys Lys Leu Ser Leu Ser Leu Ser Pro Ser Pro Gln
 1               5                   10                  15
Thr Gly Lys Pro Ser Met Arg Thr Pro Leu Arg Glu Leu Thr Leu Gln
            20                  25                  30
Pro Gly Ala Leu Thr Thr Ser Gly Lys Arg Ser Pro Ala Cys Ser Ser
        35                  40                  45
Leu Thr Pro Ser Leu Cys Lys Leu Gly Leu Gln Glu Gly Ser Asn Asn
    50                  55                  60
Ser Ser Pro Val Asp Phe Val Asn Asn Lys Arg Thr Asp Leu Ser Ser
65                  70                  75                  80
Glu His Phe Ser His Ser Ser Lys Trp Leu Glu Thr Cys Gln His Glu
                85                  90                  95
Ser Asp Glu Gln Pro Leu Asp Pro Ile Pro Gln Ile Ser Ser Thr Pro
            100                 105                 110
Lys Thr Ser Glu Glu Ala Val Asp Pro Leu Gly Asn Tyr Met Val Lys
        115                 120                 125
Thr Ile Val Leu Val Pro Ser Pro Leu Gly Gln Gln Asp Met Ile
    130                 135                 140
Phe Glu Ala Arg Leu Asp Thr Met Ala Glu Thr Asn Ser Ile Ser Leu
145                 150                 155                 160
Asn Gly Pro Leu Arg Thr Asp Asp Leu Val Arg Glu Glu Val Ala Pro
                165                 170                 175
Cys Met Gly Asp Arg Phe Ser Glu Val Ala Ala Val Ser Glu Lys Pro
            180                 185                 190
Ile Phe Gln Glu Ser Pro Ser His Leu Leu Glu Glu Ser Pro Pro Asn
        195                 200                 205
Pro Cys Ser Glu Gln Leu His Cys Ser Lys Glu Ser Leu Ser Ser Arg
    210                 215                 220
Thr Glu Ala Val Arg Glu Asp Leu Val Pro Ser Glu Ser Asn Ala Phe
225                 230                 235                 240
Leu Pro Ser Ser Val Leu Trp Leu Ser Pro Ser Thr Ala Leu Ala Ala
                245                 250                 255
Asp Phe Arg Val Asn His Val Asp Pro Glu Glu Glu Ile Val Glu His
            260                 265                 270
Gly Ala Met Glu Glu Arg Glu Met Arg Phe Pro Thr His Pro Lys Glu
        275                 280                 285
Ser Glu Thr Glu Asp Gln Ala Leu Val Ser Ser Val Glu Asp Ile Leu
    290                 295                 300
Ser Thr Cys Leu Thr Pro Asn Leu Val Glu Met Glu Ser Gln Glu Ala
305                 310                 315                 320
Pro Gly Pro Ala Val Glu Asp Val Gly Arg Ile Leu Gly Ser Asp Thr
                325                 330                 335
Glu Ser Trp Met Ser Pro Leu Ala Trp Leu Glu Lys Gly Val Asn Thr
            340                 345                 350
Ser Val Met Leu Glu Asn Leu Arg Gln Ser Leu Ser Leu Pro Ser Met
        355                 360                 365
Leu Arg Asp Ala Ala Ile Gly Thr Thr Pro Phe Ser Thr Cys Ser Val
    370                 375                 380
Gly Thr Trp Phe Thr Pro Ser Ala Pro Gln Glu Lys Ser Thr Asn Thr
385                 390                 395                 400
Ser Gln Thr Gly Leu Val Gly Thr Lys His Ser Thr Ser Glu Thr Glu
```

405 410 415
Gln Leu Leu Cys Gly Arg Pro Pro Asp Leu Thr Ala Leu Ser Arg His
420 425 430
Asp Leu Glu Asp Asn Leu Leu Ser Ser Leu Val Ile Val Glu Phe Leu
435 440 445
Ser Arg Gln Leu Arg Asp Trp Lys Ser Gln Leu Ala Val Pro His Pro
450 455 460
Glu Thr Gln Asp Ser Ser Thr Gln Thr Asp Thr Ser His Ser Gly Ile
465 470 475 480
Thr Asn Lys Leu Gln His Leu Lys Glu Ser His Glu Met Gly Gln Ala
485 490 495
Leu Gln Gln Ala Arg Asn Val Met Gln Ser Trp Val Leu Ile Ser Lys
500 505 510
Glu Leu Ile Ser Leu Leu His Leu Ser Leu Leu His Leu Glu Glu Asp
515 520 525
Lys Thr Thr Val Asn Gln Glu Ser Arg Arg Ala Glu Thr Leu Val Cys
530 535 540
Cys Cys Phe Asp Leu Leu Lys Lys Leu Arg Ala Lys Leu Gln Ser Leu
545 550 555 560
Lys Ala Glu Arg Glu Glu Ala Arg His Arg Glu Glu Met Ala Leu Arg
565 570 575
Gly Lys Asp Ala Ala Glu Ile Val Leu Glu Ala Phe Cys Ala His Ala
580 585 590
Ser Gln Arg Ile Ser Gln Leu Glu Gln Asp Leu Ala Ser Met Arg Glu
595 600 605
Phe Arg Gly Leu Leu Lys Asp Ala Gln Thr Gln Leu Val Gly Leu His
610 615 620
Ala Lys Gln Glu Glu Leu Val Gln Gln Thr Val Ser Leu Thr Ser Thr
625 630 635 640
Leu Gln Gln Asp Trp Arg Ser Met Gln Leu Asp Tyr Thr Thr Trp Thr
645 650 655
Ala Leu Leu Ser Arg Ser Arg Gln Leu Thr Glu Lys Leu Thr Val Lys
660 665 670
Ser Gln Gln Ala Leu Gln Glu Arg Asp Val Ala Ile Glu Glu Lys Gln
675 680 685
Glu Val Ser Arg Val Leu Glu Gln Val Ser Ala Gln Leu Glu Glu Cys
690 695 700
Lys Gly Gln Thr Glu Gln Leu Glu Leu Glu Asn Ile Arg Leu Ala Thr
705 710 715 720
Asp Leu Arg Ala Gln Leu Gln Ile Leu Ala Asn Met Asp Ser Gln Leu
725 730 735
Lys Glu Leu Gln Ser Gln His Thr His Cys Ala Gln Asp Leu Ala Met
740 745 750
Lys Asp Glu Leu Leu Cys Gln Leu Thr Gln Ser Asn Glu Glu Gln Ala
755 760 765
Ala Gln Cys Val Lys Glu Glu Met Ala Leu Lys His Met Gln Ala Glu
770 775 780
Leu Gln Gln Gln Gln Ala Val Leu Ala Lys Glu Val Arg Asp Leu Lys
785 790 795 800
Glu Thr Leu Glu Phe Ala Asp Gln Glu Asn Gln Val Ala His Leu Glu
805 810 815
Leu Gly Gln Val Glu Cys Gln Leu Lys Thr Thr Leu Glu Val Leu Arg
820 825 830
Glu Arg Ser Leu Gln Cys Glu Asn Leu Lys Asp Thr Val Glu Asn Leu

835 840 845
Thr Ala Lys Leu Ala Ser Thr Ile Ala Asp Asn Gln Glu Gln Asp Leu
850 855 860
Glu Lys Thr Arg Gln Tyr Ser Gln Lys Leu Gly Leu Leu Thr Glu Gln
865 870 875 880
Leu Gln Ser Leu Thr Leu Phe Leu Gln Thr Lys Leu Lys Glu Lys Thr
885 890 895
Glu Gln Glu Thr Leu Leu Leu Ser Thr Ala Cys Pro Pro Thr Gln Glu
900 905 910
His Pro Leu Pro Asn Asp Arg Thr Phe Leu Gly Ser Ile Leu Thr Ala
915 920 925
Val Ala Asp Glu Glu Pro Glu Ser Thr Pro Val Pro Leu Leu Gly Ser
930 935 940
Asp Lys Ser Ala Phe Thr Arg Val Ala Ser Met Val Ser Leu Gln Pro
945 950 955 960
Ala Glu Thr Pro Gly Met Glu Glu Ser Leu Ala Glu Met Ser Ile Met
965 970 975
Thr Thr Glu Leu Gln Ser Leu Cys Ser Leu Leu Gln Glu Ser Lys Glu
980 985 990
Glu Ala Ile Arg Thr Leu Gln Arg Lys Ile Cys Glu Leu Gln Ala Arg
995 1000 1005
Leu Gln Ala Gln Glu Glu Gln His Gln Glu Val Gln Lys Ala Lys Glu
1010 1015 1020
Ala Asp Ile Glu Lys Leu Asn Gln Ala Leu Cys Leu Arg Tyr Lys Asn
1025 1030 1035 1040
Glu Lys Glu Leu Gln Glu Val Ile Gln Gln Asn Glu Lys Ile Leu Glu
1045 1050 1055
Gln Ile Asp Lys Ser Gly Glu Leu Ile Ser Leu Arg Glu Glu Val Thr
1060 1065 1070
His Leu Thr Arg Ser Leu Arg Arg Ala Glu Thr Glu Thr Lys Val Leu
1075 1080 1085
Gln Glu Ala Trp Gln Ala Ser Trp Thr Pro Thr Ala Ser Leu Trp Pro
1090 1095 1100
Pro Ile Gly Ser Arg Arg Lys Cys Gly Ser Leu Arg Arg Trp Thr Asn
1105 1110 1115 1120

<210> 675
<211> 540
<212> PRT
<213> Homo sapiens

<400> 675
Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
1 5 10 15
Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
20 25 30
Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
35 40 45
Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
50 55 60
His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65 70 75 80
Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
85 90 95

```
Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
            100                 105                 110
Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
        115                 120                 125
Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
    130                 135                 140
Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145                 150                 155                 160
Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
                165                 170                 175
Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
            180                 185                 190
Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
        195                 200                 205
Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
    210                 215                 220
Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225                 230                 235                 240
Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
                245                 250                 255
Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
            260                 265                 270
Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
        275                 280                 285
Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
    290                 295                 300
Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305                 310                 315                 320
Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
                325                 330                 335
Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
            340                 345                 350
Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
        355                 360                 365
Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
    370                 375                 380
Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385                 390                 395                 400
Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
                405                 410                 415
Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
            420                 425                 430
Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
        435                 440                 445
Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
    450                 455                 460
Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465                 470                 475                 480
Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
                485                 490                 495
Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
            500                 505                 510
Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
        515                 520                 525
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```
Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
    530                 535                 540

&lt;210&gt; 676
&lt;211&gt; 462
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;400&gt; 676
Met Gly Lys Glu Lys Thr His Ile Asn Ile Val Val Ile Gly His Val
 1               5                  10                  15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
            20                  25                  30
Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
        35                  40                  45
Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
    50                  55                  60
Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
65                  70                  75                  80
Glu Thr Ser Lys Tyr Tyr Val Thr Ile Ile Asp Ala Pro Gly His Arg
                85                  90                  95
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
            100                 105                 110
Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
        115                 120                 125
Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
    130                 135                 140
Val Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
145                 150                 155                 160
Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile Val Lys Glu Val Ser Thr
                165                 170                 175
Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Asp Thr Val Ala Phe Val Pro
            180                 185                 190
Ile Ser Gly Trp Asn Gly Asp Asn Met Leu Glu Pro Ser Ala Asn Met
        195                 200                 205
Pro Trp Phe Lys Gly Trp Lys Val Thr Arg Lys Asp Gly Asn Ala Ser
    210                 215                 220
Gly Thr Thr Leu Leu Glu Ala Val Asp Cys Ile Leu Pro Pro Thr Arg
225                 230                 235                 240
Pro Thr Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile
                245                 250                 255
Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu
            260                 265                 270
Lys Pro Gly Met Val Val Thr Phe Ala Pro Val Asn Val Thr Thr Glu
        275                 280                 285
Val Lys Ser Val Glu Met His His Glu Ala Leu Ser Glu Ala Leu Pro
    290                 295                 300
Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Val
305                 310                 315                 320
Arg Arg Gly Asn Val Ala Gly Asp Ser Lys Asn Asp Pro Pro Met Glu
                325                 330                 335
Ala Ala Gly Phe Thr Ala Gln Val Ile Ile Leu Asn His Pro Gly Gln
            340                 345                 350
Ile Ser Ala Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ala His Ile
```

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        355                 360                 365
Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
    370                 375                 380
Lys Lys Leu Glu Asp Gly Pro Lys Phe Leu Lys Ser Gly Asp Ala Ala
385                 390                 395                 400
Ile Val Asp Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
                405                 410                 415
Asp Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
            420                 425                 430
Val Ala Val Gly Val Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala
        435                 440                 445
Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Lys
    450                 455                 460
```

<210> 677
<211> 2328
<212> PRT
<213> Homo sapiens

<400> 677

```
Lys Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val
 1               5                  10                  15
Ala Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr
            20                  25                  30
Gln Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val
        35                  40                  45
Cys Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro
    50                  55                  60
Glu Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg
65                  70                  75                  80
Val Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys
                85                  90                  95
Thr Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn
            100                 105                 110
Arg Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg
        115                 120                 125
Arg Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly
    130                 135                 140
Asn Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe
145                 150                 155                 160
Asp His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys
                165                 170                 175
Pro Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly
            180                 185                 190
Ser Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp
        195                 200                 205
Thr Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn
    210                 215                 220
Arg Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu
225                 230                 235                 240
Trp Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser
                245                 250                 255
Gly Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His
            260                 265                 270
```

Pro Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val
275 280 285
Tyr Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met
290 295 300
Leu Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val
305 310 315 320
Thr Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro
325 330 335
Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg
340 345 350
Gln Asp Gly His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp
355 360 365
Gln Lys Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Gln
370 375 380
Gly Gly Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn
385 390 395 400
Asn His Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met
405 410 415
Lys Trp Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly
420 425 430
Phe Cys Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly
435 440 445
Val Met Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly
450 455 460
His Met Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr
465 470 475 480
Cys Ile Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile
485 490 495
Thr Tyr Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His
500 505 510
Met Leu Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys
515 520 525
Asp Pro Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln
530 535 540
Ile Gly Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys
545 550 555 560
Tyr Cys Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln
565 570 575
Thr Tyr Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr
580 585 590
Pro Ser Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro
595 600 605
Ser His Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val
610 615 620
Gly Arg Trp Lys Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr
625 630 635 640
Ile Lys Gly Leu Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser
645 650 655
Ile Gln Gln Tyr Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr
660 665 670
Thr Ser Thr Ser Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr
675 680 685
Thr Pro Phe Ser Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile
690 695 700

Thr Ala Ser Ser Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val
705 710 715 720
Ser Gly Phe Arg Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro
725 730 735
Gln Tyr Leu Asp Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp
740 745 750
Leu Leu Pro Gly Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu
755 760 765
Asp Gly Glu Gln Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro
770 775 780
Asp Ala Pro Pro Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile
785 790 795 800
Val Val Arg Trp Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile
805 810 815
Val Tyr Ser Pro Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro
820 825 830
Glu Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln
835 840 845
Tyr Asn Ile Thr Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro
850 855 860
Val Val Ile Gln Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val
865 870 875 880
Pro Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val
885 890 895
Thr Ile Met Trp Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val
900 905 910
Asp Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro
915 920 925
Ile Ser Arg Asn Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val
930 935 940
Thr Tyr Tyr Phe Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys
945 950 955 960
Pro Leu Thr Ala Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu
965 970 975
Gln Phe Val Asn Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro
980 985 990
Pro Arg Ala Gln Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg
995 1000 1005
Arg Gly Gln Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr
1010 1015 1020
Pro Leu Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val
1025 1030 1035 1040
Ala Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr
1045 1050 1055
Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr
1060 1065 1070
Glu Thr Thr Ile Val Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe
1075 1080 1085
Lys Leu Gly Val Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg Glu Val
1090 1095 1100
Thr Ser Asp Ser Gly Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val
1105 1110 1115 1120
Glu Tyr Val Tyr Thr Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp
1125 1130 1135

Ala Pro Ile Val Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn
1140 1145 1150
Leu His Leu Glu Ala Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp
1155 1160 1165
Glu Arg Ser Thr Thr Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr
1170 1175 1180
Pro Thr Asn Gly Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala
1185 1190 1195 1200
Asp Gln Ser Ser Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr
1205 1210 1215
Asn Val Ser Val Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile
1220 1225 1230
Ser Asp Thr Ile Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe
1235 1240 1245
Thr Asn Ile Gly Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro
1250 1255 1260
Ser Ile Asp Leu Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn
1265 1270 1275 1280
Glu Glu Asp Val Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val
1285 1290 1295
Val Leu Thr Asn Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser
1300 1305 1310
Ser Val Tyr Glu Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys
1315 1320 1325
Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala
1330 1335 1340
Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly
1345 1350 1355 1360
Tyr Arg Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu
1365 1370 1375
Asp Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
1380 1385 1390
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu
1395 1400 1405
Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro
1410 1415 1420
Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser
1425 1430 1435 1440
Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly
1445 1450 1455
Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser
1460 1465 1470
Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
1475 1480 1485
Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser
1490 1495 1500
Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
1505 1510 1515 1520
Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu
1525 1530 1535
Pro Ser Ser Ser Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys
1540 1545 1550
Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr
1555 1560 1565

Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser
    1570   1575   1580
Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr
1585   1590   1595   1600
Ala Val Thr Asn Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val
                1605   1610   1615
Asp Val Asp Ser Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val
            1620   1625   1630
Ser Arg Tyr Arg Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu
        1635   1640   1645
Leu Phe Pro Ala Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly
    1650   1655   1660
Leu Arg Pro Gly Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp
1665   1670   1675   1680
Asp Met Glu Ser Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro
                1685   1690   1695
Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser
            1700   1705   1710
Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg
        1715   1720   1725
Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala
    1730   1735   1740
Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys
1745   1750   1755   1760
Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro
                1765   1770   1775
Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg
            1780   1785   1790
Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg
        1795   1800   1805
Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala
    1810   1815   1820
Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser
1825   1830   1835   1840
Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu
                1845   1850   1855
Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala
            1860   1865   1870
Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr
        1875   1880   1885
Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr
    1890   1895   1900
Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val
1905   1910   1915   1920
Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu
                1925   1930   1935
Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn
            1940   1945   1950
Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro
        1955   1960   1965
Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu
    1970   1975   1980
Asp Val Pro Ser Thr Val Gln Lys Thr Pro Phe Val Thr His Pro Gly
1985   1990   1995   2000

Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly Gln Gln
2005 2010 2015
Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg
2020 2025 2030
Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro
2035 2040 2045
Tyr Pro Pro Asn Val Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser
2050 2055 2060
Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro
2065 2070 2075 2080
Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser
2085 2090 2095
Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile
2100 2105 2110
Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu
2115 2120 2125
Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr
2130 2135 2140
Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly
2145 2150 2155 2160
Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln
2165 2170 2175
Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp
2180 2185 2190
Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg
2195 2200 2205
Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly
2210 2215 2220
Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp
2225 2230 2235 2240
Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly
2245 2250 2255
Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys
2260 2265 2270
Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr
2275 2280 2285
Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn
2290 2295 2300
Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln
2305 2310 2315 2320
Ala Asp Arg Glu Asp Ser Arg Glu
2325

<210> 678
<211> 188
<212> PRT
<213> Homo sapiens

<400> 678
His Gln Thr His Lys Glu Gly Gly Ser Thr His Ala Ser Ala Asp Ala
1 5 10 15
Trp Glu Ile Ile Glu Leu Glu Thr Glu Ile Glu Lys Phe Lys Ala Glu
20 25 30
Asn Ala Ser Leu Ala Lys Leu Arg Ile Glu Arg Glu Ser Ala Leu Glu

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        35                  40                  45
Lys Leu Arg Lys Glu Ile Ala Asp Phe Glu Gln Gln Lys Ala Lys Glu
    50                  55                  60
Leu Ala Arg Ile Glu Glu Phe Lys Lys Glu Glu Met Arg Lys Leu Gln
65                  70                  75                  80
Lys Glu Arg Lys Val Phe Glu Lys Tyr Thr Thr Ala Ala Arg Thr Phe
                85                  90                  95
Pro Asp Lys Lys Glu Arg Glu Glu Ile Gln Thr Leu Lys Gln Gln Ile
            100                 105                 110
Ala Asp Leu Arg Glu Asp Leu Lys Arg Lys Glu Thr Lys Trp Ser Ser
        115                 120                 125
Thr His Ser Arg Leu Arg Ser Gln Ile Gln Met Leu Val Arg Glu Asn
    130                 135                 140
Thr Asp Leu Arg Glu Glu Ile Lys Val Met Glu Arg Phe Arg Leu Asp
145                 150                 155                 160
Ala Trp Lys Arg Ala Glu Ala Ile Glu Ser Ser Leu Glu Val Glu Lys
                165                 170                 175
Lys Asp Lys Leu Ala Asn Thr Ser Val Arg Phe Gln
            180                 185

&lt;210&gt; 679
&lt;211&gt; 284
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;400&gt; 679
Met Glu Pro Gly Asn Tyr Ala Thr Leu Asp Gly Ala Lys Asp Ile Glu
 1               5                  10                  15
Gly Leu Leu Gly Ala Gly Gly Gly Arg Asn Leu Val Ala His Ser Pro
            20                  25                  30
Leu Thr Ser His Pro Ala Ala Pro Thr Leu Met Pro Ala Val Asn Tyr
        35                  40                  45
Ala Pro Leu Asp Leu Pro Gly Ser Ala Glu Pro Pro Lys Gln Cys His
    50                  55                  60
Pro Cys Pro Gly Val Pro Gln Gly Thr Ser Pro Ala Pro Val Pro Tyr
65                  70                  75                  80
Gly Tyr Phe Gly Gly Gly Tyr Tyr Ser Cys Arg Val Ser Arg Ser Ser
                85                  90                  95
Leu Lys Pro Cys Ala Gln Ala Ala Thr Leu Ala Ala Tyr Pro Ala Glu
            100                 105                 110
Thr Pro Thr Ala Gly Glu Glu Tyr Pro Ser Arg Pro Thr Glu Phe Ala
        115                 120                 125
Phe Tyr Pro Gly Tyr Pro Gly Thr Tyr His Ala Met Ala Ser Tyr Leu
    130                 135                 140
Asp Val Ser Val Val Gln Thr Leu Gly Ala Pro Gly Glu Pro Arg His
145                 150                 155                 160
Asp Ser Leu Leu Pro Val Asp Ser Tyr Gln Ser Trp Ala Leu Ala Gly
                165                 170                 175
Gly Trp Asn Ser Gln Met Cys Cys Gln Gly Glu Gln Asn Pro Pro Gly
            180                 185                 190
Pro Phe Trp Lys Ala Ala Phe Ala Asp Ser Ser Gly Gln His Pro Pro
        195                 200                 205
Asp Ala Cys Ala Phe Arg Arg Gly Arg Lys Lys Arg Ile Pro Tyr Ser
    210                 215                 220
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Lys Gly Gln Leu Arg Glu Leu Glu Arg Glu Tyr Ala Ala Asn Lys Phe
225 230 235 240
Ile Thr Lys Asp Lys Arg Arg Lys Ile Ser Ala Ala Thr Ser Leu Ser
245 250 255
Glu Arg Gln Ile Thr Ile Trp Phe Gln Asn Arg Arg Val Lys Glu Lys
260 265 270
Lys Val Leu Ala Lys Val Lys Asn Ser Ala Thr Pro
275 280

<210> 680
<211> 676
<212> PRT
<213> Homo sapiens

<400> 680
Met Asp Lys Tyr Asp Asp Leu Gly Leu Glu Ala Ser Lys Phe Ile Glu
1 5 10 15
Asp Leu Asn Met Tyr Glu Ala Ser Lys Asp Gly Leu Phe Arg Val Asp
20 25 30
Lys Gly Ala Gly Asn Asn Pro Glu Phe Glu Glu Thr Arg Arg Val Phe
35 40 45
Ala Thr Lys Met Ala Lys Ile His Leu Gln Gln Gln Gln Gln Gln Leu
50 55 60
Leu Gln Glu Glu Thr Leu Pro Arg Gly Ser Arg Gly Pro Val Asn Gly
65 70 75 80
Gly Gly Arg Leu Gly Pro Gln Ala Arg Trp Glu Val Val Gly Ser Lys
85 90 95
Leu Thr Val Asp Gly Ala Ala Lys Pro Pro Leu Ala Ala Ser Thr Gly
100 105 110
Ala Pro Gly Ala Val Thr Thr Leu Ala Ala Gly Gln Pro Pro Tyr Pro
115 120 125
Pro Gln Glu Gln Arg Ser Arg Pro Tyr Leu His Gly Thr Arg His Gly
130 135 140
Ser Gln Asp Cys Gly Ser Arg Glu Ser Leu Ala Thr Ser Glu Met Ser
145 150 155 160
Ala Phe His Gln Pro Gly Pro Cys Glu Asp Pro Ser Cys Leu Thr His
165 170 175
Gly Asp Tyr Tyr Asp Asn Leu Ser Leu Ala Ser Pro Lys Trp Gly Asp
180 185 190
Lys Pro Gly Val Ser Pro Ser Ile Gly Leu Ser Val Gly Ser Gly Trp
195 200 205
Pro Ser Ser Pro Gly Ser Asp Pro Pro Leu Pro Lys Pro Cys Gly Asp
210 215 220
His Pro Leu Asn His Arg Gln Leu Ser Leu Ser Ser Ser Arg Ser Ser
225 230 235 240
Glu Gly Ser Leu Gly Gly Gln Asn Ser Gly Ile Gly Gly Arg Ser Ser
245 250 255
Glu Lys Pro Thr Gly Leu Trp Ser Thr Ala Ser Ser Gln Arg Val Ser
260 265 270
Pro Gly Leu Pro Ser Pro Asn Leu Glu Asn Gly Ala Pro Ala Val Gly
275 280 285
Pro Val Gln Pro Arg Thr Pro Ser Val Ser Ala Pro Leu Ala Leu Ser
290 295 300
Cys Pro Arg Gln Gly Gly Leu Pro Arg Ser Asn Ser Gly Leu Gly Gly

305 310 315 320
Glu Val Ser Gly Val Met Ser Lys Pro Asn Val Asp Pro Gln Pro Trp
325 330 335
Phe Gln Asp Gly Pro Lys Ser Tyr Leu Ser Ser Ser Ala Pro Ser Ser
340 345 350
Ser Pro Ala Gly Leu Asp Gly Ser Gln Gln Gly Ala Val Pro Gly Leu
355 360 365
Gly Pro Lys Pro Gly Cys Thr Asp Leu Gly Thr Gly Pro Lys Leu Ser
370 375 380
Pro Thr Ser Leu Val His Pro Val Met Ser Thr Leu Pro Glu Leu Ser
385 390 395 400
Cys Lys Glu Gly Pro Leu Gly Trp Ser Ser Asp Gly Ser Leu Gly Ser
405 410 415
Val Leu Leu Asp Ser Pro Ser Ser Pro Arg Val Arg Leu Pro Cys Gln
420 425 430
Pro Leu Val Pro Gly Pro Glu Leu Arg Pro Ser Ala Ala Glu Leu Lys
435 440 445
Leu Glu Ala Leu Thr Gln Arg Leu Glu Arg Glu Met Asp Ala His Pro
450 455 460
Lys Ala Asp Tyr Phe Gly Ala Cys Val Lys Cys Ser Lys Gly Val Phe
465 470 475 480
Gly Ala Gly Gln Ala Cys Gln Ala Met Gly Asn Leu Tyr His Asp Thr
485 490 495
Cys Phe Thr Cys Ala Ala Cys Ser Arg Lys Leu Arg Gly Lys Ala Phe
500 505 510
Tyr Phe Val Asn Gly Lys Val Phe Cys Glu Glu Asp Phe Leu Tyr Ser
515 520 525
Gly Phe Gln Gln Ser Ala Asp Arg Cys Phe Leu Cys Gly His Leu Ile
530 535 540
Met Asp Met Ile Leu Gln Ala Leu Gly Lys Ser Tyr His Pro Gly Cys
545 550 555 560
Phe Arg Cys Val Ile Cys Asn Glu Cys Leu Asp Gly Val Pro Phe Thr
565 570 575
Val Asp Ser Glu Asn Lys Ile Tyr Cys Val Arg Asp Tyr His Lys Val
580 585 590
Leu Ala Pro Lys Cys Ala Ala Cys Gly Leu Pro Ile Leu Pro Pro Glu
595 600 605
Gly Ser Asp Glu Thr Ile Arg Val Val Ser Met Asp Arg Asp Tyr His
610 615 620
Val Glu Cys Tyr His Cys Glu Asp Cys Gly Leu Glu Leu Asn Asp Glu
625 630 635 640
Asp Gly His Arg Cys Tyr Pro Leu Glu Asp His Leu Phe Cys His Ser
645 650 655
Cys His Val Lys Arg Leu Glu Lys Arg Pro Ser Ser Thr Ala Leu His
660 665 670
Gln His His Phe
675

<210> 681
<211> 296
<212> PRT
<213> Homo sapiens

<400> 681

Ser Thr Gly Ser Glu Phe Pro Leu Cys Thr Lys Ala Ser Pro Cys Ser
1 5 10 15
Ala Ala Arg Ala Gly Gly Arg Ala Leu Gly Trp Arg Leu Gln Gln Gln
20 25 30
Arg Glu Thr Arg Gly Asn Pro Gly Asn Pro Gly Leu Gly Val Ala Ala
35 40 45
Thr Met Thr Gly Ser Asn Met Ser Asp Ala Leu Ala Asn Ala Val Cys
50 55 60
Gln Arg Cys Gln Ala Arg Phe Ser Pro Ala Glu Arg Ile Val Asn Ser
65 70 75 80
Asn Gly Glu Leu Tyr His Glu His Cys Phe Val Cys Ala Gln Cys Phe
85 90 95
Arg Pro Phe Pro Glu Gly Leu Phe Tyr Glu Phe Glu Gly Arg Lys Tyr
100 105 110
Cys Glu His Asp Phe Gln Met Leu Phe Ala Pro Cys Cys Gly Ser Cys
115 120 125
Gly Glu Phe Ile Ile Gly Arg Val Ile Lys Ala Met Asn Asn Asn Trp
130 135 140
His Pro Gly Cys Phe Arg Cys Glu Leu Cys Asp Val Glu Leu Ala Asp
145 150 155 160
Leu Gly Phe Val Lys Asn Ala Gly Arg His Leu Cys Arg Pro Cys His
165 170 175
Asn Arg Glu Lys Ala Lys Gly Leu Gly Lys Tyr Ile Cys Gln Arg Cys
180 185 190
His Leu Val Ile Asp Glu Gln Pro Leu Met Phe Arg Ser Asp Ala Tyr
195 200 205
His Pro Asp His Phe Asn Cys Thr His Cys Gly Lys Glu Leu Thr Ala
210 215 220
Glu Ala Arg Glu Leu Lys Gly Glu Leu Tyr Cys Leu Pro Cys His Asp
225 230 235 240
Lys Met Gly Val Pro Ile Cys Gly Ala Cys Arg Arg Pro Ile Glu Gly
245 250 255
Arg Val Val Asn Ala Leu Gly Lys Gln Trp His Val Glu His Phe Val
260 265 270
Cys Ala Lys Cys Glu Lys Pro Phe Leu Gly His Arg His Tyr Glu Lys
275 280 285
Lys Gly Leu Ala Tyr Cys Glu Leu
290 295

<210> 682
<211> 500
<212> PRT
<213> Homo sapiens

<400> 682
Met Gly Ile Gly Leu Ser Ala Gln Gly Val Asn Met Asn Arg Leu Pro
1 5 10 15
Gly Trp Asp Lys His Ser Tyr Gly Tyr His Gly Asp Asp Gly His Ser
20 25 30
Phe Cys Ser Ser Gly Thr Gly Gln Pro Tyr Gly Pro Thr Phe Thr Thr
35 40 45
Gly Asp Val Ile Gly Cys Cys Val Asn Leu Ile Asn Asn Thr Cys Phe
50 55 60
Tyr Thr Lys Asn Gly His Ser Leu Gly Ile Ala Phe Thr Asp Leu Pro

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65                  70                  75                  80
Pro Asn Leu Tyr Pro Thr Val Gly Leu Gln Thr Pro Gly Glu Val Val
                85                  90                  95
Asp Ala Asn Phe Gly Gln His Pro Phe Val Phe Asp Ile Glu Asp Tyr
            100                 105                 110
Met Arg Glu Trp Arg Thr Lys Ile Gln Ala Gln Ile Asp Arg Phe Pro
        115                 120                 125
Ile Gly Asp Arg Glu Gly Glu Trp Gln Thr Met Ile Gln Lys Met Val
    130                 135                 140
Ser Ser Tyr Leu Val His His Gly Tyr Cys Ala Thr Ala Glu Ala Phe
145                 150                 155                 160
Ala Arg Ser Thr Asp Gln Thr Val Leu Glu Glu Leu Ala Ser Ile Lys
                165                 170                 175
Asn Arg Gln Arg Ile Gln Lys Leu Val Leu Ala Gly Arg Met Gly Glu
            180                 185                 190
Ala Ile Glu Thr Thr Gln Gln Leu Tyr Pro Ser Leu Leu Glu Arg Asn
        195                 200                 205
Pro Asn Leu Leu Phe Thr Leu Lys Val Arg Gln Phe Ile Glu Met Val
    210                 215                 220
Asn Gly Thr Asp Ser Glu Val Arg Cys Leu Gly Gly Arg Ser Pro Lys
225                 230                 235                 240
Ser Gln Asp Ser Tyr Pro Val Ser Pro Arg Pro Phe Ser Ser Pro Ser
                245                 250                 255
Met Ser Pro Ser His Gly Met Asn Ile His Asn Leu Ala Ser Gly Lys
            260                 265                 270
Gly Ser Thr Ala His Phe Ser Gly Phe Glu Ser Cys Ser Asn Gly Val
        275                 280                 285
Ile Ser Asn Lys Ala His Gln Ser Tyr Cys His Ser Asn Lys His Gln
    290                 295                 300
Ser Ser Asn Leu Asn Val Pro Glu Leu Asn Ser Ile Asn Met Ser Arg
305                 310                 315                 320
Ser Gln Gln Val Asn Asn Phe Thr Ser Asn Asp Val Asp Met Glu Thr
                325                 330                 335
Asp His Tyr Ser Asn Gly Val Gly Glu Thr Ser Ser Asn Gly Phe Leu
            340                 345                 350
Asn Gly Ser Ser Lys His Asp His Glu Met Glu Asp Cys Asp Thr Glu
        355                 360                 365
Met Glu Val Asp Ser Ser Gln Leu Arg Arg Gln Leu Cys Gly Gly Ser
    370                 375                 380
Gln Ala Ala Ile Glu Arg Met Ile His Phe Gly Arg Glu Leu Gln Ala
385                 390                 395                 400
Met Ser Glu Gln Leu Arg Arg Asp Cys Gly Lys Asn Thr Ala Asn Lys
                405                 410                 415
Lys Met Leu Lys Asp Ala Phe Ser Leu Leu Ala Tyr Ser Asp Pro Trp
            420                 425                 430
Asn Ser Pro Val Gly Asn Gln Leu Asp Pro Ile Gln Arg Glu Pro Val
        435                 440                 445
Cys Ser Ala Leu Asn Ser Ala Ile Leu Glu Thr His Asn Leu Pro Lys
    450                 455                 460
Gln Pro Pro Leu Ala Leu Ala Met Gly Gln Ala Thr Gln Cys Leu Gly
465                 470                 475                 480
Leu Met Ala Arg Ser Gly Ile Gly Ser Cys Ala Phe Ala Thr Val Glu
                485                 490                 495
Asp Tyr Leu His
```

500

<210> 683
<211> 387
<212> PRT
<213> Homo sapiens

<400> 683
Met Ala Thr Ser Gly Val Leu Pro Gly Gly Gly Phe Val Ala Ser Ala
1 5 10 15
Ala Ala Val Ala Gly Pro Glu Met Gln Thr Gly Arg Asn Asn Phe Val
20 25 30
Ile Arg Arg Asn Pro Ala Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser
35 40 45
His Arg Ile Gln Cys Ala Ala Gly Tyr Glu Gln Ser Glu His Asn Val
50 55 60
Cys Gln Asp Ile Asp Glu Cys Thr Ala Gly Thr His Asn Cys Arg Ala
65 70 75 80
Asp Gln Val Cys Ile Asn Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro
85 90 95
Pro Gly Tyr Gln Lys Arg Gly Glu Gln Cys Val Asp Ile Asp Glu Cys
100 105 110
Thr Ile Pro Pro Tyr Cys His Gln Arg Cys Val Asn Thr Pro Gly Ser
115 120 125
Phe Tyr Cys Gln Cys Ser Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr
130 135 140
Thr Cys Val Asp Ile Asn Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln
145 150 155 160
Gln Cys Tyr Asn Ile Leu Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly
165 170 175
Tyr Glu Leu Ser Ser Asp Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys
180 185 190
Arg Thr Ser Ser Tyr Leu Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly
195 200 205
Lys Phe Ser Cys Met Cys Pro Gln Gly Tyr Gln Val Val Arg Ser Arg
210 215 220
Thr Cys Gln Asp Ile Asn Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu
225 230 235 240
Asp Glu Met Cys Trp Asn Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg
245 250 255
Asn Pro Cys Gln Asp Pro Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val
260 265 270
Cys Pro Val Ser Asn Ala Met Cys Arg Glu Leu Pro Gln Ser Ile Val
275 280 285
Tyr Lys Tyr Met Ser Ile Arg Ser Asp Arg Ser Val Pro Ser Asp Ile
290 295 300
Phe Gln Ile Gln Ala Thr Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe
305 310 315 320
Arg Ile Lys Ser Gly Asn Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr
325 330 335
Ser Pro Val Ser Ala Met Leu Val Leu Val Lys Ser Leu Ser Gly Pro
340 345 350
Arg Glu His Ile Val Asp Leu Glu Met Leu Thr Val Ser Ser Ile Gly
355 360 365

Thr Phe Arg Thr Ser Ser Val Leu Arg Leu Thr Ile Ile Val Gly Pro
370 375 380
Phe Ser Phe
385

<210> 684
<211> 531
<212> PRT
<213> Homo sapiens

<400> 684
Met Ser Lys Pro His Ser Glu Ala Gly Thr Ala Phe Ile Gln Thr Gln
1 5 10 15
Gln Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg
20 25 30
Leu Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile
35 40 45
Cys Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met
50 55 60
Ile Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr
65 70 75 80
His Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu
85 90 95
Ser Phe Ala Ser Asp Pro Tyr Leu Tyr Arg Pro Val Ala Val Ala Leu
100 105 110
Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly
115 120 125
Thr Ala Glu Leu Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu
130 135 140
Asp Asn Ala Tyr Met Glu Lys Cys Asp Glu Asn Ile Leu Trp Leu Asp
145 150 155 160
Tyr Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val
165 170 175
Asp Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe
180 185 190
Leu Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly
195 200 205
Val Asn Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys
210 215 220
Asp Ile Gln Asp Leu Lys Phe Gly Val Glu Gln Asp Val Asp Met Val
225 230 235 240
Phe Ala Ser Phe Ile Arg Lys Ala Ser Asp Val His Glu Val Arg Lys
245 250 255
Val Leu Gly Glu Lys Gly Lys Asn Ile Lys Ile Ile Ser Lys Ile Glu
260 265 270
Asn His Glu Gly Val Arg Arg Phe Asp Glu Ile Leu Glu Ala Ser Asp
275 280 285
Gly Ile Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu
290 295 300
Lys Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala
305 310 315 320
Gly Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys
325 330 335
Lys Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val

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            340                             345                             350
Leu Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly
        355                             360                             365
Asp Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu
    370                             375                             380
Ala Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg
385                             390                             395                             400
Leu Ala Pro Ile Thr Ser Asp Pro Thr Glu Ala Thr Ala Val Gly Ala
                405                             410                             415
Val Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr
            420                             425                             430
Lys Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala
        435                             440                             445
Pro Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His
    450                             455                             460
Leu Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu
465                             470                             475                             480
Ala Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val
                485                             490                             495
Gly Lys Ala Arg Gly Phe Phe Lys Lys Gly Asp Val Val Ile Val Leu
            500                             505                             510
Thr Gly Trp Arg Pro Gly Ser Gly Phe Thr Asn Thr Met Arg Val Val
        515                             520                             525
Pro Val Pro
    530

<210> 685
<211> 480
<212> PRT
<213> Homo sapiens

<400> 685
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
 1               5                  10                  15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
            20                  25                  30
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
        35                  40                  45
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
    50                  55                  60
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
65                  70                  75                  80
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
                85                  90                  95
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
            100                 105                 110
Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
        115                 120                 125
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
    130                 135                 140
Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145                 150                 155                 160
Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
                165                 170                 175
```

Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190
Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
195 200 205
Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
210 215 220
Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
225 230 235 240
Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
245 250 255
Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
260 265 270
Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
275 280 285
Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
290 295 300
Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
305 310 315 320
Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
325 330 335
Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350
Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
355 360 365
Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380
Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400
Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415
Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
435 440 445
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
450 455 460
Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
465 470 475 480

<210> 686
<211> 572
<212> PRT
<213> Homo sapiens

<400> 686
Met Ala Ala Pro Arg Pro Ser Pro Ala Ile Ser Val Ser Val Ser Ala
1 5 10 15
Pro Ala Phe Tyr Ala Pro Gln Lys Lys Phe Gly Pro Val Val Ala Pro
20 25 30
Lys Pro Lys Val Asn Pro Phe Arg Pro Gly Asp Ser Glu Pro Pro Pro
35 40 45
Ala Pro Gly Ala Gln Arg Ala Gln Met Gly Arg Val Gly Glu Ile Pro
50 55 60
Pro Pro Pro Pro Glu Asp Phe Pro Leu Pro Pro Pro Pro Leu Ala Gly

```
65                  70                  75                  80
Asp Gly Asp Asp Ala Glu Gly Ala Leu Gly Gly Ala Phe Pro Pro Pro
                85                  90                  95
Pro Pro Pro Ile Glu Glu Ser Phe Pro Pro Ala Pro Leu Glu Glu Glu
            100                 105                 110
Ile Phe Pro Ser Pro Pro Pro Pro Pro Glu Glu Glu Gly Gly Pro Glu
        115                 120                 125
Ala Pro Ile Pro Pro Pro Pro Gln Pro Arg Glu Lys Val Ser Ser Ile
    130                 135                 140
Asp Leu Glu Ile Asp Ser Leu Ser Ser Leu Leu Asp Asp Met Thr Lys
145                 150                 155                 160
Asn Asp Pro Phe Lys Ala Arg Val Ser Ser Gly Tyr Val Pro Pro Pro
                165                 170                 175
Val Ala Thr Pro Phe Ser Ser Lys Ser Ser Thr Lys Pro Ala Ala Gly
            180                 185                 190
Gly Thr Ala Pro Leu Pro Pro Trp Lys Ser Pro Ser Ser Ser Gln Pro
        195                 200                 205
Leu Pro Gln Val Pro Ala Pro Ala Gln Ser Gln Thr Gln Phe His Val
    210                 215                 220
Gln Pro Gln Pro Gln Pro Lys Pro Gln Val Gln Leu His Val Gln Ser
225                 230                 235                 240
Gln Thr Gln Pro Val Ser Leu Ala Asn Thr Gln Pro Arg Gly Pro Pro
                245                 250                 255
Ala Ser Ser Pro Ala Pro Ala Pro Lys Phe Ser Pro Val Thr Pro Lys
            260                 265                 270
Phe Thr Pro Val Ala Ser Lys Phe Ser Pro Gly Ala Pro Gly Gly Ser
        275                 280                 285
Gly Ser Gln Pro Asn Gln Lys Leu Gly His Pro Glu Ala Leu Ser Ala
    290                 295                 300
Gly Thr Gly Ser Pro Gln Pro Pro Ser Phe Thr Tyr Ala Gln Gln Arg
305                 310                 315                 320
Glu Lys Pro Arg Val Gln Glu Lys Gln His Pro Val Pro Pro Pro Ala
                325                 330                 335
Gln Asn Gln Asn Gln Val Arg Ser Pro Gly Ala Pro Gly Pro Leu Thr
            340                 345                 350
Leu Lys Glu Val Glu Glu Leu Glu Gln Leu Thr Gln Gln Leu Met Gln
        355                 360                 365
Asp Met Glu His Pro Gln Arg Gln Asn Val Ala Val Asn Glu Leu Cys
    370                 375                 380
Gly Arg Cys His Gln Pro Leu Ala Arg Ala Gln Pro Ala Val Arg Ala
385                 390                 395                 400
Leu Gly Gln Leu Phe His Ile Ala Cys Phe Thr Cys His Gln Cys Ala
                405                 410                 415
Gln Gln Leu Gln Gly Gln Gln Phe Tyr Ser Leu Glu Gly Ala Pro Tyr
            420                 425                 430
Cys Glu Gly Cys Tyr Thr Asp Thr Leu Glu Lys Cys Asn Thr Cys Gly
        435                 440                 445
Glu Pro Ile Thr Asp Arg Met Leu Arg Ala Thr Gly Lys Ala Tyr His
    450                 455                 460
Pro His Cys Phe Thr Cys Val Val Cys Ala Arg Pro Leu Glu Gly Thr
465                 470                 475                 480
Ser Phe Ile Val Asp Gln Ala Asn Arg Pro His Cys Val Pro Asp Tyr
                485                 490                 495
His Lys Gln Tyr Ala Pro Arg Cys Ser Val Cys Ser Glu Pro Ile Met
```

500 505 510
Pro Glu Pro Gly Arg Asp Glu Thr Val Arg Val Val Ala Leu Asp Lys
515 520 525
Asn Phe His Met Lys Cys Tyr Lys Cys Glu Asp Cys Gly Lys Pro Leu
530 535 540
Ser Ile Glu Ala Asp Asp Asn Gly Cys Phe Pro Leu Asp Gly His Val
545 550 555 560
Leu Cys Arg Lys Cys His Thr Ala Arg Ala Gln Thr
565 570

<210> 687
<211> 2861
<212> PRT
<213> Homo sapiens

<400> 687
Met Lys Ala Met Asp Val Leu Pro Ile Leu Lys Glu Lys Val Ala Tyr
1 5 10 15
Leu Ser Gly Gly Arg Asp Lys Arg Gly Gly Pro Ile Leu Thr Phe Pro
20 25 30
Ala Arg Ser Asn His Asp Arg Ile Arg Gln Glu Asp Leu Arg Arg Leu
35 40 45
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<210> 697
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<400> 700
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cgg 63

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Val Glu Thr Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg
1 5 10 15
Lys

<210> 704
<211> 15
<212> PRT
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Asn Lys Arg Thr Gly Gly Lys Arg Lys Glu Ile Leu Ser Ala Leu
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1 5 10

<210> 706
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Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys Leu Pro
1 5 10 15

<210> 707
<211> 15
<212> PRT
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<220>
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<400> 707
Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln Cys Gly Gln
1 5 10 15

<210> 708
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Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn
1 5 10

<210> 709
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<210> 710
<211> 13
<212> PRT
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<220>
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Ala Cys Gly Lys Ser Met Met Ser Ser Val Ser Leu Met
1 5 10

<210> 711
<211> 18

<212> PRT
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<220>
<223> peptide from Zmax1 sequence (SEQ ID NO: 3)

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Pro Tyr

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<211> 15
<212> PRT
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Ser Gly Trp Asn Glu Cys Ala Ser Ser Asn Gly His Cys Ser His
1   5   10   15

<210> 713
<211> 14
<212> PRT
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<220>
<223> peptide from Zmax1 sequence (SEQ ID NO: 3)

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<400> 714
Ile Lys Arg Ala Lys Asp Asp Gly Thr Gln Pro Phe Val Leu Thr Ser
1   5   10   15
Leu Ser Gln Gly Gln Asn
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<210> 724
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<400> 736

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<400> 737
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<400> 738
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Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
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Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
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Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
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Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala Leu Asp Pro
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Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
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Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
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Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
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Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
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Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
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Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
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Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys
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Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser
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Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
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Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr
305 310 315 320
Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly Arg Thr Cys
325 330 335
Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg Thr Asp Leu
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Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
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Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg
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Gly Phe Pro Glu Cys Ala Asp Gln Ser Asp Glu Glu Gly Cys Pro Val
1285 1290 1295
Cys Ser Ala Ser Gln Phe Pro Cys Ala Arg Gly Gln Cys Val Asp Leu
1300 1305 1310
Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp Arg Ser Asp Glu
1315 1320 1325
Ala Asn Cys Asp Ala Val Cys Leu Pro Asn Gln Phe Arg Cys Thr Ser

1330 1335 1340
Gly Leu Phe Val Met Gly Gly Val Tyr Phe Val Cys Gln Arg Val Met
1345 1350 1355 1360
Cys Gln Arg Tyr Thr Gly Ala Ser Gly Pro Phe Pro His Glu Tyr Val
1365 1370 1375
Gly Gly Ala Pro His Val Pro Leu Asn Phe Ile Ala Pro Gly Gly Ser
1380 1385 1390
Gln His Gly Pro Phe Pro Gly Ile Pro Cys Ser Lys Ser Val Met Ser
1395 1400 1405
Ser Met Ser Leu Val Gly Gly Arg Gly Ser Val Pro Leu Tyr Asp Arg
1410 1415 1420
Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser Ser Ser Thr Lys Ala
1425 1430 1435 1440
Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro Pro Ser Pro Ala Thr Asp
1445 1450 1455
Pro Ser Leu Tyr Asn Val Asp Val Phe Tyr Ser Ser Gly Ile Pro Ala
1460 1465 1470
Thr Ala Arg Pro Tyr Arg Pro Tyr Val Ile Arg Gly Met Ala Pro Pro
1475 1480 1485
Thr Thr Pro Cys Ser Thr Asp Val Cys Asp Ser Asp Tyr Ser Ile Ser
1490 1495 1500
Arg Trp Lys Ser Ser Lys Tyr Tyr Leu Asp Leu Asn Ser Asp Ser Asp
1505 1510 1515 1520
Pro Tyr Pro Pro Pro Pro Thr Pro His Ser Gln Tyr Leu Ser Ala Glu
1525 1530 1535
Asp Ser Cys Pro Pro Ser Pro Gly Thr Glu Arg Ser Tyr Cys His Leu
1540 1545 1550
Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp Ser Ser
1555 1560

<210> 763
<211> 1665
<212> PRT
<213> Homo sapiens

<400> 763
Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala Ala Ala Ser
20 25 30
Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala
35 40 45
Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
50 55 60
Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
65 70 75 80
Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
85 90 95
Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
100 105 110
Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
115 120 125
Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val

130 135 140
Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala Leu Asp Pro
145 150 155 160
Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
165 170 175
Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
180 185 190
Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
195 200 205
Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
210 215 220
Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
225 230 235 240
Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
245 250 255
Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys
260 265 270
Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser
275 280 285
Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
290 295 300
Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr
305 310 315 320
Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly Arg Thr Cys
325 330 335
Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg Thr Asp Leu
340 345 350
Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln
355 360 365
Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
370 375 380
Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala
385 390 395 400
Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn
405 410 415
Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp
420 425 430
Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr
435 440 445
Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
450 455 460
Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu
465 470 475 480
Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val
485 490 495
Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu
500 505 510
Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
515 520 525
Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
530 535 540
Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp
545 550 555 560
Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala

565 570 575
Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
580 585 590
Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
595 600 605
Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
610 615 620
Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
625 630 635 640
Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His
645 650 655
Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile Pro Leu Thr
660 665 670
Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His
675 680 685
Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg Ala Phe Met
690 695 700
Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro
705 710 715 720
Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp
725 730 735
Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg
740 745 750
Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu
755 760 765
Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro
770 775 780
Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val
785 790 795 800
Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln
805 810 815
Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn
820 825 830
Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu Pro His Pro
835 840 845
Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn
850 855 860
Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr
865 870 875 880
Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His
885 890 895
Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln
900 905 910
Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys
915 920 925
Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro
930 935 940
Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile
945 950 955 960
Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu
965 970 975
Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr
980 985 990
Trp Val Asp Gly Arg Gln Asn Phe Ser Gln Lys Ser Ala Ile Asn Arg

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        995                 1000                1005
Met Val Ile Asp Glu Gln Gln Ser Pro Asp Ile Ile Leu Pro Ile His
    1010                1015                1020
Ser Leu Arg Asn Val Arg Ala Ile Asp Tyr Asp Pro Leu Asp Lys Gln
1025                1030                1035                1040
Leu Tyr Trp Ile Asp Ser Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp
                1045                1050                1055
Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro
            1060                1065                1070
Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu
        1075                1080                1085
Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu Ser
    1090                1095                1100
Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro Arg
1105                1110                1115                1120
Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn Met
                1125                1130                1135
Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr Glu
            1140                1145                1150
Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu Val
        1155                1160                1165
Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu Lys
    1170                1175                1180
Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu Glu
1185                1190                1195                1200
Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys His
                1205                1210                1215
Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu Lys
            1220                1225                1230
Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His Leu
        1235                1240                1245
Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser Ala
    1250                1255                1260
His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile Ala
1265                1270                1275                1280
Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val Leu
                1285                1290                1295
Leu Gln Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro Asp
            1300                1305                1310
Gln Phe Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala Trp
        1315                1320                1325
Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu Gly
    1330                1335                1340
Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln Cys
1345                1350                1355                1360
Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp Arg
                1365                1370                1375
Ser Asp Glu Ala Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe Arg
            1380                1385                1390
Cys Ala Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser Phe
        1395                1400                1405
Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr Lys
    1410                1415                1420
Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro Val
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1425                1430                1435                1440
Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe Val
                1445                1450                1455
Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro Phe
            1460                1465                1470
Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe Ile
        1475                1480                1485
Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys Gly
    1490                1495                1500
Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly Val
1505                1510                1515                1520
Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser
                1525                1530                1535
Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro Pro
            1540                1545                1550
Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr Ser
        1555                1560                1565
Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile Arg
    1570                1575                1580
Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp Ser
1585                1590                1595                1600
Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp Leu
                1605                1610                1615
Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser Gln
            1620                1625                1630
Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu Arg
        1635                1640                1645
Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp Ser
    1650                1655                1660
Ser
1665


<210> 764
<211> 1613
<212> PRT
<213> Homo sapiens

<400> 764
Met Gly Ala Val Leu Arg Ser Leu Leu Ala Cys Ser Phe Cys Val Leu
 1               5                  10                  15
Leu Arg Ala Ala Pro Leu Leu Leu Tyr Ala Asn Arg Arg Asp Leu Arg
            20                  25                  30
Leu Val Asp Ala Thr Asn Gly Lys Glu Asn Ala Thr Ile Val Val Gly
        35                  40                  45
Gly Leu Glu Asp Ala Ala Ala Val Asp Phe Val Phe Ser His Gly Leu
    50                  55                  60
Ile Tyr Trp Ser Asp Val Ser Glu Glu Ala Ile Lys Arg Thr Glu Phe
65                  70                  75                  80
Asn Lys Thr Glu Ser Val Gln Asn Val Val Val Ser Gly Leu Leu Ser
                85                  90                  95
Pro Asp Gly Leu Ala Cys Asp Trp Leu Gly Glu Lys Leu Tyr Trp Thr
            100                 105                 110
Asp Ser Glu Thr Asn Arg Ile Glu Val Ser Asn Leu Asp Gly Ser Leu
```

115 120 125
Arg Lys Val Leu Phe Trp Gln Glu Leu Asp Gln Pro Arg Ala Ile Ala
130 135 140
Leu Asp Pro Ser Ser Gly Phe Met Tyr Trp Thr Asp Trp Gly Glu Val
145 150 155 160
Pro Lys Ile Glu Arg Ala Gly Met Asp Gly Ser Ser Arg Phe Ile Ile
165 170 175
Ile Asn Ser Glu Ile Tyr Trp Pro Asn Gly Leu Thr Leu Asp Tyr Glu
180 185 190
Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Asn Phe Ile His Lys
195 200 205
Ser Asn Leu Asp Gly Thr Asn Arg Gln Ala Val Val Lys Gly Ser Leu
210 215 220
Pro His Pro Phe Ala Leu Thr Leu Phe Glu Asp Ile Leu Tyr Trp Thr
225 230 235 240
Asp Trp Ser Thr His Ser Ile Leu Ala Cys Asn Lys Tyr Thr Gly Glu
245 250 255
Gly Leu Arg Glu Ile His Ser Asp Ile Phe Ser Pro Met Asp Ile His
260 265 270
Ala Phe Ser Gln Gln Arg Gln Pro Asn Ala Thr Asn Pro Cys Gly Ile
275 280 285
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Met Ser Pro Val Lys Pro
290 295 300
Phe Tyr Gln Cys Ala Cys Pro Thr Gly Val Lys Leu Leu Glu Asn Gly
305 310 315 320
Lys Thr Cys Lys Asp Gly Ala Thr Glu Leu Leu Leu Leu Ala Arg Arg
325 330 335
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
340 345 350
Val Leu Gln Leu Glu Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp
355 360 365
Pro Val Glu Gly Tyr Ile Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile
370 375 380
Arg Arg Ser Phe Ile Asp Gly Ser Gly Ser Gln Phe Val Val Thr Ala
385 390 395 400
Gln Ile Ala His Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn
405 410 415
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu
420 425 430
Asn Gly Thr Met Arg Lys Ile Leu Ile Ser Glu Asp Leu Glu Glu Pro
435 440 445
Arg Ala Ile Val Leu Asp Pro Met Val Gly Tyr Met Tyr Trp Thr Asp
450 455 460
Trp Gly Glu Ile Pro Lys Ile Glu Arg Ala Ala Leu Asp Gly Ser Asp
465 470 475 480
Arg Val Val Leu Val Asn Thr Ser Leu Gly Trp Pro Asn Gly Leu Ala
485 490 495
Leu Asp Tyr Asp Glu Gly Lys Ile Tyr Trp Gly Asp Ala Lys Thr Asp
500 505 510
Lys Ile Glu Val Met Asn Thr Asp Gly Thr Gly Arg Arg Val Leu Val
515 520 525
Glu Asp Lys Ile Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Tyr
530 535 540
Val Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys

545 550 555 560
Arg Ser Ala Glu Arg Glu Val Ile Ile Asp Gln Leu Pro Asp Leu Met
565 570 575
Gly Leu Lys Ala Thr Asn Val His Arg Val Ile Gly Ser Asn Pro Cys
580 585 590
Ala Glu Glu Asn Gly Gly Cys Ser His Leu Cys Leu Tyr Arg Pro Gln
595 600 605
Gly Leu Arg Cys Ala Cys Pro Ile Gly Phe Glu Leu Ile Ser Asp Met
610 615 620
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Leu Phe Ser Arg Arg Ala
625 630 635 640
Asp Ile Arg Arg Ile Ser Leu Glu Thr Asn Asn Asn Asn Val Ala Ile
645 650 655
Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Thr
660 665 670
Asp Asn Arg Ile Tyr Trp Thr Asp Ile Ser Leu Lys Thr Ile Ser Arg
675 680 685
Ala Phe Met Asn Gly Ser Ala Leu Glu His Val Val Glu Phe Gly Leu
690 695 700
Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Leu Gly Lys Asn Leu Tyr
705 710 715 720
Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ser Lys Leu Asp Gly
725 730 735
Gln His Arg Gln Val Leu Val Trp Lys Asp Leu Asp Ser Pro Arg Ala
740 745 750
Leu Ala Leu Asp Pro Ala Glu Gly Phe Met Tyr Trp Thr Glu Trp Gly
755 760 765
Gly Lys Pro Lys Ile Asp Arg Ala Ala Met Asp Gly Ser Glu Arg Thr
770 775 780
Thr Leu Val Pro Asn Val Gly Arg Ala Asn Gly Leu Thr Ile Asp Tyr
785 790 795 800
Ala Lys Arg Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Leu Ile Glu
805 810 815
Ser Ser Asn Met Leu Gly Leu Asn Arg Glu Val Ile Ala Asp Asp Leu
820 825 830
Pro His Pro Phe Gly Leu Thr Gln Tyr Gln Asp Tyr Ile Tyr Trp Thr
835 840 845
Asp Trp Ser Arg Arg Ser Ile Glu Arg Ala Asn Lys Thr Ser Gly Gln
850 855 860
Asn Arg Thr Ile Ile Gln Gly His Leu Asp Tyr Val Met Asp Ile Leu
865 870 875 880
Val Phe His Ser Ser Arg Gln Ser Gly Trp Asn Glu Cys Ala Ser Ser
885 890 895
Asn Gly His Cys Ser His Leu Cys Leu Ala Val Pro Val Gly Gly Phe
900 905 910
Val Cys Gly Cys Pro Ala His Tyr Ser Leu Asn Ala Asp Asn Arg Thr
915 920 925
Cys Ser Ala Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile
930 935 940
Asn Arg Met Val Ile Asp Glu Gln Gln Ser Pro Asp Ile Ile Leu Pro
945 950 955 960
Ile His Ser Leu Arg Asn Val Arg Ala Ile Asp Tyr Asp Pro Leu Asp
965 970 975
Lys Gln Leu Tyr Trp Ile Asp Ser Arg Gln Asn Met Ile Arg Lys Ala

980 985 990
Gln Glu Asp Gly Ser Gln Gly Phe Thr Val Val Val Ser Ser Val Pro
995 1000 1005
Ser Gln Asn Leu Glu Ile Gln Pro Tyr Asp Leu Ser Ile Asp Ile Tyr
1010 1015 1020
Ser Arg Tyr Ile Tyr Trp Thr Cys Glu Ala Thr Asn Val Ile Asn Val
1025 1030 1035 1040
Thr Arg Leu Asp Gly Arg Ser Val Gly Val Val Leu Lys Gly Glu Gln
1045 1050 1055
Asp Arg Pro Arg Ala Ile Val Val Asn Pro Glu Lys Gly Tyr Met Tyr
1060 1065 1070
Phe Thr Asn Leu Gln Glu Arg Ser Pro Lys Ile Glu Arg Ala Ala Leu
1075 1080 1085
Asp Gly Thr Glu Arg Glu Val Leu Phe Phe Ser Gly Leu Ser Lys Pro
1090 1095 1100
Ile Ala Leu Ala Leu Asp Ser Arg Leu Gly Lys Leu Phe Trp Ala Asp
1105 1110 1115 1120
Ser Asp Leu Arg Arg Ile Glu Ser Ser Asp Leu Ser Gly Ala Asn Arg
1125 1130 1135
Ile Val Leu Glu Asp Ser Asn Ile Leu Gln Pro Val Gly Leu Thr Val
1140 1145 1150
Phe Glu Asn Trp Leu Tyr Trp Ile Asp Lys Gln Gln Gln Met Ile Glu
1155 1160 1165
Lys Ile Asp Met Thr Gly Arg Glu Gly Arg Thr Lys Val Gln Ala Arg
1170 1175 1180
Ile Ala Gln Leu Ser Asp Ile His Ala Val Lys Glu Leu Asn Leu Gln
1185 1190 1195 1200
Glu Tyr Arg Gln His Pro Cys Ala Gln Asp Asn Gly Gly Cys Ser His
1205 1210 1215
Ile Cys Leu Val Lys Gly Asp Gly Thr Thr Arg Cys Ser Cys Pro Met
1220 1225 1230
His Leu Val Leu Leu Gln Asp Glu Leu Ser Cys Gly Glu Pro Pro Thr
1235 1240 1245
Cys Ser Pro Gln Gln Phe Thr Cys Phe Thr Gly Glu Ile Asp Cys Ile
1250 1255 1260
Pro Val Ala Trp Arg Cys Asp Gly Phe Thr Glu Cys Glu Asp His Ser
1265 1270 1275 1280
Asp Glu Leu Asn Cys Pro Val Cys Ser Glu Ser Gln Phe Gln Cys Ala
1285 1290 1295
Ser Gly Gln Cys Ile Asp Gly Ala Leu Arg Cys Asn Gly Asp Ala Asn
1300 1305 1310
Cys Gln Asp Lys Ser Asp Glu Lys Asn Cys Glu Val Leu Cys Leu Ile
1315 1320 1325
Asp Gln Phe Arg Cys Ala Asn Gly Gln Cys Ile Gly Lys His Lys Lys
1330 1335 1340
Cys Asp His Asn Val Asp Cys Ser Asp Lys Ser Asp Glu Leu Asp Cys
1345 1350 1355 1360
Tyr Pro Thr Glu Glu Pro Ala Pro Gln Ala Thr Asn Thr Val Gly Ser
1365 1370 1375
Val Ile Gly Val Ile Val Thr Ile Phe Val Ser Gly Thr Val Tyr Phe
1380 1385 1390
Ile Cys Gln Arg Met Leu Cys Pro Arg Met Lys Gly Asp Gly Glu Thr
1395 1400 1405
Met Thr Asn Asp Tyr Val Val His Gly Pro Ala Ser Val Pro Leu Gly

```
    1410                1415                1420
Tyr Val Pro His Pro Ser Ser Leu Ser Gly Ser Leu Pro Gly Met Ser
1425                1430                1435                1440
Arg Gly Lys Ser Met Ile Ser Ser Leu Ser Ile Met Gly Gly Ser Ser
                1445                1450                1455
Gly Pro Pro Tyr Asp Arg Ala His Val Thr Gly Ala Ser Ser Ser Ser
            1460                1465                1470
Ser Ser Ser Thr Lys Gly Thr Tyr Phe Pro Ala Ile Leu Asn Pro Pro
        1475                1480                1485
Pro Ser Pro Ala Thr Glu Arg Ser His Tyr Thr Met Glu Phe Gly Tyr
    1490                1495                1500
Ser Ser Asn Ser Pro Ser Thr His Arg Ser Tyr Ser Tyr Arg Pro Tyr
1505                1510                1515                1520
Ser Tyr Arg His Phe Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val
                1525                1530                1535
Cys Asp Ser Asp Tyr Ala Pro Ser Arg Arg Met Thr Ser Val Ala Thr
            1540                1545                1550
Ala Lys Gly Tyr Thr Ser Asp Leu Asn Tyr Asp Ser Glu Pro Val Pro
        1555                1560                1565
Pro Pro Pro Thr Pro Arg Ser Gln Tyr Leu Ser Ala Glu Glu Asn Tyr
    1570                1575                1580
Glu Ser Cys Pro Pro Ser Pro Tyr Thr Glu Arg Ser Tyr Ser His His
1585                1590                1595                1600
Leu Tyr Pro Pro Pro Pro Ser Pro Cys Thr Asp Ser Ser
                1605                1610
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<210> 765
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> cytoplasmic domain and portion of transmembrane domain

<400> 765

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Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro Phe Pro His
1               5                   10                  15
Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe Ile Ala Pro
            20                  25                  30
Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys Gly Lys Ser
        35                  40                  45
Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly Val Pro Leu
    50                  55                  60
Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser Ser Ser
65                  70                  75                  80
Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro Pro Ser Pro
                85                  90                  95
Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr Ser Ser Asn
            100                 105                 110
Ile Pro Ala Thr Val Arg Pro Tyr Arg Pro Tyr Ile Ile Arg Gly Met
        115                 120                 125
Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp Ser Asp Tyr
    130                 135                 140
```

```
Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp Leu Asn Ser
145                 150                 155                 160
Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser Gln Tyr Leu
                165                 170                 175
Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu Arg Ser Tyr
            180                 185                 190
Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp Ser Ser
        195                 200                 205
```